

Match length 127 % identity 80

NCBI Description DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL

4-REDUCTASE) >gi_499018_emb_CAA53578_ (X75964) dihydroflavonol reductase [Vitis vinifera]

Seq. No. 213941

Seq. ID LIB3146-033-Q1-K1-E7

Method BLASTX
NCBI GI g4455129
BLAST score 279
E value 8.0e-25
Match length 83
% identity 57

NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]

Seq. No. 213942

Seq. ID LIB3146-033-Q1-K1-F1

Method BLASTX
NCBI GI 94530585
BLAST score 196
E value 4.0e-15
Match length 49
% identity 71

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 213943

Seq. ID LIB3146-033-Q1-K1-F10

Method BLASTN
NCBI GI g3510339
BLAST score 46
E value 7.0e-17
Match length 183
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 213944

Seq. ID LIB3146-033-Q1-K1-F12

Method BLASTX
NCBI GI g1172873
BLAST score 423
E value 6.0e-44
Match length 114
% identity 76

NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 213945

Seq. ID LIB3146-033-Q1-K1-F2

Method BLASTX
NCBI GI g2493045
BLAST score 351
E value 3.0e-33
Match length 86



% identity

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>qi 1655484 dbj BAA13601 (D88376) delta-prime subunit of

mitochondrial FI-ATPase [Arabidopsis thaliana]

Seq. No. 213946

Seq. ID LIB3146-033-Q1-K1-F3

Method BLASTX NCBI GI q3335337 BLAST score 375 E value 4.0e-36 114

Match length 67 % identity

(AC004512) Similar to acyl carrier protein, mitochondrial NCBI Description

> precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330

come from this gene

Seq. No. 213947

Seq. ID LIB3146-033-Q1-K1-F4

Method BLASTX NCBI GI g2267567 BLAST score 394 2.0e-38 E value Match length 85 87 % identity

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

213948 Seq. No.

Seq. ID LIB3146-033-Q1-K1-F6

Method BLASTX NCBI GI a1684851 BLAST score 232 2.0e-19 E value Match length 81

% identity 57

(U77935) DnaJ-like protein [Phaseolus vulgaris] NCBI Description

Seq. No. 213949

Seq. ID LIB3146-033-Q1-K1-F7

Method BLASTX NCBI GI g2462746 BLAST score 472 E value 2.0e-47 Match length 121 % identity

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 213950

Seq. ID LIB3146-033-Q1-K1-F8

Method BLASTN NCBI GI g3985949

BLAST score 35



```
3.0e-10 .
E value
Match length
                  43
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOB24, complete sequence [Arabidopsis thaliana]
                  213951
Seq. No.
Seq. ID
                  LIB3146-033-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2811278
BLAST score
                  470
E value
                  2.0e-58
Match length
                  115
                  95
% identity
NCBI Description
                  (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  213952
                  LIB3146-033-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510426
BLAST score
                  304
E value
                  9.0e-28
Match length
                  125
% identity
                  56
NCBI Description
                  (AC006929) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213953
Seq. ID
                  LIB3146-033-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2501182
BLAST score
                  210
                  6.0e-17
E value
Match length
                  43
% identity
                  86
NCBI Description
                  OSMOTIN-LIKE PROTEIN PRECURSOR >gi 2129934 pir
                  osmotin-like protein - tomato >gi 1220537 (L76632)
                  osmotin-like protein [Lycopersicon esculentum]
Seq. No.
                  213954
Seq. ID
                  LIB3146-033-Q1-K1-G4
                  BLASTX
Method
                  g729974
NCBI GI
BLAST score
                  302
E value
                  1:0e-27
Match length
                  128
                  53
% identity
                  FLORAL HOMEOTIC PROTEIN PMADS1 (GREEN PETAL HOMEOTIC
NCBI Description
                  PROTEIN) >gi_322773_pir__S31693 transcription factor gp -
                  garden petunia >gi 22665_emb_CAA49567_ (X69946) GP (green
                  petal) [Petunia x hybrida]
```

Seq. No. 213955

Seq. ID LIB3146-033-Q1-K1-H10

Method BLASTX
NCBI GI g1076427
BLAST score 296
E value 4.0e-27



 Match length 68 % identity NCBI Description

ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis

thaliana

Seq. No.

213956

Seq. ID

LIB3146-033-Q1-K1-H11

Method BLASTX NCBI GI g2832675 BLAST score 245 E value 3.0e-21 Match length 54

% identity 76

NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.

213957

Seq. ID

LIB3146-033-Q1-K1-H6

Method BLASTX NCBI GI g1703200 BLAST score 574 E value 2.0e-59 Match' length 129 % identity

PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase NCBI Description

[Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)

protein kinase [Arabidopsis thaliana]

>gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)

[Arabidopsis thaliana]

213958 Seq. No.

Seq. ID LIB3146-033-Q1-K1-H9

Method BLASTX NCBI GI g3024020 BLAST score 336 E value 3.0e - 34Match length 78 % identity 96

INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) NCBI Description

>gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

213959 Seq. No.

Seq. ID LIB3146-034-Q1-K1-A12

Method BLASTX g3461820 NCBI GI BLAST score 206 1.0e-16 E value Match length 52 % identity 65

(AC004138) unknown protein [Arabidopsis thaliana] NCBI Description

213960 Seq. No.

Seq. ID LIB3146-034-Q1-K1-A3

Method BLASTX NCBI GI g2827558 BLAST score 270 E value 9.0e-24



Match length 107 % identity 50

NCBI Description (AL021635) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 213961

Seq. ID LIB3146-034-Q1-K1-A4

Method BLASTX
NCBI GI g1173256
BLAST score 216
E value 5.0e-18
Match length 46
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal

protein S4 - upland cotton > gi 488739 emb CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e)

[Gossypium hirsutum]

Seq. No. 213962

Seq. ID LIB3146-034-Q1-K1-A6

Method BLASTX
NCBI GI g401322
BLAST score 366
E value 2.0e-35
Match length 72
% identity 100

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]

Seq. No. 213963

Seq. ID LIB3146-034-Q1-K1-A7

Method BLASTX
NCBI GI g401322
BLAST score 320
E value 1.0e-38
Match length 103
% identity 81

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]

Seq. No. 213964

Seq. ID LIB3146-034-Q1-K1-A8

Method BLASTX
NCBI GI g3021485
BLAST score 443
E value 3.0e-44
Match length 91
% identity 99

NCBI Description (AJ224932) histone H2B-3 [Lycopersicon esculentum]

Seq. No. 213965

Seq. ID LIB3146-034-Q1-K1-B10

Method BLASTX NCBI GI g2493321 BLAST score 136



E value 1.0e-08
Match length 35
% identity 80

NCBI Description L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)

>gi 2129952 pir S66353 L-ascorbate oxidase (EC 1.10.3.3)

precursor - common tobacco >gi_599594_dbj_BAA07734

(D43624) ascorbate oxidase precursor [Nicotiana tabacum]

Seq. No. 213966

Seq. ID LIB3146-034-Q1-K1-B2

Method BLASTX
NCBI GI g3080428
BLAST score 252
E value 1.0e-21
Match length 72
% identity 56

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 213967

Seq. ID LIB3146-034-Q1-K1-B3

Method BLASTX
NCBI GI g3860277
BLAST score 390
E value 8.0e-38
Match length 83
% identity 90

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 213968

Seq. ID LIB3146-034-Q1-K1-B4

Method BLASTX
NCBI GI g4103963
BLAST score 257
E value 2.0e-22
Match length 51
% identity 100

NCBI Description (AF030035) calmodulin [Phaseolus vulgaris]

Seq. No. 213969

Seq. ID LIB3146-034-Q1-K1-B5

Method BLASTX
NCBI GI g1771162
BLAST score 351
E value 3.0e-33
Match length 114
% identity 60

NCBI Description (X98930) SBT2 [Lycopersicon esculentum]

>gi 3687307 emb CAA07000 (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 213970

Seq. ID LIB3146-034-Q1-K1-B6

Method BLASTX NCBI GI g2341028 BLAST score 161



```
E value
                  3.0e-11
Match length
                  31
                  100
% identity
NCBI Description
                  (AC000104) Strong similarity to 60S ribosomal protein L17
                  (gb_X01694). EST gb_AA042332 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  213971
Seq. ID
                  LIB3146-034-Q1-K1-B9
Method
                  BLASTN
NCBI GI
                  q2326340
BLAST score
                  38
                  6.0e-12
E value
Match length
                  134
                  82
% identity
NCBI Description A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
Seq. No.
                  213972
Seq. ID
                  LIB3146-034-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g543565
                                 450
BLAST score
                  288
E value
                  7.0e-26
                  90
Match length
% identity
                  58
NCBI Description
                  hypothetical 10.0K protein - Zinnia elegans
                  >gi 493721 dbj BAA06462 (D30802) TED4 [Zinnia elegans]
                  >gi 641903 (U19266) putative nonspecific lipid transfer;
                  auxin induced gene [Zinnia elegans]
Seq. No.
                  213973
Seq. ID
                  LIB3146-034-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2244835
BLAST score
                  395
E value
                  2.0e-38
Match length
                  122
                  59
% identity
NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
Seq. No.
                  213974
```

Seq. ID LIB3146-034-Q1-K1-C4

Method BLASTX g3786324 NCBI GI BLAST score 356 E value 5.0e-34 Match length 102 % identity 62

NCBI Description (AB015139) chlorophyll a oxygenase [Chlamydomonas

reinhardtii]

Seq. No. 213975

Seq. ID LIB3146-034-Q1-K1-D12

Method BLASTX NCBI GI g4512432 BLAST score 276 E value 2.0e-24

```
Match length
                  53
% identity
                  (AB017508) rplQ homologue (identity of 84% to B. subtilis )
NCBI Description
                  [Bacillus halodurans]
                  213976
Seq. No.
Seq. ID
                  LIB3146-034-Q1-K1-E1
Method
                  BLASTX
                  g3273764
NCBI GI
BLAST score
                  174
                  8.0e-16
E value
                  80
Match length
                  64
% identity
                  (AF061870) Dc3 promoter-binding factor-3 [Helianthus
NCBI Description
                  annuus]
                  213977
Seq. No.
                  LIB3146-034-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  q4105798
NCBI GI
BLAST score
                  383
E value
                  3.0e-37
Match length
                  94
% identity
                  62
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
                  213978
Seq. No.
                  LIB3146-034-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g4105798
NCBI GI
BLAST score
                  236
E value
                  6.0e-32
Match length
                  113
% identity
                  56
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
```

Seq. No. 213979

Seq. ID LIB3146-034-Q1-K1-E8

BLASTX Method NCBI GI g1213629 BLAST score 552 E value 8.0e-57 130 Match length 78 % identity

NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 213980

LIB3146-034-Q1-K1-F11 Seq. ID

BLASTN Method NCBI GI q488738 BLAST score 48 E value 7.0e-19 Match length 56 96 % identity

NCBI Description G.hirsutum (DPL 62) mRNA for ribosomal protein small



```
213981
Seq. No.
Seq. ID
                  LIB3146-034-Q1-K1-F12
                  BLASTN
Method
NCBI GI
                  g2924651
BLAST score
                  41
                  9.0e-14
E value
                  65
Match length
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213982
                  LIB3146-034-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g4510383
NCBI GI
BLAST score
                  451
E value
                  4.0e-45
Match length
                  111
% identity
                  80
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213983
Seq. ID
                  LIB3146-034-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2695711
BLAST score
                  246
                  5.0e-21
E value
Match length
                  52
% identity
                  81
                  (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
                  213984
Seq. No.
Seq. ID
                  LIB3146-034-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g3288721
BLAST score
                  272
                  1.0e-24
E value
Match length
                  70
% identity
                  60
                  (AB015872) chalcone synthase [Vitis vinifera]
NCBI Description
                  213985
Seq. No.
Seq. ID
                  LIB3146-034-Q1-K1-F6
Method
                  BLASTX
                  g2341028
NCBI GI
BLAST score
                  161
                  3.0e-11
E value
Match length
                  31
                  100
% identity
                  (AC000104) Strong similarity to 60S ribosomal protein L17
NCBI Description
                   (gb X01694). EST gb AA042332 comes from this gene.
```

[Arabidopsis thaliana]

Seq. No. 213986

Seq. ID LIB3146-034-Q1-K1-F7

Method BLASTX NCBI GI g2252841

BLAST score

Match length

% identity

E value

214

116

41

3.0e-17



```
BLAST score
E value
                  5.0e-18
Match length
                  69
% identity
                  58
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213987
Seq. ID
                  LIB3146-034-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g4105798
                  276
BLAST score
                  4.0e-25
E value
Match length
                  72
% identity
                  61
NCBI Description
                  (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                  213988
Seq. ID
                  LIB3146-034-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g401322
BLAST score
                  589
E value
                  3.0e-61
Match length
                  114
                  99
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                  subunit [Gossypium hirsutum]
Seq. No.
                  213989
Seq. ID
                  LIB3146-034-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2981131
BLAST score
                  495
                  4.0e-50
E value
Match length
                  124
% identity
                  80
NCBI Description
                  (AF052570) AGAMOUS homolog [Populus balsamifera subsp.
                  trichocarpa]
Seq. No.
                  213990
Seq. ID
                  LIB3146-034-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  424
                  8.0e-42
E value
                  112
Match length
% identity
                  71
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  213991
Seq. ID
                  LIB3146-034-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4220514
```



NCBI Description (AL035356) putative protein [Arabidopsis thaliana] Seq. No. 213992 Seq. ID LIB3146-034-Q1-K1-G8 Method BLASTX NCBI GI q3759184 BLAST score 625 E value 2.0e-65 Match length 127 % identity 87 NCBI Description (AB018441) phi-1 [Nicotiana tabacum] Seq. No. 213993 Seq. ID LIB3146-034-Q1-K1-H1 Method BLASTX NCBI GI g1944319 BLAST score 416 6.0e-41 E value Match length 125 % identity 65 NCBI Description (D31700) cysteine proteinase inhibitor [Glycine max] >gi_1944342_dbj_BAA19610_ (D64115) cysteine proteinase inhibitor [Glycine max] 213994 Seq. No. Seq. ID LIB3146-034-Q1-K1-H2 Method BLASTX NCBI GI g1076560 BLAST score 385 E value 2.0e-37 Match length 113 % identity 68 NCBI Description cysteine proteinase inhibitor - castor bean 213995 Seq. No. Seq. ID LIB3146-034-Q1-K1-H4 Method BLASTX NCBI GI q4539390 BLAST score 648 E value 4.0e-68 Match length 135 90 % identity NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana] Seq. No. 213996

Seq. ID LIB3146-034-Q1-K1-H5

Method BLASTX NCBI GI g2499932 BLAST score 305 E value 2.0e-28 Match length 70 % identity 83

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 726305

(U22442) adenine phosphoribosyltransferase form 1 [Triticum

aestivum



Seq. No.

213997

```
Seq. ID
                   LIB3146-034-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   598
E value
                   3.0e-62
Match length
                   127
% identity
                   84
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   213998
Seq. ID
                   LIB3146-034-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1702983
BLAST score
                   210
E value
                   3.0e-17
Match length
                   53
% identity
                   70
                   AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850
NCBI Description
                   hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria
                   x ananassa] >gi 927034 (L44142) auxin-repressed protein
                   [Fragaria ananassa]
Seq. No.
                   213999
Seq. ID
                   LIB3146-034-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   g2462758
BLAST score
                   355
E value
                   9.0e-34
Match length
                   120
% identity
                   62
                   (AC002292) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214000
Seq. ID
                   LIB3146-035-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q421941
BLAST score
                   444
E value
                   2.0e-44
Match length
                   101
% identity
                   84
NCBI Description
                   GTP-binding protein, ras-related - common tobacco
                   >gi_296878_emb_CAA50609 (X71609) ras-related GTP-binding
                   protein [Nicotiana tabacum]
Seq. No.
                   214001
                   LIB3146-035-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g549750
BLAST score
                   198
E value
                   2.0e-15
Match length
                   73
% identity
                   52
NCBI Description
                   HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
```

>gi_539221 pir_ S38045 hypothetical protein YKL207w - yeast



68

% identity

NCBI Description

(Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

214002 Seq. No. Seq. ID LIB3146-035-P1-K1-C6 Method BLASTX NCBI GI g4263791 189 BLAST score 3.0e-14 E value 38 Match length 97 % identity (AC006068) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 214003 Seq. No. LIB3146-035-P1-K1-F1 Seq. ID ${\tt BLASTX}$ Method NCBI GI g3643604 132 BLAST score 4.0e-10 E value 57 Match length % identity 58 (AC005395) receptor-like protein kinase [Arabidopsis NCBI Description thaliana] 214004 Seq. No. Seq. ID LIB3146-035-P1-K1-F8 Method BLASTX g2979544 NCBI GI 173 BLAST score 2.0e-12 E value Match length 66 % identity 50 (AC003680) putative cytochrome P-450 [Arabidopsis thaliana] NCBI Description 214005 Seq. No. Seq. ID LIB3146-035-P1-K1-G5 BLASTX Method NCBI GI g3176965 BLAST score 417 5.0e-41 E value Match length 120 72 % identity NCBI Description (AF067967) pyrroline-5-carboxylate synthetase [Mesembryanthemum crystallinum] 214006 Seq. No. LIB3146-035-P1-K1-H7 Seq. ID Method BLASTX q2388582 NCBI GI BLAST score 254 E value 7.0e-24 Match length 81

29808

(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb U76557). [Arabidopsis thaliana]

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214007
Seq. No.
                  LIB3146-036-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  q3249070
NCBI GI
BLAST score
                  188
                  2.0e-14
E value
                  79
Match length
                  59
% identity
NCBI Description
                  (AC004473) Contains similarity to siah binding protein 1
                  (SiahBP1) qb U51586 from Homo sapiens. ESTs qb T43314,
                  gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]
                  214008
Seq. No.
Seq. ID
                  LIB3146-036-P1-K1-B6
                  BLASTX
Method
                  g2369766
NCBI GI
                  381
BLAST score
                  8.0e-37
E value
                  132
Match length
                  60
% identity
NCBI Description
                  (AJ001304) hypothetical protein [Citrus x paradisi]
                  214009
Seq. No.
                  LIB3146-036-P1-K1-C3
Seq. ID
                  BLASTN
Method
                  g2696018
NCBI GI
BLAST score
                  32
                  1.0e-08
E value
                  56
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
                  214010
Seq. No.
                  LIB3146-036-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811025
BLAST score
                  378
                  1.0e-36
E value
                   97
Match length
                   69
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607_
NCBI Description
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  214011
                  LIB3146-036-P1-K1-D4
Seq. ID
Method
                  BLASTX
                   q3023419
NCBI GI
BLAST score
                   405
                   1.0e-39
E value
Match length
                   102
% identity
                  76
                  CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA
NCBI Description
```

29809

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)

O-methyltransferase [Eucalyptus gunnii]

>gi 1934859 emb CAA72911 (Y12228) caffeoyl-CoA



```
214012
Seq. No.
Seq. ID
                  LIB3146-036-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3319278
BLAST score
                  330
E value
                  8.0e-31
Match length
                  101
                  66
% identity
NCBI Description
                  (AF046122) caffeoyl-CoA 3-O-methyltransferase; CCOMT;
                  S-adenosyl-L-methionine:caffeoyl-CoA 3-O-methyltransferase
                  [Eucalyptus globulus]
```

214013

Seq. No. Seq. ID LIB3146-036-P1-K1-E3

Method BLASTX NCBI GI q3947985 BLAST score 154 E value 1.0e-15 Match length 60 % identity 78

NCBI Description (U78948) MADS-box protein 2 [Malus domestica]

Seq. No. 214014

Seq. ID LIB3146-036-P1-K1-E6

Method BLASTN NCBI GI q3821780 BLAST score 36 E value 6.0e-11 Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 214015

Seq. ID LIB3146-036-P1-K1-F1

Method BLASTX NCBI GI q1175252 BLAST score 141 E value 1.0e-08 Match length 92 37 % identity

NCBI Description HYPOTHETICAL PROTEIN HI0488 >gi_1074418_pir__D64008

hypothetical protein HI0488 - Haemophilus influenzae (strain Rd KW20) >gi 1573468 (U32731) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No. 214016

LIB3146-036-P1-K1-F7 Seq. ID

Method BLASTX NCBI GI g1350944 BLAST score 389 E value 1.0e-37 Match length 80 % identity 96

NCBI Description 40S RIBOSOMAL PROTEIN S17

Seq. No. 214017

Seq. ID LIB3146-036-P1-K1-G1

E value

Match length

1.0e-25

```
BLASTX
Method
NCBI GI
                   g4538980
BLAST score
                   349
                   5.0e-33
E value
                   79
Match length
                   71
% identity
NCBI Description
                   (AL049487) putative protein [Arabidopsis thaliana]
Seq. No.
                   214018
Seq. ID
                  LIB3146-036-P1-K1-G2
Method
                  BLASTX
                   g4538979
NCBI GI
BLAST score
                   178
E value
                   3.0e-13
Match length
                   61
% identity
                   51
                   (AL049487) putative protein [Arabidopsis thaliana]
NCBI Description
                   214019
Seq. No.
Seq. ID
                   LIB3146-036-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g4249382
BLAST score
                   568
E value
                   1.0e-58
Match length
                   132
                   77
% identity
NCBI Description
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   214020
Seq. ID
                   LIB3146-036-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g3461815
BLAST score
                   220
                   6.0e-18
E value
                   57
Match length
                   77
% identity
NCBI Description
                   (AC004138) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   214021
                   LIB3146-036-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1402947
BLAST score
                   198
                   9.0e-16
E value
Match length
                   77
                   39
% identity
NCBI Description
                  (X98404) calmodulin-2 [Capsicum annuum]
Seq. No.
                   214022
Seq. ID
                   LIB3146-036-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4220524
BLAST score
                   285
```



2.0e-16

74

% identity NCBI Description (AL035356) putative protein [Arabidopsis thaliana] Seq. No. 214023 Seq. ID LIB3146-036-P1-K1-H4 Method BLASTX NCBI GI g1708971 BLAST score 207

% identity 53 (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR NCBI Description (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -black cherry >gi_288116_emb_CAA51194_ (X72617) mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi 1090776 prf 2019441A mandelonitrile lyase

[Prunus serotina]

Seq. No. 214024

E value Match length

Seq. ID LIB3146-036-P1-K1-H5

Method BLASTN NCBI GI q10621 BLAST score 38 E value 6.0e-12 Match length 137 24 % identity

NCBI Description Trypanosoma cruzi hsp70 gene

Seq. No. 214025

Seq. ID LIB3146-036-P1-K1-H6

Method BLASTX NCBI GI g2443890 BLAST score 254 7.0e-22 E value Match length 120 56 % identity

NCBI Description (AC002294) similar to NAM (qp X92205 1321924) and CUC2 (gp AB002560 1944132) proteins [Arabidopsis thaliana]

Seq. No. 214026

Seq. ID LIB3146-037-P1-K1-A1

Method BLASTX NCBI GI g3540180 BLAST score 368 E value 3.0e-35 Match length 137 % identity

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 214027

LIB3146-037-P1-K1-A12 Seq. ID

Method BLASTX NCBI GI q4455223 BLAST score 389 E value 8.0e-38



```
Match length
% identity
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  214028
Seq. ID
                  LIB3146-037-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q1353769
                  35
BLAST score
E value
                  2.0e-10
Match length
                  71
% identity
                  87
NCBI Description
                  Arabidopsis thaliana profilin 1 mRNA, complete cds
                  214029
Seq. No.
Seq. ID
                  LIB3146-037-P1-K1-A3
Method
                  BLASTX
                  g1076625
NCBI GI
BLAST score
                  325
E value
                  3.0e-30
                  123
Match length
                  49
% identity
                  glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) precursor
NCBI Description
                  - common tobacco >gi_473102 emb CAA82271 (Z28697)
                  beta-1,3-glucanase [Nicotiana tabacum]
                  214030
Seq. No.
Seq. ID
                  LIB3146-037-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3643607
BLAST score
                  554
E value
                  5.0e-57
Match length
                  137
% identity
                  74
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
                  214031
Seq. No.
                  LIB3146-037-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346802
BLAST score
                  142
E value
                  5.0e-09
Match length
                  74
% identity
                  43
                  PROFILIN 1 >gi 1076516 pir S49351 profilin - kidney bean
NCBI Description
                  >gi_556836_emb_CAA57508_ (X81982) profilin [Phaseolus
                  vulgaris]
Seq. No.
                  214032
Seq. ID
                  LIB3146-037-P1-K1-A7
```

Method BLASTX NCBI GI q1168728 BLAST score 239 E value 4.0e-20 Match length 68 % identity 87



CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) NCBI Description cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

214033 Seq. No.

Seq. ID LIB3146-037-P1-K1-A9

Method BLASTX NCBI GI g1351271 BLAST score 160 E value 4.0e-11 Match length 46 72

% identity

TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) NCBI Description

>gi 1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi 806312 (L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

Seq. No. 214034

LIB3146-037-P1-K1-B6 Seq. ID

Method BLASTX NCBI GI g4455293 BLAST score 384 E value 4.0e-37 Match length 123 67 % identity

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

214035 Seq. No.

Seq. ID LIB3146-037-P1-K1-B7

Method BLASTX NCBI GI g3367522 BLAST score 336 E value 2.0e-31 Match length 133 % identity 49

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 214036

Seq. ID LIB3146-037-P1-K1-C12

Method BLASTX NCBI GI g3551247 BLAST score 170 E value 3.0e-12 Match length 103 43 % identity

NCBI Description (AB012703) 181 [Daucus carota]

Seq. No. 214037

Seq. ID LIB3146-037-P1-K1-C4

Method BLASTX NCBI GI g122106 BLAST score 301 1.0e-27 E value Match length 61 % identity 100

NCBI Description HISTONE H4 >gi_70771 pir HSZM4 histone H4 - maize





```
>gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana
>gi_2119028_pir__S60475 histone H4 - garden pea
>gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
(M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone
H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914
(Z79638) histone H4 homologue [Sesbania rostrata]
>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4
[Arabidopsis thaliana]
```

```
Seq. No.
                  214038
Seq. ID
                  LIB3146-037-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2191141
BLAST score
                  595
E value
                  7.0e-62
Match length
                  130
% identity
NCBI Description
                  (AF007269) A IG002N01.21 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  214039
Seq. ID
                  LIB3146-037-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g117188
BLAST score
                  310
E value
                  2.0e-28
Match length
                  127
% identity
                  CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)
NCBI Description
                  >gi 81423 pir A35867 cytochrome P450 71A1 - avocado
```

 Seq. No.
 214040

 Seq. ID
 LIB3146-037-P1-K1-D11

 Method
 BLASTX

 NCBI GI
 g3319921

 BLAST score
 256

 E value
 4.0e-22

 Match length
 96

% identity 58
NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]

>gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber

particle protein [Hevea brasiliensis]

Seq. No. 214041

Seq. ID LIB3146-037-P1-K1-D12

Method BLASTX
NCBI GI g3927838
BLAST score 407
E value 7.0e-40



Match length 100 % identity 79

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. 214042

Seq. ID LIB3146-037-P1-K1-D5

Method BLASTX
NCBI GI g2146727
BLAST score 195
E value 6.0e-15
Match length 67
% identity 82

NCBI Description cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 -

Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 214043

Seq. ID LIB3146-037-P1-K1-D6

Method BLASTX
NCBI GI 94538944
BLAST score 165
E value 2.0e-11
Match length 75
% identity 44

NCBI Description (ALO49483) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 214044

Seq. ID LIB3146-037-P1-K1-D9

Method BLASTX
NCBI GI g1934730
BLAST score 223
E value 2.0e-29
Match length 98
% identity 66

NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No. 214045

Seq. ID LIB3146-037-P1-K1-E1

Method BLASTX
NCBI GI g629602
BLAST score 364
E value 6.0e-35
Match length 104
% identity 68

NCBI Description probable imbibition protein - wild cabbage

>gi_488787_emb_CAA55893_ (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No. 214046

Seq. ID LIB3146-037-P1-K1-E10

Method BLASTX
NCBI GI g1518540
BLAST score 699
E value 5.0e-74
Match length 147
% identity 86

Method

NCBI GI

BLASTN

g1263029



```
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                  214047
Seq. No.
Seq. ID
                  LIB3146-037-P1-K1-E6
                  BLASTX
Method
NCBI GI
                  g2570338
BLAST score
                  152
E value
                  6.0e-10
Match length
                  49
% identity
                  59
NCBI Description
                  (U90927) glyoxalase II isozyme [Arabidopsis thaliana]
Seq. No.
                  214048
Seq. ID
                  LIB3146-037-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1881585
BLAST score
                  264
                  5.0e-23
E value
                  90
Match length
% identity
                  58
NCBI Description
                  (U72489) remorin [Solanum tuberosum]
Seq. No.
                  214049
Seq. ID
                  LIB3146-037-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2828267
BLAST score
                  741
E value
                  6.0e-79
Match length
                  148
% identity
                  94
NCBI Description
                  (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
Seq. No.
                  214050
Seq. ID
                  LIB3146-037-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2558962
BLAST score
                  282
E value
                  3.0e-25
                  57
Match length
% identity
                  98
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
Seq. No.
                  214051
Seq. ID
                  LIB3146-037-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q3650032
BLAST score
                  215
E value
                  2.0e-17
Match length
                  66
                  56
% identity
NCBI Description
                  (AC005396) gibberellin-regulated protein GAST1-like
                  [Arabidopsis thaliana]
Seq. No.
                  214052
                  LIB3146-037-P1-K1-F9
Seq. ID
```

Method

NCBI GI

BLASTX

g3121867



```
BLAST score
                  4.0e-31
E value
Match length
                  74
                  99
% identity
                  Tetrameles nudiflora 18S ribosomal RNA gene, complete
NCBI Description
                  sequence
                  214053
Seq. No.
                  LIB3146-037-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3650032
BLAST score
                  229
                  5.0e-19
E value
                  49
Match length
                   69
% identity
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
                  214054
Seq. No.
Seq. ID
                  LIB3146-037-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q974782
BLAST score
                  752
                  3.0e-80
E value
                  149
Match length
                  97
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
Seq. No.
                  214055
                  LIB3146-037-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  g629735
NCBI GI
BLAST score
                  226
                  1.0e-18
E value
Match length
                   64
% identity
                   67
                  fill protein - garden snapdragon >gi 406309 emb CAA40553
NCBI Description
                   (X57296) FIL1 [Antirrhinum majus]
Seq. No.
                  214056
Seq. ID
                  LIB3146-037-P1-K1-G12
Method
                  BLASTX
                  g112717
NCBI GI
BLAST score
                  195
E value
                   5.0e-15
Match length
                   62
                  58
% identity
NCBI Description
                  21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
                  hypothetical protein precursor - carrot
                  >gi_18312_emb_CAA36642 (X52395) precursor polypeptide (AA
                  -22 to 171) [Daucus carota]
Seq. No.
                  214057
                  LIB3146-037-P1-K1-G4
Seq. ID
```



BLAST score E value 6.0e-13 Match length 54 % identity 63

COP1 REGULATORY PROTEIN >gi_1694900_emb_CAA70768_ (Y09579) NCBI Description

Cop1 protein [Pisum sativum]

214058 Seq. No.

Seq. ID LIB3146-037-P1-K1-G5

Method BLASTX NCBI GI q4102634 BLAST score 198 E value 2.0e-15 Match length 32 94 % identity

NCBI Description (AF014396) Snakin-1 [Solanum tuberosum]

Seq. No. 214059

Seq. ID LIB3146-037-P1-K1-G6

Method BLASTX NCBI GI g1169012 BLAST score 580 E value 4.0e-60 Match length 128 % identity 87

COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1) >qi 402685 NCBI Description

(L24437) regulatory protein [Arabidopsis thaliana]

Seq. No. 214060

Seq. ID LIB3146-037-P1-K1-G8

Method BLASTX NCBI GI g3024127 BLAST score 538 E value 3.0e-55 Match length 127

% identity 80

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

Seq. No. 214061

Seq. ID LIB3146-037-P1-K1-H11

Method BLASTX NCBI GI q417103 BLAST score 665 E value 5.0e-70 Match length 135 % identity

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2



[Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 214062 Seq. ID LIB3146-037-P1-K1-H3 Method BLASTX NCBI GI g1498053 BLAST score 466 1.0e-48 E value 127 Match length 83 % identity NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 214063

Seq. ID LIB3146-037-P1-K1-H5

Method BLASTX NCBI GI q3702620 BLAST score 640 4.0e-67 E value Match length 127

86 % identity

NCBI Description (Y17329) calnexin [Pisum sativum]

214064 Seq. No.

Seq. ID LIB3146-037-P1-K1-H7

Method BLASTX NCBI GI q3914435 BLAST score 380 8.0e-37 E value Match length 83 % identity 87

NCBI Description PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin

[Glycine max]

Seq. No. 214065

LIB3146-037-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI q3402722 BLAST score 364 8.0e-35 E value Match length 123 % identity 61

NCBI Description (AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No. 214066

Seq. ID LIB3146-038-P1-K1-A10

Method BLASTX NCBI GI g480450

% identity

69



```
BLAST score
                  9.0e-22
E value
                  59
Match length
                  85
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  214067
Seq. No.
                  LIB3146-038-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  q2462834
NCBI GI
                  237
BLAST score
                  7.0e-20
E value
                  87
Match length
                  54
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  214068
Seq. No.
                  LIB3146-038-P1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1698548
BLAST score
                  268
E value
                  1.0e-25
                  104
Match length
                  64
% identity
                  (U58971) calmodulin-binding protein [Nicotiana tabacum]
NCBI Description
                  214069
Seq. No.
                  LIB3146-038-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2583108
BLAST score
                  387
E value
                  1.0e-37
                  107
Match length
                  69
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                  214070
Seq. No.
                  LIB3146-038-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2443751
BLAST score
                  664
E value
                  6.0e-70
Match length
                  141
                  89
% identity
                  (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
                  214071
Seq. No.
                  LIB3146-038-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  g1173218
NCBI GI
BLAST score
                  288
E value
                  6.0e-26
Match length
                  90
```

40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal NCBI Description protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] Seq. No. 214072 Seq. ID LIB3146-038-P1-K1-B2 Method BLASTX q4008159 NCBI GI BLAST score 655 6.0e-69 E value Match length 131 % identity 92 (AB015601) DnaJ homolog [Salix gilgiana] NCBI Description Seq. No. 214073 LIB3146-038-P1-K1-B3 Seq. ID Method BLASTX NCBI GI q4217999 BLAST score 609 E value 2.0e-63 Match length 138 84 % identity (AC006135) putative ubiquitin--protein ligase NCBI Description (ubiquitin-conjugating enzyme) [Arabidopsis thaliana] Seq. No. 214074 Seq. ID LIB3146-038-P1-K1-B5

BLASTN Method g167116 NCBI GI BLAST score 34 E value 1.0e-09 Match length 86 % identity

B.napus plastid 60-kDa chaperonin-60 beta-polypeptide NCBI Description

(cpn-60 beta) mRNA, partial cds

214075 Seq. No.

Seq. ID LIB3146-038-P1-K1-B8

BLASTX Method NCBI GI q547886 BLAST score 380 5.0e-44 E value Match length 122 75 % identity

NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)

> (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi 542102 pir S42939 malate dehydrogenase

(oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor - Flaveria pringlei >gi 1084444 pir S52016

malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria pringlei >gi 459441 emb CAA54986

(X78069) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Flaveria pringlei]

Seq. No. 214076

LIB3146-038-P1-K1-B9 Seq. ID

Method BLASTX



q3650032 NCBI GI BLAST score 181 2.0e-13 E value Match length 60 % identity 55

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 214077

Seq. ID LIB3146-038-P1-K1-C1

BLASTX Method NCBI GI g2370232 BLAST score 484 E value 7.0e-49 123 Match length 74 % identity

NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No. 214078

Seq. ID LIB3146-038-P1-K1-C11

Method BLASTX NCBI GI q3551247. 404 BLAST score 2.0e-39 E value Match length 142 % identity 58

NCBI Description (AB012703) 181 [Daucus carota]

Seq. No. 214079

LIB3146-038-P1-K1-C12 Seq. ID

Method BLASTX NCBI GI q2388689 BLAST score 517 1.0e-52 E value 128 Match length

% identity 78

NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 214080

Seq. ID LIB3146-038-P1-K1-C2

Method BLASTX NCBI GI g3522929 BLAST score 588 E value 3.0e-61 Match length 115 % identity 97

NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase

> [Arabidopsis thaliana] >qi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 214081

Seq. ID LIB3146-038-P1-K1-C3

Method BLASTX NCBI GI g2598599 BLAST score 284 E value 2.0e-25 Match length 82

NCBI Description

thaliana]



```
% identity
NCBI Description
                  (Y15372) MtN4 [Medicago truncatula]
                   214082
Seq. No.
                  LIB3146-038-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1946364
BLAST score
                   384
E value
                   4.0e-37
Match length
                   125
% identity
                   60
NCBI Description
                  (U93215) lipase isolog [Arabidopsis thaliana]
Seq. No.
                  214083
                  LIB3146-038-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3452263
BLAST score
                  138
E value
                   8.0e-09
Match length
                   63
% identity
                   48
NCBI Description
                   (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
                  thaliana]
                  214084
Seq. No.
Seq. ID
                  LIB3146-038-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3249109
BLAST score
                  176
E value
                  1.0e-26
Match length
                  111
% identity
                   60
                   (AC003114) Contains similarity to pre-mRNA splicing factor
NCBI Description
                   (SF2), P33 subunit gb M72709 from Homo sapiens. ESTs
                   gb_T42588 and gb_R65514 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                  214085
Seq. ID
                  LIB3146-038-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1762914
BLAST score
                  261
E value
                   9.0e-23
Match length
                   65
% identity
                  72
NCBI Description
                  (U65973) alcohol dehydrogenase A [Washingtonia robusta]
Seq. No.
                  214086
                  LIB3146-038-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1732509
BLAST score
                  257
E value
                  2.0e-22
Match length
                  70
% identity
                  67
```

(U62741) putative cytoskeletal protein [Arabidopsis

Method

NCBI GI

BLASTX

q2244771



```
Seq. No.
                  214087
Seq. ID
                  LIB3146-038-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                   450
                  5.0e-45
E value
Match length
                  107
% identity
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  214088
                  LIB3146-038-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1694976
BLAST score
                  393
E value
                  4.0e-38
Match length
                  110
% identity
                  67
NCBI Description
                  (Y09482) HMG1 [Arabidopsis thaliana]
                  >gi_2832361_emb_CAA74402 (Y14073) HMG protein [Arabidopsis
                  thaliana]
Seq. No.
                  214089
Seq. ID
                  LIB3146-038-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g100481
BLAST score
                  247
                  5.0e-21
E value
Match length
                  69
% identity
                  67
NCBI Description fill protein - garden snapdragon
Seq. No.
                  214090
Seq. ID
                  LIB3146-038-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1518540
BLAST score
                  400
E value
                  6.0e-50
Match length
                  139
% identity
                  68
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  214091
Seq. ID
                  LIB3146-038-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4455129
BLAST score
                  141
E value
                  1.0e-08
Match length
                  53
% identity
NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
Seq. No.
                  214092
Seq. ID
                  LIB3146-038-P1-K1-E7
```



```
BLAST score
E value
                   8.0e-15
Match length
                   112
                   44
% identity
NCBI Description
```

(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.

214093

Seq. ID

LIB3146-038-P1-K1-E9

Method BLASTX g2781363 NCBI GI 209 BLAST score 1.0e-16 E value

Match length 41 90 % identity

NCBI Description (AC003113) F2401.19 [Arabidopsis thaliana]

Seq. No.

214094

Seq. ID

LIB3146-038-P1-K1-F1

Method BLASTX NCBI GI g4263790 BLAST score 572 3.0e-59 E value 130 Match length

% identity 88

NCBI Description (AC006068) putative ch-TOG protein [Arabidopsis thaliana]

Seq. No.

214095 LIB3146-038-P1-K1-F3 Seq. ID

Method BLASTX NCBI GI g1076303 BLAST score 194 7.0e-15 E value 110 Match length 46

% identity NCBI Description

RNA-binding protein cp29 precursor - Arabidopsis thaliana

ź

>gi 681902 dbj BAA06518 (D31710) cp29 [Arabidopsis

thaliana]

Seq. No. 214096

Seq. ID LIB3146-038-P1-K1-G12

Method BLASTX NCBI GI g2661840 BLAST score 272 5.0e-24 E value Match length 73 % identity 73

NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 214097

LIB3146-038-P1-K1-G3 Seq. ID

Method BLASTN NCBI GI g2244731 BLAST score 36 E value 9.0e-11 Match length 52 92 % identity

NCBI Description Cotton mRNA for endo-xyloglucan transferase, clone CF101,



partial cds

```
Seq. No.
                  214098
Seq. ID
                  LIB3146-038-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3075399
BLAST score
                  269
                  1.0e-23
E value
Match length
                  138
% identity
                   45
                  (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214099
Seq. ID
                  LIB3146-038-P1-K1-H1
                  BLASTX
Method
NCBI GI
                  g462195
BLAST score
                   297
                   3.0e-27
E value
Match length
                  83
% identity
                  73
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
                  214100
Seq. No.
Seq. ID
                  LIB3146-038-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g416758
BLAST score
                   490
                   1.0e-49
E value
                   120
Match length
                   71
% identity
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
NCBI Description
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
Seq. No.
                   214101
Seq. ID
                  LIB3146-038-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g1514977
BLAST score
                   549
E value
                   2.0e-56
Match length
                   138
% identity
NCBI Description
                  (D84669) VM23 [Raphanus sativus]
Seq. No.
                   214102
Seq. ID
                  LIB3146-038-P1-K1-H7
Method
                  BLASTX
NCBI GI
                   g115874
BLAST score
                   227
                   1.0e-21
E value
```

29827

....

Match length

% identity

75



```
SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-WIII) >gi 170704
NCBI Description
                  (J02817) gibberellin responsive protein [Triticum aestivum]
                  214103
Seq. No.
Seq. ID
                  LIB3146-038-P1-K1-H8
Method
                  BLASTX
                  g135860
NCBI GI
BLAST score
                  654
E value
                  1.0e-68
Match length
                  147
                  86
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi 445129 prf 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
Seq. No.
                  214104
                  LIB3146-039-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  q3292849
NCBI GI
                  396
BLAST score
E value
                  7.0e-39
                  90
Match length
                  84
% identity
                  (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214105
Seq. ID
                  LIB3146-039-Q1-K1-A12
                  BLASTX
Method
                  g2388689
NCBI GI
BLAST score
                  259
                  1.0e-22
E value
                  81
Match length
                  67
% identity
                  (AF016633) GH1 protein [Glycine max]
NCBI Description
                  214106
Seq. No.
Seq. ID
                  LIB3146-039-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1076317
                  577
BLAST score
                  1.0e-59
E value
                  130
Match length
                  79
% identity
                  dihydrodipicolinate synthase (EC 4.2.1.52) precursor -
NCBI Description
                  Arabidopsis thaliana
                  214107
```

BLASTX NCBI GI q595780

Seq. No. Seq. ID

Method

BLAST score 104

LIB3146-039-Q1-K1-A6

BLAST score

Match length

E value

330

92

4.0e-31



```
1.0e-10
E value
                  83
Match length
                  45
% identity
NCBI Description (U13871) lacZ alpha peptide [Cloning vector]
                  214108
Seq. No.
Seq. ID
                  LIB3146-039-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2493046
                  357
BLAST score
                  3.0e-34
E value
                  99
Match length
                  68
% identity
                  ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                  3.6.1.34) delta' chain precursor - sweet potato
                  >gi 217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                  delta subunit [Ipomoea batatas]
                  214109
Seq. No.
                  LIB3146-039-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3451075
                  169
BLAST score
                  6.0e-12
E value
                  120
Match length
% identity
                  43
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                  214110
Seq. No.
                  LIB3146-039-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760347
                  344
BLAST score
                  5.0e-33
E value
                  71
Match length
                  16
% identity
NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  214111
Seq. ID
                  LIB3146-039-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2062691
BLAST score
                  37
                  2.0e-11
E value
                  40
Match length
% identity
NCBI Description
                  Human sodium phosphate transporter (NPT4) mRNA, complete
                  cds
Seq. No.
                  214112
Seq. ID
                  LIB3146-039-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3249096
```



Seq. No. 214113

Seq. ID LIB3146-039-Q1-K1-C5

Method BLASTX
NCBI GI 94336434
BLAST score 341
E value 3.0e-32
Match length 103
% identity 66

NCBI Description (AF092431) nodule-enhanced protein phosphatase type 2C

[Lotus japonicus]

Seq. No. 214114

Seq. ID LIB3146-039-Q1-K1-C8

Method BLASTX
NCBI GI g731285
BLAST score 153
E value 4.0e-10
Match length 93
% identity 35

NCBI Description HYPOTHETICAL 27.1 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION

>gi_1077483_pir__S51970 hypothetical protein YAL049c yeast (Saccharomyces cerevisiae) >gi_595535 (U12980)

Yal049cp [Saccharomyces cerevisiae]

Seq. No. 214115

Seq. ID LIB3146-039-Q1-K1-D11

Method BLASTX
NCBI GI g1351791
BLAST score 370
E value 2.0e-35
Match length 131
% identity 19

NCBI Description HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN

CPR4-SSK22 INTERGENIC REGION >gi_83249_pir__S19487 hypothetical protein YCR072c - yeast (Saccharomyces cerevisiae) >gi_1907211_emb_CAA42270_ (X59720) YCR072c, len:515 [Saccharomyces cerevisiae]

Seq. No. 214116

Seq. ID LIB3146-039-Q1-K1-D12

Method BLASTX
NCBI GI g3687833
BLAST score 399
E value 7.0e-39
Match length 121
% identity 14

NCBI Description (AF069737) notchless [Xenopus laevis]

Seq. No. 214117

Seq. ID LIB3146-039-Q1-K1-D2

Method BLASTX

```
NCBI GI
                   g2896801
BLAST score
                   246
                   6.0e-21
E value
                   125
Match length
% identity
                   42
NCBI Description
```

(AC004155) ERCC4 MOUSE [Mus musculus]

214118 Seq. No. Seq. ID LIB3146-039-Q1-K1-D3

Method BLASTX NCBI GI q2129726 BLAST score 450 6.0e - 45E value Match length 109 % identity 79

RNA polymerase II third largest chain RPB35.5A -NCBI Description

Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II

third largest subunit [Arabidopsis thaliana]

>gi_4544370_gb_AAD22281.1 AC006920 5 (AC006920) RNA

polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No. 214119

Seq. ID LIB3146-039-Q1-K1-D5

Method BLASTX NCBI GI q1172571 BLAST score 668 E value 2.0e-70 Match length 130 % identity 95

PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) NCBI Description

>gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase

(ATP) (EC 4.1.1.49) - cucumber >gi 567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No. 214120

Seq. ID LIB3146-039-Q1-K1-D6

BLASTX Method NCBI GI g4126405 BLAST score 353 2.0e-33 E value 72 Match length 96 % identity

NCBI Description (AB011798) homolog to defender against apoptotic death 1

[Citrus unshiu]

Seq. No. 214121

Seq. ID LIB3146-039-Q1-K1-D7

Method BLASTX NCBI GI g1351357 BLAST score 289 3.0e-26 E value 66 Match length % identity 85

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN NCBI Description

(CR14) >gi 633681 emb CAA55863 (X79276)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

Method

NCBI GI

BLASTX

g3075399



```
214122
Seq. No.
Seq. ID
                  LIB3146-039-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3851636
BLAST score
                  145
E value
                  2.0e-14
                  55
Match length
                  80
% identity
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                  214123
Seq. No.
                  LIB3146-039-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2326772
BLAST score
                  169
E value
                  5.0e-12
Match length
                  46
% identity
                  76
NCBI Description
                  (Y14507) anther-specific protein [Nicotiana sylvestris]
                  >gi_2326774_emb_CAA74846_ (Y14506) anther-specific protein
                   [Nicotiana sylvestris]
Seq. No.
                  214124
Seq. ID
                  LIB3146-039-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g485512
BLAST score
                  379
                  1.0e-36
E value
Match length
                  96
% identity
                  72
NCBI Description
                  salt-associated protein csaA - sweet orange
Seq. No.
                  214125
Seq. ID
                  LIB3146-039-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4455180
BLAST score
                  145
                  3.0e-09
E value
Match length
                  33
% identity
NCBI Description
                  (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                  214126
                  LIB3146-039-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760322
BLAST score
                  509
                  8.0e-52
E value
                  126
Match length
% identity
                  75
NCBI Description
                  (AC002130) F1N21.7 [Arabidopsis thaliana]
Seq. No.
                  214127
                  LIB3146-039-Q1-K1-F7
Seq. ID
```

% identity

NCBI Description

38



```
BLAST score
E value
                  2.0e-11
Match length
                   54
% identity
                   69
                  (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
                  214128
Seq. No.
                  LIB3146-039-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1931655
BLAST score
                   625
E value
                  2.0e-65
Match length
                  136
                   82
% identity
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]
                  214129
Seq. No.
Seq. ID
                  LIB3146-039-Q1-K1-G11
                  {\tt BLASTX}
Method
NCBI GI
                  g3953471
BLAST score
                   474
E value
                  1.0e-47
                  133
Match length
                   61
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
                  214130
Seq. No.
Seq. ID
                  LIB3146-039-Q1-K1-G3
                  BLASTX
Method
NCBI GI
                  g629735
BLAST score
                   248
E value
                   4.0e-21
Match length
                  71
% identity
                   66
NCBI Description
                  fill protein - garden snapdragon >gi 406309 emb CAA40553
                   (X57296) FIL1 [Antirrhinum majus]
Seq. No.
                  214131
Seq. ID
                  LIB3146-039-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4220537
BLAST score
                   606
E value
                   4.0e-63
Match length
                  135
% identity
NCBI Description
                  (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
Seq. No.
                  214132
Seq. ID
                  LIB3146-039-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q1402888
BLAST score
                  189
E value
                  3.0e-14
Match length
                  125
```

29833

(X98130) unknown [Arabidopsis thaliana]

```
Seq. No.
                   214133
Seq. ID
                  LIB3146-039-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   6.0e-11
Match length
                   36
% identity
                   100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   214134
```

 Seq. No.
 214134

 Seq. ID
 LIB3146-039-Q1-K1-G8

 Method
 BLASTX

 NCBI GI
 g2827039

 BLAST score
 326

BLAST score 326
E value 1.0e-30
Match length 66
% identity 94

NCBI Description (AF008444) chloroplast processing enzyme [Arabidopsis

thaliana]

 Seq. No.
 214135

 Seq. ID
 LIB3146-039-Q1-K1-H2

 Method
 BLASTX

 NCBI GI
 g4490331

 BLAST score
 265

BLAST score 265 E value 3.0e-23 Match length 72 % identity 68

NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No. 214136

Seq. ID LIB3146-039-Q1-K1-H4

Method BLASTX
NCBI GI g3860277
BLAST score 431
E value 1.0e-42
Match length 91
% identity 91

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

The same

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 214137

Seq. ID LIB3146-039-Q1-K1-H5

Method BLASTX
NCBI GI g2827536
BLAST score 294
E value 1.0e-26
Match length 136
% identity 43

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 214138

Seq. ID LIB3146-040-Q1-K1-A12

Method BLASTN NCBI GI g2829205



```
BLAST score
E value
                  1.0e-60
Match length
                  181
% identity
                  23
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  214139
Seq. No.
Seq. ID
                  LIB3146-040-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3560183
BLAST score
                  161
E value
                  4.0e-11
                  57
Match length
                  54
% identity
NCBI Description
                  (AL031517) conserved hypothetical protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  214140
Seq. ID
                  LIB3146-040-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2914698
BLAST score
                  176
E value
                  9.0e-13
                  74
Match length
% identity
                  46
NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  214141
Seq. ID
                  LIB3146-040-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3540180
BLAST score
                  366
E value
                  3.0e-35
Match length
                  92
% identity
                  71
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  214142
                  LIB3146-040-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                                                                        3
NCBI GI
                  g477430
BLAST score
                  258
E value
                  9.0e-23
Match length
                  76
                  67
% identity
NCBI Description nucleolar protein p120 - mouse (fragment)
Seq. No.
                  214143
Seq. ID
                  LIB3146-040-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q477430
BLAST score
                  281
E value
                  3.0e-25
Match length
                  98
                  58
% identity
```

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NCBI Description nucleolar protein p120 - mouse (fragment)

Seq. No.

Seq. ID

214149

LIB3146-040-Q1-K1-D2



```
214144
Seq. No.
Seq. ID
                  LIB3146-040-Q1-K1-B7
Method
                  BLASTX
                  g2072023
NCBI GI
                  240
BLAST score
                  2.0e-20
E value
                  90
Match length
                   61
% identity
                  (U93506) symbiosis-related protein [Laccaria bicolor]
NCBI Description
                   214145
Seq. No.
                  LIB3146-040-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                   g2924507
NCBI GI
                   332
BLAST score
                   4.0e-31
E value
                   110
Match length
                   62
% identity
                   (AL022023) cyclophilin - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   214146
Seq. No.
                   LIB3146-040-Q1-K1-C11
Seq. ID
                   BLASTN
Method
                   g407800
NCBI GI
BLAST score
                   245
                   1.0e-135
E value
                   263
Match length
                   99
% identity
                   G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                   (RL41)
                   214147
Seq. No.
Seq. ID
                   LIB3146-040-Q1-K1-D1
Method
                   BLASTX
                   g3695383
NCBI GI
                   603
BLAST score
                   9.0e-63
E value
                   122
Match length
                   90
% identity
                   (AF096370) similar to inorganic pyrophosphatase (Pfam:
NCBI Description
                   PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
                   thaliana]
                   214148
Seq. No.
Seq. ID
                   LIB3146-040-Q1-K1-D11
                   BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
                   7.0e-11
E value
Match length
                   37
% identity
                   61
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
```



```
BLASTX
Method
                   g3695383
NCBI GI
BLAST score
                   128
E value
                   3.0e-13
                   83
Match length
                   58
% identity
                   (AF096370) similar to inorganic pyrophosphatase (Pfam:
NCBI Description
                   PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
                   thaliana]
                   214150
Seq. No.
                   LIB3146-040-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g4406770
NCBI GI
BLAST score
                   434
E value
                   5.0e-43
                   121
Match length
                   60
% identity
                   (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                   214151
Seq. No.
                   LIB3146-040-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   q2583121
NCBI GI
BLAST score
                   150
                   1.0e-14
E value
                   63
Match length
                   70
% identity
                   (AC002387) putative phosphotransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214152
                   LIB3146-040-Q1-K1-E2
Seq. ID
Method
                   BLASTX
                   g3281853
NCBI GI
                   351
BLAST score
                   3.0e-33
E value
                   104
Match length
                   82
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214153
Seq. ID
                   LIB3146-040-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2736348
                   183
BLAST score
                   2.0e-13
E value
Match length
                   130
                   36
% identity
                   (AF039035) contains similarity to 4-nitrophenylphosphatases
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   214154
```

LIB3146-040-Q1-K1-F11 Seq. ID

Method BLASTX NCBI GI q3789917 BLAST score 144

NCBI Description

```
6.0e-09
E value
                  70
Match length
                  41
% identity
                   (AF084928) erythroblast macrophage protein EMP [Homo
NCBI Description
                  sapiens]
                  214155
Seq. No.
                  LIB3146-040-Q1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244833
BLAST score
                  146
                  2.0e-09
E value
                  97
Match length
                  32
% identity
                  (Z97337) centromere protein homolog [Arabidopsis thaliana]
NCBI Description
                   214156
Seq. No.
                  LIB3146-040-Q1-K1-G7
Seq. ID
                  BLASTN
Method
                   g4519195
NCBI GI
BLAST score
                   39
E value
                   1.0e-12
                   279
Match length
                   82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MQC12, complete sequence
                   214157
Seq. No.
Seq. ID
                   LIB3146-040-Q1-K1-H11
                   BLASTN
Method
NCBI GI
                   g167346
                   59
BLAST score
                   1.0e-24
E value
                   253
Match length
                   85
% identity
                   Gossypium hirsutum Lea5-A late embryogenesis-abundant
NCBI Description
                   protein (Lea5-A) gene, complete cds
                   214158
Seq. No.
                   LIB3146-040-Q1-K1-H4
Seq. ID
Method
                   BLASTN
                   q2244733
NCBI GI
BLAST score
                   63
                   1.0e-27
E value
                   79
Match length
                   95
% identity
                  Cotton mRNA for actin, clone CF456, partial cds
NCBI Description
Seq. No.
                   214159
                   LIB3146-040-Q1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244734
BLAST score
                   554
                   4.0e-57
E value
Match length
                   117
% identity
                   93
```

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(D88414) actin [Gossypium hirsutum]



```
Seq. No.
                  214160
                  LIB3146-041-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549893
BLAST score
                  187
E value
                  5.0e-14
Match length
                  43
% identity
                  (U09342) homeobox protein [Arabidopsis thaliana]
NCBI Description
                  214161
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3551257
BLAST score
                  178
E value
                  2.0e-13
Match length
                  40
% identity
NCBI Description
                  (AB012708) 98b [Daucus carota]
                  214162
Seq. No.
                  LIB3146-041-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2688824
BLAST score
                  395
                  1.0e-38
E value
Match length
                  93
% identity
NCBI Description
                  (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
Seq. No.
                  214163
                  LIB3146-041-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024127
BLAST score
                  585
                  8.0e-61
E value
Match length
                  116
% identity
                  94
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                  >gi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
Seq. No.
                  214164
                  LIB3146-041-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262149
BLAST score
                  439
                  1.0e-43
E value
Match length
                  112
% identity
                  70
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
```

Seq. No. 214165

[Arabidopsis thaliana]



```
LIB3146-041-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4007792
BLAST score
                  254
E value
                  6.0e-22
Match length
                  130
                  39
% identity
NCBI Description
                   (AL034463) Xenopus 14s cohesin smc1 subunit homolog
                   [Schizosaccharomyces pombe]
Seq. No.
                  214166
Seq. ID
                  LIB3146-041-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                  g2191174
BLAST score
                  418
                  4.0e-41
E value
                  132
Match length
% identity
                  67
                  (AF007270) similar to the peptidase family S16 [Arabidopsis
NCBI Description
                  thaliana]
                  214167
Seq. No.
                  LIB3146-041-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402835
                  155
BLAST score
E value
                  9.0e-11
                  34
Match length
                  91
% identity
NCBI Description
                  (U60148) plasma membrane major intrinsic protein 2 [Beta
                  vulgaris]
                  214168
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-B4
Method
                  BLASTN
NCBI GI
                  g1906829
BLAST score
                  33
                  5.0e-09
E value
Match length
                  45
                  93
% identity
NCBI Description A.thaliana hsp88.1 gene
Seq. No.
                  214169
Seq. ID
                  LIB3146-041-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2500380
BLAST score
                  161
                  6.0e-11
E value
                  29
Match length
                  100
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal
                  protein RL44 - upland cotton >gi 1553129 (U64677) ribosomal
                  protein L44 isoform a [Gossypium hirsutum] >gi 1553131
                   (U64678) ribosomal protein L44 isoform b [Gossypium
```

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hirsutum]

214170

Seq. No.



```
LIB3146-041-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q122070
                  320
BLAST score
E value
                  6.0e-30
Match length
                  66
% identity
                  HISTONE H3 >qi 82483 pir A25564 histone H3 - rice
NCBI Description
                  >qi 169793 (M15664) histone 3 [Oryza sativa] >qi 940018
                  (U25664) histone H3 [Oryza sativa]
                  214171
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-B9
                  BLASTN
Method
                  g1069999
NCBI GI
                  33
BLAST score
                  6.0e-09
E value
                  73
Match length
                  86
% identity
                  B.napus mRNA for biotin carboxyl carrier protein (pBP1)
NCBI Description
                  >gi 3715063 emb A59872.1 A59872 Sequence 1 from Patent
                  WO9707222
                  214172
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-C1
                  BLASTN
Method
                  g2924257
NCBI GI
                  44
BLAST score
                  2.0e-15
E value
                  197
Match length
                  90
% identity
NCBI Description
                  Tobacco chloroplast genome DNA
                  214173
Seq. No.
                  LIB3146-041-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281855
BLAST score
                   269
E value
                  1.0e-23
                  100
Match length
                   58
% identity
                  (AL031004) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   214174
Seq. No.
                  LIB3146-041-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                   a475048
BLAST score
                   629
                   8.0e-66
E value
Match length
                  139
% identity
NCBI Description
                   (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
                   [Arabidopsis thaliana]
```

Seq. No. 214175

Seq. ID LIB3146-041-Q1-K1-C6

Method BLASTX

```
q2275199
NCBI GI
BLAST score
                   466
E value
                   1.0e-46
                   142
Match length
% identity
                   71
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  214176
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-C7
                  BLASTX
Method
NCBI GI
                  g2244826
                   366
BLAST score
E value
                   3.0e-35
Match length
                   82
% identity
                   (Z97336) replication control protein homolog [Arabidopsis
NCBI Description
                   thaliana]
                   214177
Seq. No.
                  LIB3146-041-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220521
BLAST score
                   283
                   3.0e-25
E value
                   63
Match length
                   86
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   214178
Seq. No.
Seq. ID
                   LIB3146-041-Q1-K1-C9
Method
                   BLASTX
                   q2119042
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   48
Match length
% identity
                   94
                   glycine-rich RNA-binding protein RGP-la - wood tobacco
NCBI Description
                   >qi 469070 dbj BAA03741 (D16204) RNA-binding glycine-rich
                   protein-1 (RGP-1a) [Nicotiana sylvestris]
Seq. No.
                   214179
Seq. ID
                   LIB3146-041-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   q1710007
BLAST score
                   750
E value
                   5.0e-80
Match length
                   135
                   100
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN1A >gi 1370203 emb CAA98187
NCBI Description
                   (Z73959) RAN1A [Lotus japonicus]
```

214180 Seq. No.

LIB3146-041-Q1-K1-D11 Seq. ID

Method BLASTX NCBI GI g3929649 BLAST score 356 3.0e-56 E value



Match length % identity 87

NCBI Description (AJ131205) mitochondrial NAD-dependent malate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 214181

Seq. ID LIB3146-041-Q1-K1-D12

Method BLASTX NCBI GI q4158230 BLAST score 233 E value 2.0e-19 Match length 80 % identity 54

NCBI Description (Y18625) amylogenin [Triticum aestivum]

Seq. No. 214182

Seq. ID LIB3146-041-Q1-K1-D3

Method BLASTX NCBI GI g2760326 BLAST score 301 E value 2.0e-27 Match length 132 % identity 46

NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No. 214183

Seq. ID LIB3146-041-Q1-K1-D4

Method BLASTX NCBI GI g464987 BLAST score 215 E value 3.0e-17 Match length 41 % identity 95

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 214184

Seq. ID LIB3146-041-Q1-K1-D6

Method BLASTX NCBI GI g1903021 BLAST score 372 E value 1.0e-35 Match length 87 % identity

(Y10216) hypothetical 3-isopropylmalate dehydrogenase NCBI Description

[Arabidopsis thaliana]

Seq. No. 214185

Seq. ID LIB3146-041-Q1-K1-D8

Method BLASTX NCBI GI g4335735 BLAST score 143



```
6.0e-09
E value
Match length
                   51
                   49
% identity
NCBI Description
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   214186
Seq. ID
                   LIB3146-041-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g3123271
BLAST score
                   444
E value
                   3.0e-44
Match length
                   84
% identity
                   96
NCBI Description
                   40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381 (Y14052)
                   ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                   214187
Seq. ID
                   LIB3146-041-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                   g3915165
BLAST score
                   489
E value
                   1.0e-49
Match length
                   110
% identity
                   85
NCBI Description
                  TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 2792520
                   (AF042320) tryptophan synthase beta subunit [Camptotheca
                   acuminata] >gi_2801771 (AF042321) tryptophan synthase beta
                   [Camptotheca acuminata]
Seq. No.
                   214188
Seq. ID
                  LIB3146-041-Q1-K1-E11
Method
                  BLASTN
NCBI GI
                  g567934
BLAST score
                   48
                  5.0e-18
E value
Match length
                  80
% identity
                   90
NCBI Description
                  Camellia sinensis mRNA for chalcone synthase (CHS1),
                  complete cds, clone VEG13
Seq. No.
                  214189
Seq. ID
                  LIB3146-041-Q1-K1-E12
Method
                  BLASTX
                  g2529668
NCBI GI
BLAST score
                  428
E value
                  2.0e-42
Match length
                  92
% identity
                  87
NCBI Description
                  (AC002535) putative photolyase/blue-light receptor
                   [Arabidopsis thaliana] >gi 3319288 (AF053366)
                  photolyase/blue light photoreceptor PHR2 [Arabidopsis
                  thaliana]
```

Seq. No. 214190 Seq. ID LIB3146-041-Q1-K1-E4

Method BLASTX NCBI GI g3434973



99

% identity

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NCBI Description

```
BLAST score
                  8.0e-25
E value
Match length
                  64
                  83
% identity
                  (AB008106) ethylene responsive element binding factor 4
NCBI Description
                  [Arabidopsis thaliana]
                  214191
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-E7
Method
                  BLASTX
                  g2982266
NCBI GI
BLAST score
                  611
                  9.0e-64
E value
Match length
                  128
% identity
                  91
                  (AF051216) probable fibrillarin [Picea mariana]
NCBI Description
Seq. No.
                  214192
Seq. ID
                  LIB3146-041-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  306
E value
                  6.0e-28
Match length
                  88
% identity
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
Seq. No.
                  214193
Seq. ID
                  LIB3146-041-Q1-K1-E9
Method
                  BLASTX
                  g2388689
NCBI GI
                  339
BLAST score
E value
                  7.0e-32
                  74
Match length
% identity
                  85
                  (AF016633) GH1 protein [Glycine max]
NCBI Description
                  214194
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1381676
BLAST score
                  259
                  2.0e-22
E value
                  57
Match length
                  89
% identity
NCBI Description
                  (U58853) small GTP-binding protein [Glycine max]
                  214195
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-F10
                  BLASTX
Method
NCBI GI
                  g1703380
BLAST score
                  489
E value
                  2.0e-49
                  95
Match length
```

29845

ADP-ribosylation factor [Oryza sativa]

ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)



```
Seq. No.
                  214196
Seq. ID
                  LIB3146-041-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3047117
BLAST score
                  158
E value
                  1.0e-10
Match length
                  30
                  97
% identity
                  (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  214197
                  LIB3146-041-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914706
BLAST score
                  371
                  1.0e-35
E value
Match length
                  107
% identity
                  63
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214198
Seq. ID
                  LIB3146-041-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2827659
BLAST score
                  477
E value
                  1.0e-48
Match length
                  137
% identity
                  78
                  (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
                  214199
Seq. No.
Seq. ID
                  LIB3146-041-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q547712
BLAST score
                  382
E value
                  7.0e-37
Match length
                  138
% identity
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                  >gi_542153_pir__S38358 translation initiation factor eIF-4A
                   - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic
                  initiation factor 4A [Oryza sativa]
Seq. No.
                  214200
Seq. ID
                  LIB3146-041-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1079720
BLAST score
                  580
E value
                  4.0e-60
Match length
                  131
% identity
                  (U39764) eukaryotic release factor 3 [Ricinus communis]
NCBI Description
```

Seq. No. 214201

Seq. ID LIB3146-041-Q1-K1-G8



```
BLASTX
Method
NCBI GI
                   g3068713
BLAST score
                   426
                   2.0e-46
E value
                   135
Match length
% identity
                   73
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   214202
Seq. No.
Seq. ID
                   LIB3146-041-Q1-K1-G9
                   BLASTX
Method
NCBI GI
                   q99749
BLAST score
                   269
                   1.0e-23
E value
                   72
Match length
                   74
% identity
NCBI Description
                   probable serine/threonine-specific protein kinase ATPK64
                   (EC 2.7.1.-) - Arabidopsis thaliana >gi_217843_dbj_BAA01731_ (D10937) protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   214203
Seq. ID
                   LIB3146-041-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   q4508073
BLAST score
                   398
E value
                   8.0e-39
Match length
                   103
% identity
                   70
                   (AC005882) 43220 [Arabidopsis thaliana]
NCBI Description
                   214204
Seq. No.
Seq. ID
                   LIB3146-041-Q1-K1-H3
Method
                   BLASTN
NCBI GI
                   q20548
BLAST score
                   36
                   7.0e-11
E value
Match length
                   80
% identity
                   89
                   P.hortense GADPH mRNA for glycolytic
NCBI Description
                   glyceraldehyde-3-phosphate
                                                          dehydrogenase
Seq. No.
                   214205
Seq. ID
                   LIB3146-041-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   g2979565
BLAST score
                   367
E value
                   4.0e-35
Match length
                   84
% identity
                   83
                   (AC003680) putative sin3 associated polypeptide (SAP18)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214206
```

Seq. ID LIB3146-041-Q1-K1-H6

Method BLASTX NCBI GI g133867



```
BLAST score
E value
                  1.0e-57
Match length
                  126
                  85
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                  214207
Seq. ID
                  LIB3146-041-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3548810
BLAST score
                  185
E value
                  5.0e-14
Match length
                  100
% identity
                  44
                  (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  214208
Seq. ID
                  LIB3146-042-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2245065
BLAST score
                  578
                  5.0e-60
E value
Match length
                  118
% identity
                  81
NCBI Description
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
                  214209
Seq. No.
Seq. ID
                  LIB3146-042-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3044218
BLAST score
                  310
                  2.0e-28
E value
Match length
                  78
% identity
                  73
NCBI Description
                  (AF057144) signal peptidase [Arabidopsis thaliana]
Seq. No.
                  214210
Seq. ID
                  LIB3146-042-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                  279
E value
                  1.0e-156
Match length
                  339
% identity
                  96
NCBI Description
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
                  partial sequence
```

Seq. No. 214211

Seq. ID LIB3146-042-Q1-K1-A8

Method BLASTX
NCBI GI g2341041
BLAST score 191
E value 3.0e-17
Match length 90



% identity NCBI Description

(AC000104) Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb AF047976). EST gb_W43451 comes from this

gene. [Arabidopsis thaliana] >gi_3687656 (AF047976) putative ethylene receptor; ERS2 [Arabidopsis thaliana]

Seq. No. 214212

Seq. ID LIB3146-042-Q1-K1-B2

Method BLASTX
NCBI GI g2342687
BLAST score 351
E value 3.0e-33
Match length 124
% identity 52

NCBI Description (AC000106) Similar to Beta integral membrane protein

(gb U43629). EST gb W43122 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 214213

Seq. ID LIB3146-042-Q1-K1-B4

Method BLASTX
NCBI GI g1345698
BLAST score 700
E value 3.0e-74
Match length 128
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

a/b-binding protein - upland cotton

>gi_452314 emb CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 214214

Seq. ID LIB3146-042-Q1-K1-B6

Method BLASTX
NCBI GI g1173234
BLAST score 327
E value 2.0e-30
Match length 72
% identity 89

NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal

protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714)

ribosomal protein S25 [Lycopersicon esculentum] >gi_1584836_prf__2123431A ribosomal protein S25

[Lycopersicon esculentum]

Seq. No. 214215

Seq. ID LIB3146-042-Q1-K1-B7

Method BLASTX
NCBI GI g1840425
BLAST score 154
E value 3.0e-10
Match length 42
% identity 67

NCBI Description (U36586) alcohol dehydrogenase [Vitis vinifera]

Seq. No. 214216



```
Seq. ID
                   LIB3146-042-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   389
E value
                   1.0e-37
Match length
                   107
% identity
                   70
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
Seq. No.
                    214217
                   LIB3146-042-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                    g3063396
BLAST score
                    449
E value
                    9.0e-45
                    111
Match length
                    77
% identity
                   (AB012947) vcCyP [Vicia faba]
NCBI Description
Seq. No.
                    214218
Seq. ID
                    LIB3146-042-Q1-K1-C5
Method
                    BLASTX
NCBI GI
                    g3122673
BLAST score
                    284
E value
                    9.0e-26
Match length
                    57
                    93
% identity
                    60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
NCBI Description
                    (Z97341) ribosomal protein [Arabidopsis thaliana]
                    214219
Seq. No.
Seq. ID
                    LIB3146-042-Q1-K1-C6
Method
                    BLASTX
                    g3242714
NCBI GI
BLAST score
                    167
                    1.0e-11
E value
                    94
Match length
                    35
% identity
                    (AC003040) hypersensitivity-related protein [Arabidopsis
NCBI Description
                    thaliana]
                    214220
Seq. No.
                    LIB3146-042-Q1-K1-D1
Seq. ID
                    BLASTX
Method
                    g2131352
NCBI GI
BLAST score
                    174
                    1.0e-12
E value
```

101 Match length 36 % identity

hypothetical protein YDL166c - yeast (Saccharomyces NCBI Description cerevisiae) >gi 1061273 emb CAA91580 (Z67750) putative

protein [Saccharomyces cerevisiae]

>gi 1431264 emb CAA98740 (Z74214) ORF YDL166c ~

[Saccharomyces cerevisiae]

Seq. No.

Seq. ID

214226

LIB3146-042-Q1-K1-E7



```
214221
Seq. No.
                  LIB3146-042-Q1-K1-D3
Seq. ID
                  BLASTN
Method
                  g3873174
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
                  114
Match length
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  214222
Seq. No.
                  LIB3146-042-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g1841870
NCBI GI
                  223
BLAST score
                  3.0e-18
E value
                  122
Match length
                  41
% identity
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
                  214223
Seq. No.
                  LIB3146-042-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g3885515
NCBI GI
                   396
BLAST score
                  8.0e-39
E value
                   92
Match length
                   79
% identity
                  (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                   sativa]
                   214224
Seq. No.
                   LIB3146-042-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3128208
NCBI GI
BLAST score
                   182
                   2.0e-13
E value
                   70
Match length
                   53
% identity
                   (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   214225
Seq. No.
                   LIB3146-042-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   q122007
NCBI GI
                   285
BLAST score
E value
                   1.0e-25
                   62
Match length
 % identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
```



BLASTX Method NCBI GI q139780 BLAST score 215 2.0e-17 E value 75 Match length % identity 61

WOUND-INDUCED PROTEIN 1 >gi 82293 pir JQ0398 wun1 protein NCBI Description

Seq. No. 214227

Seq. ID LIB3146-042-Q1-K1-F3

Method BLASTX NCBI GI q122085 BLAST score 365 E value 1.0e-38 Match length 107 % identity

HISTONE H3 >gi 81641 pir S06250 histone H3 - Arabidopsis NCBI Description

thaliana >gi_82482_pir__S04099 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays]

>gi_168497 (M13379) histone H3 [Zea mays] >gi_168506

(M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3
[Petroselinum crispum] >gi_387565 (M17130) histone H3
[Arabidopsis thaliana] >gi_387567 (M17131) histone H3
[Arabidopsis thaliana] >gi_886738 emb_CAA59111 (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi 1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414)

Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb H76511 gb H76255, gb AA712452, gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana]

>gi 225459_prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839_prf 1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 214228

Seq. ID LIB3146-042-Q1-K1-G4

Method BLASTX NCBI GI g1705826 BLAST score 184 9.0e-14 E value Match length 38 89 % identity

CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1) NCBI Description

>gi 437708 (M91193) chalcone synthase [Trifolium

subterraneum] >gi 741008 prf 2006270A chalcone synthase

[Trifolium subterraneum]

214229 Seq. No.

Seq. ID LIB3146-042-Q1-K1-G7



```
BLASTX
Method
NCBI GI
                  q3334756
BLAST score
                  510
                  6.0e-52
E value
Match length
                  113
% identity
                  87
                  (Y16672) putative arginine/serine-rich splicing factor
NCBI Description
                   [Medicago sativa]
Seq. No.
                  214230
                  LIB3146-042-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2598009
BLAST score
                  230
E value
                  3.0e-19
Match length
                  58
% identity
                  79
NCBI Description
                  (AJ222545) Rop subfamily GTPase [Nicotiana tabacum]
Seq. No.
                  214231
Seq. ID
                  LIB3146-042-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q3201613
BLAST score
                  318
E value
                  1.0e-29
Match length
                  84
% identity
                  71
NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]
                  214232
Seq. No.
                  LIB3146-042-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421096
                   409
BLAST score
E value
                   4.0e-40
                  117
Match length
                  73
% identity
                   (AF043528) 20S proteasome subunit PAG1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3885332 (AC005623) proteasome component
                   [Arabidopsis thaliana]
                  214233
Seq. No.
Seq. ID
                  LIB3146-043-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g3786011
BLAST score
                   314
                   4.0e-41
E value
Match length
                  102
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214234
```

Seq. ID LIB3146-043-Q1-K1-A3

Method BLASTX NCBI GI g1705826 BLAST score 243



E value 1.0e-20 Match length 59 % identity 81

NCBI Description CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)

>gi 437708 (M91193) chalcone synthase [Trifolium

subterraneum] >gi_741008_prf__2006270A chalcone synthase

[Trifolium subterraneum]

Seq. No. 214235

Seq. ID LIB3146-043-Q1-K1-A7

Method BLASTX
NCBI GI g2078350
BLAST score 185
E value 4.0e-23
Match length 124
% identity 52

NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 214236

Seq. ID LIB3146-043-Q1-K1-B12

Method BLASTX
NCBI GI g1263291
BLAST score 578
E value 6.0e-60
Match length 127
% identity 82

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 214237

Seq. ID LIB3146-043-Q1-K1-B4

Method BLASTX
NCBI GI g4097547
BLAST score 288
E value 5.0e-26
Match length 70
% identity 45

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

Seq. No. 214238

Seq. ID LIB3146-043-Q1-K1-B6

Method BLASTX
NCBI GI g3421087
BLAST score 610
E value 1.0e-63
Match length 125
% identity 97

NCBI Description (AF043524) 20S proteasome subunit PAE1 [Arabidopsis

thaliana]

Seq. No. 214239

Seq. ID LIB3146-043-Q1-K1-B7

Method BLASTX
NCBI GI g1354849
BLAST score 468
E value 6.0e-47
Match length 133
% identity 63





NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

 Seq. No.
 214240

 Seq. ID
 LIB3146-043-Q1-K1-B8

 Method
 BLASTX

 NCBI GI
 g133867

NCBI GI G13386/ BLAST score 440 E value 1.0e-43 Match length 103 % identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 214241

Seq. ID LIB3146-043-Q1-K1-C12

Method BLASTX
NCBI GI g3021483
BLAST score 139
E value 1.0e-08
Match length 31
% identity 97

NCBI Description (AJ224931) histone H2B-2 [Lycopersicon esculentum]

Seq. No. 214242

Seq. ID LIB3146-043-Q1-K1-C3

Method BLASTX
NCBI GI g3288823
BLAST score 361
E value 2.0e-34
Match length 122
% identity 64

NCBI Description (AF063852) FUS5 [Arabidopsis thaliana]

Seq. No. 214243

Seq. ID LIB3146-043-Q1-K1-C5

Method BLASTX
NCBI GI g119791
BLAST score 494
E value 5.0e-50
Match length 108
% identity 89

NCBI Description 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR

(3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)

>gi_1084385_pir__S22450 3-oxoacyl-[acyl-carrier-protein]
reductase (EC 1.1.1.100) precursor - Cuphea lanceolata
>gi_18046_emb_CAA45866_ (X64566) 3-oxoacyl-[acyl-carrier

protein] reductase [Cuphea lanceolata]

>gi 228929 prf 1814446A beta ketoacyl-ACP reductase

[Cuphea lanceolata]

Seq. No. 214244

Seq. ID LIB3146-043-Q1-K1-C7

Method BLASTX
NCBI GI g2326772
BLAST score 465
E value 1.0e-46



Match length % identity

NCBI Description

(Y14507) anther-specific protein [Nicotiana sylvestris] >gi 2326774 emb_CAA74846_ (Y14506) anther-specific protein

[Nicotiana sylvestris]

Seq. No.

214245

Seq. ID

LIB3146-043-Q1-K1-C9

Method NCBI GI BLASTX g547683 255

BLAST score E value

5.0e-22 84

Match length % identity

67

NCBI Description

HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum] >gi 445601 prf 1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No.

214246

Seq. ID

LIB3146-043-Q1-K1-D1

Method BLASTX g2633047 NCBI GI BLAST score 148 E value 2.0e-09

113 Match length 30 % identity

NCBI Description

(Z99107) similar to metabolite transporter [Bacillus subtilis] >gi_2633058_emb_CAB12563_ (Z99108) similar to

metabolite transporter [Bacillus subtilis]

Seq. No.

214247

Seq. ID

LIB3146-043-Q1-K1-D10

Method BLASTX NCBI GI g2583130 BLAST score 174 E value 2.0e-12 Match length 119 % identity

NCBI Description

(AC002387) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No.

214248

Seq. ID Method

LIB3146-043-Q1-K1-D11

BLASTX NCBI GI q3122228 BLAST score 324 4.0e-30 E value Match length 84 76 % identity

NCBI Description

MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR

>gi 2129837 pir S65049 low molecular weight heat shock protein precursor (clone Hsp23.9) - soybean >gi_710432

(U21722) Hsp23.9 [Glycine max]

Seq. No.

214249

Seq. ID

LIB3146-043-Q1-K1-D3



Method BLASTX
NCBI GI G116385
BLAST score 385
E value 6.0e-66
Match length 133
% identity 93
NCBI Description CVALCON

NCBI Description CHALCONE SYNTHASE A (NARINGENIN-CHALCONE SYNTHASE A)

>gi 66548 pir SYPJCN naringenin-chalcone synthase (EC

2.3.1.74) - garden petunia >gi_20542_emb_CAA27718_ (X04080)

CHS (aa 1-389) [Petunia x hybrida]

Seq. No. 214250

Seq. ID LIB3146-043-Q1-K1-D5

Method BLASTX
NCBI GI g3080420
BLAST score 126
E value 5.0e-19
Match length 90
% identity 68

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 214251

Seq. ID LIB3146-043-Q1-K1-D6

Method BLASTX
NCBI GI g3687235
BLAST score 438
E value 4.0e-46
Match length 106
% identity 95

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 214252

Seq. ID LIB3146-043-Q1-K1-D7

Method BLASTX
NCBI GI g992706
BLAST score 541
E value 2.0e-55
Match length 103
% identity 92

NCBI Description (U33758) UBC13 [Arabidopsis thaliana]

Seq. No. 214253

Seq. ID LIB3146-043-Q1-K1-E1

Method BLASTX
NCBI GI g2894598
BLAST score 395
E value 2.0e-38
Match length 120
% identity 65

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 214254

Seq. ID LIB3146-043-Q1-K1-E3

Method BLASTX NCBI GI g3757521



```
BLAST score
E value
                  6.0e-49
Match length
                  139
                  64
% identity
NCBI Description
                  (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                  214255
Seq. ID
                  LIB3146-043-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q1483218
BLAST score
                  204
E value
                  4.0e-16
Match length
                  94
                  50
% identity
NCBI Description
                   (X99793) induced upon wounding stress [Arabidopsis
                  thaliana]
Seq. No.
                  214256
                  LIB3146-043-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  g4580575
NCBI GI
                  252
BLAST score
E value
                  9.0e-22
Match length
                  102
% identity
                  54
                  (AF082176) auxin response factor 9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214257
Seq. ID
                  LIB3146-043-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q1710546
BLAST score
                  314
E value
                   6.0e-29
Match length
                  72
% identity
                  86
                  60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
NCBI Description
                  ribosomal protein [Daucus carota]
Seq. No.
                  214258
Seq. ID
                  LIB3146-043-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3859595
BLAST score
                  206
                  3.0e-16
E value
Match length
                  107
                  45
% identity
                  (AF104919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214259
Seq. ID
                  LIB3146-043-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4539324
                  436
```

Method BLASTX
NCBI GI g453932
BLAST score 436
E value 3.0e-43
Match length 115
% identity 81

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]



```
Seq. No.
                  214260
Seq. ID
                  LIB3146-043-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2760323
BLAST score
                  183
E value
                  1.0e-13
Match length
                  74
% identity
                  45
NCBI Description
                  (AC002130) F1N21.8 [Arabidopsis thaliana]
Seq. No.
                  214261
Seq. ID
                  LIB3146-043-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2462741
BLAST score
                  441
E value
                  7.0e-44
Match length
                  110
                  76
% identity
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  214262
Seq. ID
                  LIB3146-043-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2462761
BLAST score
                  144
E value
                  4.0e-09
Match length
                  62
% identity
                  44
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  214263
Seq. ID
                  LIB3146-043-Q1-K1-F6
                                                                    .. A
Method
                  BLASTX
NCBI GI
                  g3746069
BLAST score
                  157
E value
                  2.0e-10
Match length
                  123
% identity
                  31
                  (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214264
Seq. ID
                  LIB3146-043-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2792297
BLAST score
                  253
                  9.0e-22
E value
                  77
Match length
                  57
% identity
```

NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 214265

Seq. ID LIB3146-043-Q1-K1-G5

Method BLASTX

% identity

56



```
q3063396
NCBI GI
                   623
BLAST score
                   4.0e-65
E value
                   139
Match length
% identity
                   83
NCBI Description (AB012947) vcCyP [Vicia faba]
                   214266
Seq. No.
                   LIB3146-043-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3212863
BLAST score
                   519
E value
                   6.0e-53
Match length
                   132
                   76
% identity
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
                   214267
Seq. No.
Seq. ID
                   LIB3146-043-Q1-K1-H1
Method
                   BLASTN
NCBI GI
                   q19153
BLAST score
                   37
E value
                   2.0e-11
Match length
                   41
                   98
% identity
NCBI Description Tomato 17S-25S ribosomal DNA spacer
                   214268
Seq. No.
Seq. ID
                   LIB3146-043-Q1-K1-H3
Method
                   BLASTX
                   g4309734
NCBI GI
BLAST score
                   209
                   1.0e-16
E value
Match length
                   61
                   64
% identity
                   (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214269
Seq. ID
                   LIB3146-043-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   g4218991
BLAST score
                   332
                   4.0e-31
E value
Match length
                   125
% identity
                   54
                  (AF098632) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   214270
Seq. No.
Seq. ID
                   LIB3146-044-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2827661
                   257
BLAST score
                   3.0e-22
E value
Match length
                   99
```

Seq. ID

Method



```
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]
Seq. No.
                  214271
                  LIB3146-044-Q1-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                   9.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  214272
                  LIB3146-044-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                   a2281103
NCBI GI
                   189
BLAST score
E value
                   1.0e-14
                   54
Match length
                   61
% identity
                   (AC002333) Glucan endo-1,3-beta glucosidase isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214273
                   LIB3146-044-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   g2950476
NCBI GI
                   174
BLAST score
E value
                   2.0e-12
                   81
Match length
% identity
                   46
                  (AL022070) vesicle transport v-snare protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   214274
Seq. No.
Seq. ID
                   LIB3146-044-Q1-K1-B1
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
                   9.0e-11
E value
Match length
                   48
% identity
                   65
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   214275
                   LIB3146-044-Q1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g296502
BLAST score
                   557
E value
                   1.0e-57
Match length
                   106
                   99
% identity
NCBI Description (X69187) beta tubulin 3 [Anemia phyllitidis]
Seq. No.
                   214276
```

29861

LIB3146-044-Q1-K1-B12

BLASTX



```
q3297819
NCBI GI
                  636 🏤
BLAST score
                  1.0e-66
E value
                  126
Match length
% identity
                  94
NCBI Description
                   (AL031032) protein kinase - like protein [Arabidopsis
                  thaliana]
                  214277
Seq. No.
Seq. ID
                  LIB3146-044-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1699024
BLAST score
                  198
                  1.0e-15
E value
Match length
                  54
% identity
                  67
NCBI Description
                  (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
                   (U78870) unknown [Arabidopsis thaliana]
Seq. No.
                  214278
Seq. ID
                  LIB3146-044-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2369766
BLAST score
                  395
E value
                  2.0e-38
Match length
                  114
% identity
                  67
NCBI Description
                  (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                  214279
                  LIB3146-044-Q1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1399551
BLAST score
                  142
                  5.0e-74
E value
                  158
Match length
                  97
% identity
                  Adonis vernalis nuclear 26S ribosomal RNA gene, partial
NCBI Description
                  sequence
Seq. No.
                  214280
Seq. ID
                  LIB3146-044-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g457517
BLAST score
                  241
E value
                  2.0e-20
Match length
                  120
% identity
                  42
                  (L12579) alternatively spliced [Homo sapiens]
NCBI Description
                  >gi 4503169 ref NP 001904.1 pCUTL1 cut (Drosophila)-like 1
                   (CCAAT displacement protein)
Seq. No.
                  214281
```

Seq. ID LIB3146-044-Q1-K1-C1

Method BLASTN NCBI GI q2828184 BLAST score 39



E value 2.0e-12 Match length 79 % identity 87 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSN9, complete sequence [Arabidopsis thaliana] Seq. No. 214282 Seq. ID LIB3146-044-Q1-K1-C2 Method BLASTX NCBI GI q2688824 BLAST score 359 E value 3.0e-34 Match length 100 74 % identity (U93273) putative auxin-repressed protein [Prunus NCBI Description armeniaca] Seq. No. 214283 LIB3146-044-Q1-K1-C3 Seq. ID Method BLASTX g3023961 NCBI GI BLAST score 642 E value 2.0e-67 Match length 134 % identity 91 HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi_1946222_emb_CAA96512_ NCBI Description (Z71980) knotted1-like homeobox protein [Malus domestica] Seq. No. 214284 Seq. ID LIB3146-044-Q1-K1-C4 Method BLASTX NCBI GI q3023961 BLAST score 313 E value 7.0e-29 Match length 106 % identity 59 NCBI Description HOMEOBOX PROTEIN KNOTTED-1-LIKE >qi 1946222 emb CAA96512 (Z71980) knotted1-like homeobox protein [Malus domestica] Seq. No. 214285 Seq. ID LIB3146-044-Q1-K1-C5 Method BLASTX NCBI GI g3746069 BLAST score 154

E value 4.0e-10 Match length 94 % identity

NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis

thaliana]

214286 Seq. No.

Seq. ID LIB3146-044-Q1-K1-C8

Method BLASTX NCBI GI g3080389 BLAST score 178 6.0e-13 E value Match length 106



% identity 59

NCBI Description (AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No. 214287
Seq. ID LIB3146-044-Q1-K1-D1
Method BLASTX

NCBI GI g3063396
BLAST score 552
E value 8.0e-57
Match length 121
% identity 85

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 214288

Seq. ID LIB3146-044-Q1-K1-D11

Method BLASTX
NCBI GI g4490728
BLAST score 305
E value 7.0e-28
Match length 92
% identity 61

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 214289

Seq. ID LIB3146-044-Q1-K1-D12

Method BLASTX
NCBI GI g2832661
BLAST score 265
E value 3.0e-23
Match length 83
% identity 64

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 214290

Seq. ID LIB3146-044-Q1-K1-D3

Method BLASTX
NCBI GI g2507617
BLAST score 537
E value 5.0e-55
Match length 139
% identity 73

NCBI Description (U90341) chalcone synthase homolog PrChS1 [Pinus radiata]

Seq. No. 214291

Seq. ID LIB3146-044-Q1-K1-D4

Method BLASTX
NCBI GI g730450
BLAST score 540
E value 2.0e-55
Match length 120
% identity 88

NCBI Description 60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)

>gi_480649_pir__S37134 cold-induced protein BnC24B - rape >gi_398922_emb_CAA80343_ (Z22620) cold induced protein

(BnC24B) [Brassica napus]



214292 Seq. No. Seq. ID LIB3146-044-Q1-K1-D6 Method BLASTX NCBI GI g3687250 360 BLAST score 3.0e-34 E value 82 Match length 80 % identity (AC005169) putative arginine n-methyltransferase NCBI Description [Arabidopsis thaliana] 214293 Seq. No. Seq. ID LIB3146-044-Q1-K1-E12 BLASTX Method q2764941 NCBI GI BLAST score 393 3.0e-38 E value Match length 90 73 % identity (X98255) transcriptionally stimulated by gibberellins; NCBI Description expressed in meristematic region, and style [Arabidopsis thaliana] 214294 Seq. No. Seq. ID LIB3146-044-Q1-K1-F12 Method BLASTX NCBI GI q118825 BLAST score 149 E value 1.0e-09 Match length 58 53 % identity DNA POLYMERASE I (POL I) >gi_67054_pir__DJECI DNA-directed NCBI Description DNA polymerase (EC 2.7.7.7) I - Escherichia coli >gi_42461_emb_CAA23607_ (V00317) DNA polymerase I
[Escherichia coli] >gi_147312 (J01663) DNA polymerase I
[Escherichia coli] >gi_304969 (L19201) DNA polymerase I
[Escherichia coli] >gi_1790294 (AE000461) DNA polymerase I,
3' --> 5' polymerase, 5' --> 3' and 3' --> 5' exonuclease [Escherichia coli] 214295 Seq. No. Seq. ID LIB3146-044-Q1-K1-F2 Method BLASTX g3241943 NCBI GI 149 BLAST score 1.0e-09 E value

46 Match length 67 % identity

(AC004625) hypothetical protein [Arabidopsis thaliana] NCBI Description

214296 Seq. No.

Seq. ID LIB3146-044-Q1-K1-F3

Method BLASTX g2950472 NCBT GT BLAST score 197 E value 3.0e-15



```
Match length
% identity
                  51
                   (AL022070) putative autophagocytosis protein
NCBI Description
                  [Schizosaccharomyces pombe]
Seq. No.
                  214297
                  LIB3146-044-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g3063706
NCBI GI
BLAST score
                  173
                  1.0e-18
E value
Match length
                  59
% identity
                  80
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  214298
Seq. ID
                  LIB3146-044-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2104446
BLAST score
                  136
E value
                  2.0e-13
Match length
                  72
% identity
                  61
NCBI Description
                  (Z95396) WD-repeat protein [Schizosaccharomyces pombe]
Seq. No.
                  214299
Seq. ID
                  LIB3146-044-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2598049
BLAST score
                  391
                  5.0e-38
E value
Match length
                  86
% identity
                  87
                  (Y15269) chloroplast drought-induced stress protein, 34 kD)
NCBI Description
                   [Solanum tuberosum]
                  214300
Seq. No.
Seq. ID
                  LIB3146-044-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g1669341
BLAST score
                  180
E value
                  1.0e-13
Match length
                  82
% identity
                  49
                  (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                   [Cucurbita maxima]
                  214301
Seq. No.
```

Seq. ID LIB3146-044-Q1-K1-G3

BLASTX Method NCBI GI g2501850 BLAST score 727 2.0e-77 E value 139 Match length 96 % identity

NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]



```
Seq. No.
                  214302
Seq. ID
                  LIB3146-044-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1617206
BLAST score
                  403
E value
                  2.0e-39
Match length
                  122
% identity
                  66
NCBI Description
                  (Z72489) CP12 [Pisum sativum]
Seq. No.
                  214303
Seq. ID
                  LIB3146-044-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q3420055
BLAST score
                  416
E value
                  7.0e-41
Match length>
                  ÷101
% identity
                  79
NCBI Description
                  (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  214304
Seq. ID
                  LIB3146-044-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q4335750
BLAST score
                  277
E value
                  1.0e-24
Match length
                  78
                  59
% identity
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
                  214305
Seq. No.
Seq. ID
                  LIB3146-044-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                   359
                   3.0e-34
E value
Match length
                  88
% identity
                  78
                   (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214306
Seq. ID
                  LIB3146-044-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                  150
E value
                   9.0e-10
                   92
Match length
% identity
                   41
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214307
                  LIB3146-044-Q1-K1-H12
```

Seq. ID

BLASTX Method

NCBI GI g4204793 BLAST score 597



```
E value
                  4.0e-62
                  136
Match length
% identity
                  42
                  (U52079) P-glycoprotein [Solanum tuberosum]
NCBI Description
Seq. No.
                  214308
Seq. ID
                  LIB3146-044-Q1-K1-H2
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  214309
Seq. ID
                  LIB3146-044-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q4056437
BLAST score
                  410
E value
                  3.0e-40
Match length
                  120
% identity
NCBI Description
                  (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  214310
Seq. ID
                  LIB3146-044-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2500574
BLAST score
                  157
                  2.0e-10
E value
Match length
                  56
                  27
% identity
NCBI Description
                  NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4
                  >gi 2131274 pir S66820 heterogeneous nuclear
                  ribonucleoprotein HRP1 - yeast (Saccharomyces cerevisiae)
                  >gi 1016290 (U35737) nuclear polyadenylated RNA-binding
                  protein [Saccharomyces cerevisiae]
                  >gi 1420003 emb CAA99142 (Z74865) ORF YOL123w
                   [Saccharomyces cerevisiae] >gi 1550721 emb CAA64546
                   (X95258) RNA binding protein [Saccharomyces cerevisiae]
                  >gi_1657691 (U38535) Hrp1p [Saccharomyces cerevisiae]
Seq. No.
                  214311
Seq. ID
                  LIB3146-044-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g122007
BLAST score
                  348
```

6.0e-33 E value Match length 93 75 % identity

HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley NCBI Description >gi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 214312

```
Seq. ID
                  LIB3146-044-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q2605932
BLAST score
                  539
                  3.0e-55
E value
                  134
Match length
% identity
                  79
                  (AF029898) aspartate aminotransferase [Lotus corniculatus]
NCBI Description
                  214313
Seq. No.
Seq. ID
                  LIB3146-044-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2244900
                  314
BLAST score
                  2.0e-29
E value
Match length
                  74
                  81
% identity
                  (Z97338) similarity to hypothetical protein HYP1 -
NCBI Description
                  Arabidopsis [Arabidopsis thaliana]
                  214314
                  LIB3146-044-Q1-K1-H9
                  BLASTX
```

 Seq. No.
 214344

 Seq. ID
 LIB3146-044-Q1-K1-H9

 Method
 BLASTX

 NCBI GI
 g3294469

 BLAST score
 270

 E value
 4.0e-24

 Match length
 66

 % identity
 85

NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]

214315 Seq. No. Seq. ID LIB3146-046-Q1-K1-A1 Method BLASTX NCBI GI q3914052 BLAST score 543 E value 9.0e-56 Match length 134 80 % identity

NCBI Description DNA MISMATCH REPAIR PROTEIN MSH6 >gi_2104549 (AF001535) AGAA.3 [Arabidopsis thaliana]

AGAA.3 [Arabidopsis thaile

Seq. No. 214316

Seq. ID LIB3146-046-Q1-K1-A10

Method BLASTX
NCBI GI g2924520
BLAST score 628
E value 1.0e-65
Match length 130
% identity 91

NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)

[Arabidopsis thaliana]

Seq. No. 214317

Seq. ID LIB3146-046-Q1-K1-A11

Method BLASTX NCBI GI g1168251 BLAST score 631

Match length

% identity

69

74



```
4.0e-66
E value
                  135
Match length
                  87
% identity
                  PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR
NCBI Description
                  >gi 1076384 pir S46535 probable cysteine proteinase (EC
                  3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment)
                  >gi_516865_emb_CAA52403_ (X74359) putative thiol protease
                  [Arabidopsis thaliana]
Seq. No.
                  214318
Seq. ID
                  LIB3146-046-Q1-K1-A12
Method
                  BLASTX
                  q2501492
NCBI GI
                  576
BLAST score
                  1.0e-59
E value
                  140
Match length
% identity
                  75
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE 2 (UDP-GLUCOSE FLAVONOID
NCBI Description
                  3-O-GLUCOSYLTRANSFERASE 2) >gi 542018 pir S41954
                  UTP-glucose glucosyltransferase - cassava (fragment)
                  >gi_453255_emb_CAA54611_ (X77461) UTP-glucose
                  glucosyltransferase [Manihot esculenta]
                  214319
Seq. No.
                  LIB3146-046-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  q1651862
NCBI GI
BLAST score
                  196
                  4.0e-15
E value
                  132
Match length
                  32
% identity
                  (D90900) lysine decarboxylase [Synechocystis sp.]
NCBI Description
                  214320
Seq. No.
                  LIB3146-046-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337175
                  236
BLAST score
                  9.0e-20
E value
                  69
Match length
                  68
% identity
                  (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
                  214321
Seq. No.
Seq. ID
                  LIB3146-046-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g70753
BLAST score
                  247
                  3.0e-21
E value
```

NCBI Description histone H3 - garden pea >gi 82610 pir S00373 histone H3 -



```
Seq. No.
                  214322
Seq. ID
                  LIB3146-046-Q1-K1-A6
                  BLASTX
Method
                  g2323353
NCBI GI
BLAST score
                  498
E value
                  2.0e-50
Match length
                  118
                  79
% identity
                  (AF015885) anthocyanidin synthase [Callistephus chinensis]
NCBI Description
Seq. No.
                  214323
Seq. ID
                  LIB3146-046-Q1-K1-A7
Method
                  BLASTN
                  g3150006
NCBI GI
BLAST score
                  111
                  2.0e-55
E value
Match length
                  119
% identity
                  44
                  CIC5B11.1 check: 4870 from: 1 to: 167234, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
                  214324
Seq. No.
Seq. ID
                  LIB3146-046-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3980407
BLAST score
                  151
E value
                  8.0e-10
Match length
                  117
% identity
                  32
NCBI Description
                  (AC004561) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  214325
Seq. ID
                  LIB3146-046-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2665890
BLAST score
                  378
                  2.0e-36
E value
Match length
                  90
                  79
% identity
                  (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                  ananassa]
Seq. No.
                  214326
Seq. ID
                  LIB3146-046-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4235430
BLAST score
                  248
E value
                  3.0e-21
                  128
Match length
% identity
                  48
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
```

Seq. No. 214327

Seq. ID LIB3146-046-Q1-K1-B5

Method BLASTX NCBI GI g4388829



BLAST score 298
E value 5.0e-27
Match length 136
% identity 47

NCBI Description (AC006528) putative pol polyprotein with a Zn-finger CCHC

type domain (prosite:QDOC50158) and a DDE integrase

signature motif [Arabidopsis thaliana]

Seq. No. 214328

Seq. ID LIB3146-046-Q1-K1-B6

Method BLASTX
NCBI GI g1617274
BLAST score 408
E value 2.0e-46
Match length 130
% identity 71

NCBI Description (272152) AMP-binding protein [Brassica napus]

Seq. No. 214329

Seq. ID LIB3146-046-Q1-K1-B7

Method BLASTX
NCBI GI g462195
BLAST score 381
E value 8.0e-37
Match length 94
% identity 81

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi_100682_pir__S21636 GOS2 protein - rice

>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]

>gi 3789950 (AF094774) translation initiation factor [Oryza

satīva]

Seq. No. 214330

Seq. ID LIB3146-046-Q1-K1-B9

Method BLASTX
NCBI GI 94204313
BLAST score 277
E value 1.0e-24
Match length 82
% identity 68

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 214331

Seq. ID LIB3146-046-Q1-K1-C1

Method BLASTX
NCBI GI g4049349
BLAST score 212
E value 6.0e-17
Match length 78
% identity 54

NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein

[Arabidopsis thaliana]

Seq. No. 214332

Seq. ID LIB3146-046-Q1-K1-C11

Method BLASTX



```
q3334320
NCBI GI
                  342
BLAST score
                  3.0e-32
E value
                  66
Match length
                  97
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  214333
Seq. ID
                  LIB3146-046-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1771778
BLAST score
                  338
E value
                  7.0e-32
Match length
                  100
% identity
                  73
NCBI Description
                   (X99320) 23 kDa oxygen evolving protein of photosystem II
                   [Solanum tuberosum]
Seq. No.
                  214334
Seq. ID
                  LIB3146-046-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3024501
BLAST score
                  541
E value
                  1.0e-55
Match length
                  131
% identity
NCBI Description
                  RAS-RELATED PROTEIN RAB11C >qi 1370146 emb CAA98179
                   (Z73951) RAB11C [Lotus japonicus]
Seq. No.
                  214335
Seq. ID
                  LIB3146-046-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4139230
BLAST score
                  225
                  2.0e-18
E value
Match length
                  81
% identity
                  52
NCBI Description (AF109243) mismatch repair protein [Arabidopsis thaliana]
Seq. No.
                  214336
Seq. ID
                  LIB3146-046-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g629735
BLAST score
                  248
                  3.0e-21
E value
Match length
                  71
% identity
                  66
NCBI Description
                  fill protein - garden snapdragon >gi 406309 emb CAA40553
                  (X57296) FIL1 [Antirrhinum majus]
Seq. No.
                  214337
```

Seq. ID LIB3146-046-Q1-K1-C8

Method BLASTX NCBI GI g1710780 BLAST score 355 E value 9.0e-34



Match length % identity 80 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433_ NCBI Description (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina] Seq. No. 214338 LIB3146-046-Q1-K1-C9 Seq. ID Method BLASTX NCBI GI g3297818 BLAST score 474 E value 1.0e-47 Match length 135 % identity 70 (AL031032) putative protein [Arabidopsis thaliana] NCBI Description 214339 Seq. No. LIB3146-046-Q1-K1-D1 Seq. ID Method BLASTX NCBI GI q3659907 BLAST score 344 E value 2.0e-32 Match length 104 % identity 68 NCBI Description (AF091857) protein translation factor SUI1 homolog [Pimpinella brachycarpa] 214340 Seq. No. LIB3146-046-Q1-K1-D11 Seq. ID Method BLASTX NCBI GI q3212871 BLAST score 565 E value 2.0e-58 Match length 135 79 % identity NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana] Seq. No. 214341 Seq. ID LIB3146-046-Q1-K1-D12 Method BLASTX NCBI GI g2497492 BLAST score 330 E value 9.0e-31 Match length 131 % identity 58 NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_1653646_dbj_BAA18558_ (D90915) uridine monophosphate kinase [Synechocystis sp.]

214342 Seq. No.

Seq. ID LIB3146-046-Q1-K1-D2

Method BLASTX NCBI GI g4432854 BLAST score 267 E value 2.0e-23 Match length 131

```
% identity
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  214343
Seq. No.
                  LIB3146-046-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  g2660668
NCBI GI
BLAST score
                  146
                  2.0e-10
E value
Match length
                  78
% identity
                  41
                  (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214344
                  LIB3146-046-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377797
BLAST score
                  527
E value
                  7.0e-54
Match length
                  132
                  78
% identity
NCBI Description
                  (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  214345
                  LIB3146-046-Q1-K1-D6
                  BLASTX
                  g4218144
                  249
                  4.0e-31
Match length
                  115
% identity
                  64
```

Seq. ID Method NCBI GI BLAST score E value

(AJ132398) glutathione transferase, GST 10b [Arabidopsis NCBI Description

thaliana]

214346 Seq. No.

Seq. ID LIB3146-046-Q1-K1-D8

BLASTX Method NCBI GI g2827651 BLAST score 263 6.0e-23E value Match length 120 19 % identity

(AL021637) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

214347

LIB3146-046-Q1-K1-D9 Seq. ID

Method BLASTX NCBI GI g3212871 BLAST score 659 2.0e-69 E value Match length 138 88 % identity

(AC004005) putative translation initiation factor NCBI Description

29875

Ţ.,



[Arabidopsis thaliana]

```
214348
Seq. No.
Seq. ID
                  LIB3146-046-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3121825
BLAST score
                   549
                  2.0e-56
E value
Match length
                  120
% identity
                   88
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
Seq. No.
                  214349
Seq. ID
                  LIB3146-046-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g118390
BLAST score
                   165
E value
                  2.0e-11
Match length
                   40
% identity
                  80
NCBI Description
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
                  >gi_2144526_pir__DCZMP pyruvate decarboxylase (EC 4.1.1.1)
                   - maize >gi_22395_emb_CAA42120_ (X59546) pyruvate
                  decarboxylase [Zea mays]
Seq. No.
                  214350
Seq. ID
                  LIB3146-046-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2454184
BLAST score
                  212
E value
                   6.0e-17
Match length
                  53
% identity
                  81
NCBI Description
                   (U80186) pyruvate dehydrogenase El beta subunit
                   [Arabidopsis thaliana]
Seq. No.
                  214351
Seq. ID
                  LIB3146-046-Q1-K1-E5
Method
                  BLASTX
                  g1350720
NCBI GI
BLAST score
                  393
E value
                  3.0e-38
Match length
                  87
                  84
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                  214352
Seq. ID
                  LIB3146-046-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4455342
BLAST score
                  438
E value
                  2.0e-43
Match length
                  133
```

29876

NCBI Description (AL035522) O-methyltransferase-like protein [Arabidopsis

56

% identity

NCBI GI



thaliana]

```
Seq. No.
                   214353
Seq. ID
                   LIB3146-046-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g2352084
BLAST score
                   385
E value
                   3.0e-37
Match length
                   110
% identity
                   72
                   (U96613) serine/threonine kinase [Arabidopsis thaliana]
NCBI Description
                   214354
Seq. No.
Seq. ID
                   LIB3146-046-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g3451074
BLAST score
                   549
E value
                   2.0e-56
Match length
                   131
                   76
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214355
Seq. ID
                   LIB3146-046-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   g1483218
BLAST score
                   196
E value
                   4.0e-15
Match length
                   136
% identity
                   39
                   (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214356
Seq. ID
                   LIB3146-046-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3927836
BLAST score
                   371
                   1.0e-35
E value
Match length
                   94
                   71
% identity
NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
Seq. No.
                   214357
Seq. ID
                   LIB3146-046-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g2431769
BLAST score
                   240
                   3.0e-20
E value
                   107
Match length
                   50
% identity
NCBI Description
                   (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                   214358
Seq. ID
                   LIB3146-046-Q1-K1-F8
Method
                   BLASTX
```

29877

g2244973



```
BLAST score
E value
                  1.0e-36
Match length
                  135
% identity
                  61
NCBI Description
                  (Z97340) similarity to extensin class 1 protein
                  [Arabidopsis thaliana]
Seq. No.
                  214359
Seq. ID
                  LIB3146-046-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q3738329
BLAST score
                  413
E value
                  2.0e-40
Match length
                  129
% identity
                  69
NCBI Description
                  (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                  214360
Seq. ID
                  LIB3146-046-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q2267567
BLAST score
                  395
E value
                  2.0e-38
Match length
                  87
% identity
                  86
NCBI Description
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                  214361
Seq. ID
                  LIB3146-046-Q1-K1-G2
Method
                  BLASTN
NCBI GI
                  g3402745
BLAST score
                  44
E value
                  2.0e-15
Match length
                  72
% identity
                  90
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
NCBI Description
                  (ESSAII project)
Seq. No.
                  214362
Seq. ID
                  LIB3146-046-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2245135
BLAST score
                  423
E value
                  1.0e-41
Match length
                  115
% identity
                  67
NCBI Description
                 (Z97344) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.

214363

Seq. ID LIB3146-046-Q1-K1-G6

Method BLASTX NCBI GI g2129942 BLAST score 404 E value 2.0e-39 Match length 105



```
% identity
                  cathepsin B-like cysteine proteinase (EC 3.4.22.-) - Aztec
NCBI Description
                  tobacco
Seq. No. Seq. ID
                  214364
                  LIB3146-046-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  q3776577
BLAST score
                  440
                  1.0e-43
E value
Match length
                  129
% identity
                  64
NCBI Description (AC005388) T22H22.24 [Arabidopsis thaliana]
                  214365
Seq. No.
                  LIB3146-046-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455207
                                           1,200
BLAST score
                  421
                  2.0e-41
E value
Match length
                  89
% identity
                  89
NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                  214366
                  LIB3146-046-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334299
BLAST score
                  189
                  3.0e-14
E value
Match length
                  41
                  93
% identity
                  PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX ALPHA SUBUNIT) >gi_2315211_emb_CAA74725_ (Y14339)
                  proteasome alpha subunit [Lycopersicon esculentum]
Seq. No.
                  214367
Seq. ID
                  LIB3146-046-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q2370312
BLAST score
                  541
E value
                  1.0e-55
Match length
                   125
                  79
% identity
                  (AJ000995) DnaJ-like protein [Medicago sativa] >gi 3202020
NCBI Description
                   (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]
Seq. No.
                  214368
Seq. ID
                  LIB3146-046-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  155
```

1.0e-14 E value Match length 63 % identity 73

UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)



ubiquitin carrier protein [Lycopersicon esculentum]

214369 Seq. No. Seq. ID LIB3146-046-Q1-K1-H7 Method BLASTX NCBI GI g1369981 BLAST score 193

E value 1.0e-14 Match length 103 37 % identity

NCBI Description (X95609) mec-8 [Caenorhabditis elegans]

>gi 3874374 emb CAB02754 (Z81037) similar to mecanosensory gene mec-8; cDNA EST EMBL: T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk505h10.3 comes from this gene; cDNA EST yk2... >gi 3877217 emb CAB03111 (281084) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST

yk505h10.3 comes from this gene; cDNA EST yk2

214370 Seq. No.

Seq. ID LIB3146-046-Q1-K1-H8

Method BLASTX g1171866 NCBI GI BLAST score 296 8.0e-27 E value Match length 60 % identity

NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR NCBI Description

(COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 214371

LIB3146-047-Q1-K1-A1 Seg. ID

Method BLASTX NCBI GI q417154 BLAST score 628 E value 9.0e-66 Match length 129 % identity 94

HEAT SHOCK PROTEIN 82 >gi_100685 pir S25541 heat shock NCBI Description

protein 82 - rice (strain Taichung Native One)

>gi 20256 emb CAA77978 (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

214372 Seq. No.

Seq. ID LIB3146-047-Q1-K1-A10

BLASTX Method g1843527 NCBI GI BLAST score 372 E value 8.0e-36 Match length 101 74 % identity

NCBI Description (U73747) annexin [Gossypium hirsutum]



```
214373
Seq. No.
                  LIB3146-047-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4008159
BLAST score
                   664
E value
                  5.0e-70
Match length
                  131
                   92
% identity
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
Seq. No.
                  214374
Seq. ID
                  LIB3146-047-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1173256
BLAST score
                   381
                   9.0e-37
E value
Match length
                   97
                   80
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
Seq. No.
                   214375
                  LIB3146-047-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   a3098571
BLAST score
                   221
E value
                   5.0e-18
Match length
                   94
                   44
% identity
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
                   214376
Seq. No.
Seq. ID
                   LIB3146-047-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g3122703
BLAST score
                   297
                   6.0e-27
E value
Match length
                   80
% identity
                   75
                   60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
NCBI Description
                   protein L23a [Fritillaria agrestis]
                   214377
Seq. No.
Seq. ID
                   LIB3146-047-Q1-K1-B1
Method
                   BLASTX
                   q4049354
NCBI GI
BLAST score
                   172
                   3.0e-12
E value
Match length
                   45
                   78
% identity
```

Seq. No. 214378

NCBI Description

29881

2.1.2.1)-like protein [Arabidopsis thaliana]

(AL034567) glycine hydroxymethyltransferase (EC



```
LIB3146-047-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g166949
BLAST score
                  208
                   9.0e-25
E value
Match length
                  139
% identity
                  43
NCBI Description
                   (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea
                  americana]
Seq. No.
                  214379
Seq. ID
                  LIB3146-047-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4455202
BLAST score
                  375
E value
                  4.0e-36
Match length
                  106
% identity
                  61
NCBI Description
                  (AL035440) putative APG protein [Arabidopsis thaliana]
Seq. No.
                  214380
Seq. ID
                  LIB3146-047-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4522007
BLAST score
                  195
E value
                  6.0e-15
Match length
                  103
% identity
                  45
NCBI Description
                  (AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  214381
Seq. ID
                  LIB3146-047-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g417821
BLAST score
                  623
E value
                  4.0e-65
Match length
                  131
% identity
                  88
NCBI Description
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi 322725 pir S31959
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
                  flax >gi 22682 emb CAA50298 (X70962) acyl-[acyl-carrier
                  protein] desaturase; stearoyl-[acyl-carrier protein]
                  desaturase [Linum usitatissimum]
Seq. No.
                  214382
Seq. ID
                  LIB3146-047-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q4455246
BLAST score
                  150
                  5.0e-10
E value
Match length
                  36
                  75
% identity
```

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 214383

Seq. ID LIB3146-047-Q1-K1-B7



BLASTX Method NCBI GI g3695061 BLAST score 537 4.0e-55 E value Match length 124 % identity 84

(AF064788) rac GTPase activating protein 2 [Lotus NCBI Description

japonicus]

Seq. No. 214384

Seq. ID LIB3146-047-Q1-K1-C2

Method BLASTX NCBI GI g122085 BLAST score 503 4.0e-51 E value Match length 119 % identity 85

HISTONE H3 >gi_81641 pir S06250 histone H3 - Arabidopsis NCBI Description

thaliana >gi_82482_pir__504099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__557626 histone H3 - maize >gi_20251_emb_CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168495 (M13378) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]

>gi_168497 (M13379) histone H3 [Zea mays] >gi_168506

(M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738 emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414)

Histone H3 [Asparagus officinalis] $>\overline{gi}_1\overline{16}67592$ (U $\overline{7}7296$) histone 3 [Oryza sativa] >gi 3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb H76511 gb H76255, gb AA712452, gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana]

>qī 225459 prf 1303352A histone H3 [Helicoverpa zea] >gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 214385

LIB3146-047-Q1-K1-C4 Seq. ID

Method BLASTX NCBI GI g2088658 BLAST score 309 E value 2.0e-28 Match length 113 60 % identity

NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

Seq. No. 214386

Seq. ID LIB3146-047-Q1-K1-C5

Method BLASTX NCBI GI q2088658 BLAST score 219



```
6.0e-18
E value
Match length
                    87
% identity
                    54
NCBI Description
                   (AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.
                    214387
Seq. ID
                    LIB3146-047-Q1-K1-C7
Method
                    BLASTX
NCBI GI
                    g3075395
BLAST score
                    562
E value
                    5.0e-58
Match length
                    138
                    77
% identity
                   (AC004484) nodulin-35 homologue [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    214388
Seq. ID
                    LIB3146-047-Q1-K1-D1
Method
                    BLASTX
NCBI GI
                    g4220463
                    306
BLAST score
E value
                    5.0e-28
Match length
                    76
% identity
NCBI Description
                   (AC006216) This gene is cut off. [Arabidopsis thaliana]
Seq. No.
                    214389
Seq. ID
                    LIB3146-047-Q1-K1-D10
Method
                    BLASTX
NCBI GI
                    g464849
BLAST score
                    331
E value
                    4.0e-31
Match length
                    94
% identity
                    69
NCBI Description
                   TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
                    chain - almond >gi 2041\overline{3} emb \overline{CAA47635} (X67162)
                    alpha-tubulin [Prunus dulcis]
Seq. No.
                    214390
Seq. ID
                    LIB3146-047-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                    g2493694
BLAST score
                    262
E value
                    8.0e-23
                    107
Match length
% identity
                    53
NCBI Description
                   PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
                   6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                    of photosystem II [Spinacia oleracea]
```

Seq. No. 214391

Seq. ID LIB3146-047-Q1-K1-D3

Method BLASTX
NCBI GI g2829927
BLAST score 313
E value 7.0e-29
Match length 115



```
% identity 61
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No. 214392
Seq. ID LIB3146-047-Q1-K1-D4
```

Method BLASTX
NCBI GI g464840
BLAST score 723
E value 7.0e-77
Match length 138
% identity 98

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin

alpha-1 chain - fern (Anemia phyllitidis)

>gi 296494 emb CAA48927 (X69183) alpha tubulin [Anemia

phyllitidis]

Seq. No. 214393

Seq. ID LIB3146-047-Q1-K1-D8

Method BLASTX
NCBI GI g3668118
BLAST score 628
E value 9.0e-66
Match length 135
% identity 50

NCBI Description (AJ224078) hypothetical protein [Brassica napus]

Seq. No. 214394

Seq. ID LIB3146-047-Q1-K1-D9

Method BLASTX
NCBI GI g3668118
BLAST score 402
E value 5.0e-60
Match length 138
% identity 50

NCBI Description (AJ224078) hypothetical protein [Brassica napus]

Seq. No. 214395

Seq. ID LIB3146-047-Q1-K1-E3

Method BLASTX
NCBI GI g3023713
BLAST score 382
E value 7.0e-37
Match length 78
% identity 95

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

Seq. No. 214396

Seq. ID LIB3146-047-Q1-K1-E6

Method BLASTX
NCBI GI g2995990
BLAST score 305
E value 7.0e-28
Match length 101
% identity 59

NCBI Description (AF053746) dormancy-associated protein [Arabidopsis





thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

214397 Seq. No. LIB3146-047-Q1-K1-E7 Seq. ID Method BLASTX NCBI GI g2467088 BLAST score 278 E value 1.0e-24 Match length 98 % identity 59 NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana] Seq. No. 214398 LIB3146-047-Q1-K1-F10 Seq. ID Method BLASTX NCBI GI g3063396 BLAST score 518 E value 7.0e-53 Match length 115 % identity 84 NCBI Description (AB012947) vcCyP [Vicia faba] Seq. No. 214399 LIB3146-047-Q1-K1-F11 Seq. ID Method BLASTX NCBI GI q1688072 BLAST score 602 E value 1.0e-62 Match length 137 77 % identity (U41369) biotin holocarboxylase synthetase [Arabidopsis NCBI Description thaliana] Seq. No. Seq. ID 214400 LIB3146-047-Q1-K1-F2 BLASTX Method NCBI GI q1063684 250 BLAST score 1.0e-21 E value 80 Match length % identity 65 (U39072) AtGRP2b [Arabidopsis thaliana] NCBI Description Seq. No. 214401 Seq. ID LIB3146-047-Q1-K1-F3 BLASTX Method NCBI GI g4105772 BLAST score 493 7.0e-50 E value 110 Match length 46 % identity

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No.

214402

Seq. ID LIB3146-047-Q1-K1-F5

Method BLASTX



```
NCBI GI
                   a267120
BLAST score
                   434
                   6.0e-43
E value
Match length
                   132
% identity
NCBI Description
                   THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi 100070 pir S20929
                   thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum
                   satīvum] >gi 1388086 (U35830) thioredoxin f [Pisum sativum]
Seq. No.
Seq. ID
                   LIB3146-047-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q3068704
BLAST score
                   224
E value
                   2.0e-18
Match length
                   57
% identity
                   70
NCBI Description
                  (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   214404
Seq. ID
                   LIB3146-047-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g3023752
BLAST score
                   272
E value
                   5.0e-24
Match length
                   101
% identity
                   57
NCBI Description
                   FERREDOXIN I PRECURSOR >qi 1418982 emb CAA99756 (Z75520)
                   ferredoxin-I [Lycopersicon esculentum]
Seq. No. Seq. ID
                   214405
                   LIB3146-047-Q1-K1-F8
Method
                   BLASTN
NCBI GI
                   g4454587
BLAST score
                   33
E value
                   6.0e-09
Match length
                   164
% identity
                   Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
                   214406
Seq. No.
Seq. ID
                   LIB3146-047-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   q729252
BLAST score
                   170
                   3.0e-12
E value
Match length
                   63
                   52
% identity
                   CYTOCHROME B5 >gi 167140 (M87514) cytochrome b-5 [Brassica
NCBI Description
```

oleracea] >gi 384338 prf 1905426A cytochrome b5 [Brassica

oleracea]

214407 Seq. No.

Seq. ID LIB3146-047-Q1-K1-G12

Method BLASTX



```
NCBI GI
                   q3641837
BLAST score
                   487
E value
                   3.0e-49
                   125
Match length
                   74
% identity
NCBI Description
                   (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   214408
Seq. ID
                   LIB3146-047-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g2262149
BLAST score
                   188
E value
                   3.0e-14
Match length
                   81
% identity
                   57
NCBI Description
                   (AC002330) LUMINIDEPENDENS protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3146-047-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   q100294
BLAST score
                   313
E value
                   8.0e-29
Match length
                   134
                   33
% identity
                  ribonucleoprotein B, 29K - wood tobacco
NCBI Description
                   >gi 14135 emb CAA43428 (X61114) 29kD B ribonucleoprotein
                   [Nicotiana sylvestris]
Seq. No.
                   214410
Seq. ID
                   LIB3146-047-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g2190007
BLAST score
                   162
E value
                   4.0e-11
Match length
                   127
% identity
                   31
NCBI Description
                   (AB004109) phosphatidylserine synthase II [Cricetulus
                   griseus]
                   214411
Seq. No.
Seq. ID
                   LIB3146-047-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   q2827559
BLAST score
                   271
                   6.0e-24
E value
Match length
                   128
```

46 % identity

(AL021635) predicted protein [Arabidopsis thaliana] NCBI Description >gi 3292808 emb CAA19798 (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 214412

Seq. ID LIB3146-047-Q1-K1-G7

Method BLASTX NCBI GI g121353



BLAST score 361 E value 2.0e-34 Match length 102 % identity 73

NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)

(GLUTAMATE-AMMONIA LIGASE) >gi 68596 pir AJFBQD

glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - kidney bean >gi_21005_emb_CAA31234_ (X12738)

GS precursor protein [Phaseolus vulgaris]

Seq. No. 214413

Seq. ID LIB3146-047-Q1-K1-H10

Method BLASTX
NCBI GI g3176690
BLAST score 673
E value 5.0e-71
Match length 132
% identity 96

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 214414

Seq. ID LIB3146-047-Q1-K1-H11

Method BLASTX
NCBI GI g1350720
BLAST score 146
E value 2.0e-13
Match length 79
% identity 57

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 214415

Seq. ID LIB3146-047-Q1-K1-H5

Method BLASTX
NCBI GI g1350720
BLAST score 455
E value 2.0e-45
Match length 111
% identity 77

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 214416

Seq. ID LIB3146-047-Q1-K1-H6

Method BLASTX
NCBI GI g4406819
BLAST score 216
E value 2.0e-17
Match length 87
% identity 52

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 214417

Seq. ID LIB3146-047-Q1-K1-H8

Method BLASTX
NCBI GI g1362066
BLAST score 159



```
9.0e-11
E value
                  49
Match length
% identity
                  61
                  small GTP-binding protein - garden pea
NCBI Description
                  >gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein
                   [Pisum sativum]
                  214418
Seq. No.
Seq. ID
                  LIB3146-048-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g629670
BLAST score
                  486
E value
                  4.0e-49
Match length
                  125
                  74
% identity
NCBI Description hypothetical protein - tomato
Seq. No.
                  214419
                  LIB3146-048-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2104536
BLAST score
                  189
E value
                  2.0e-14
Match length
                  52
% identity
                  65
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214420
Seq. ID
                  LIB3146-048-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4415931
BLAST score
                  437
E value
                  2.0e-43
Match length
                  121
% identity
                  67
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  214421
Seq. ID
                  LIB3146-048-Q1-K1-A9
                  BLASTX
Method
                  g1345785
NCBI GI
BLAST score
                  554
                  4.0e-57
E value
Match length
                  108
% identity
                  98
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                  >gi 567935 dbj BAA05640 (D26593) chalcone synthase
                  [Camellia sinensis]
```

Seq. No. 214422

Seq. ID LIB3146-048-Q1-K1-B1

Method BLASTX NCBI GI g950299 BLAST score 702



```
2.0e-74
· · E value
                     134
  Match length
   % identity
                     95
                      (L46792) xyloglucan endotransglycosylase precursor
   NCBI Description
                      [Actinidia deliciosa]
                     214423
   Seq. No.
   Seq. ID
                     LIB3146-048-Q1-K1-B10
   Method
                     BLASTX
   NCBI GI
                     g629483
   BLAST score
                     186
   E value
                     6.0e-14
  Match length
                     112
   % identity
                     41
   NCBI Description
                     gene 1-Sc3 protein - European white birch
                     >qi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                     >gi^-158432^-pr^-212237^-C allergen Bet v 1-Sc3 [Betula
                     pendula]
   Seq. No.
                     214424
   Seq. ID
                     LIB3146-048-Q1-K1-B11
   Method
                     BLASTX
   NCBI GI
                     q121353
   BLAST score
                     187
   E value
                     2.0e-14
  Match length
                     69
   % identity
                     51
   NCBI Description
                     GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)
                      (GLUTAMATE-AMMONIA LIGASE) >gi 68596 pir AJFBQD
                     glutamate--ammonia ligase (EC 6.3.1.2) delta precursor,
                     chloroplast - kidney bean >gi_21005_emb_CAA31234_ (X12738)
                     GS precursor protein [Phaseolus vulgaris]
   Seq. No.
                     214425
   Seq. ID
                     LIB3146-048-Q1-K1-B4
                     BLASTX
   Method
   NCBI GI
                     q1871192
   BLAST score
                     185
                     8.0e-14
   E value
   Match length
                     61
                     66
   % identity
                      (U90439) Cys3His zinc finger protein isolog [Arabidopsis
   NCBI Description
                     thaliana]
   Seq. No.
                     214426
   Seq. ID
                     LIB3146-048-Q1-K1-C1
                     BLASTX
   Method
   NCBI GI
                     g3717946
   BLAST score
                     328
```

1.0e-30 E value Match length 110 62 % identity

NCBI Description (AJ005901) vag1 [Arabidopsis thaliana]

214427 Seq. No.

Seq. ID LIB3146-048-Q1-K1-C10

Method BLASTX



```
q170753
NCBI GI
BLAST score
                  384
                  5.0e-60
E value
                  136
Match length
                  81
% identity
NCBI Description
                  (M95819) initiation factor (iso) 4F p28 subunit [Triticum
                  aestivum]
                  214428
Seq. No.
                  LIB3146-048-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  578
E value
                  7.0e-60
                  114
Match length
                  92
% identity
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  214429
Seq. No.
                  LIB3146-048-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2506277
BLAST score
                  437
E value
                  2.0e-43
Match length
                  100
% identity
                  88
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi 806808
                  (U21139) chaperonin precursor [Pisum sativum]
Seq. No.
                  214430
                  LIB3146-048-Q1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  214431
Seq. ID
                  LIB3146-048-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4406777
BLAST score
                  238
E value
                  5.0e-20
Match length
                  45
                  96
% identity
NCBI Description
                  (AC006532) putative zinc-finger protein [Arabidopsis
                  thaliana]
Seq. No.
                  214432
```

Seq. ID LIB3146-048-Q1-K1-C6

Method BLASTX
NCBI GI g1001955
BLAST score 450
E value 7.0e-45

```
Match length 115 77 NCBI Description (U19099) unknown protein [Lycopersicon chilense ] Seq. No. 214433
```

 Seq. No.
 214433

 Seq. ID
 LIB3146-048-Q1-K1-C7

 Method
 BLASTX

 NCBI GI
 q4455365

NCBI GI g4455365
BLAST score 373
E value 7.0e-36
Match length 76
% identity 84

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 214434

Seq. ID LIB3146-048-Q1-K1-C8

Method BLASTX
NCBI GI g2501781
BLAST score 377
E value 3.0e-36
Match length 119
% identity 62

NCBI Description (U76501) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 214435

Seq. ID LIB3146-048-Q1-K1-D1

Method BLASTX
NCBI GI g3860315
BLAST score 257
E value 3.0e-22
Match length 60
% identity 80

NCBI Description (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]

Seq. No. 214436

Seq. ID LIB3146-048-Q1-K1-D12

Method BLASTX
NCBI GI g2117726
BLAST score 162
E value 4.0e-11
Match length 32
% identity 91

NCBI Description 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform

SBE2.1 precursor - Arabidopsis thaliana (fragment) >gi_619939 (U18817) starch branching enzyme class II

[Arabidopsis thaliana]

Seq. No. 214437

Seq. ID LIB3146-048-Q1-K1-D2

Method BLASTN
NCBI GI g3334755
BLAST score 53
E value 6.0e-21
Match length 119
% identity 90

NCBI Description Medicago sativa mRNA for putative arginine/serine-rich

splicing factor

NCBI Description



```
Seq. No.
                   214438
Seq. ID
                  LIB3146-048-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                   g1001955
BLAST score
                   417
E value
                   5.0e-41
                   113
Match length
% identity
                   74
                  (U19099) unknown protein [Lycopersicon chilense
NCBI Description
Seq. No.
                   214439
                  LIB3146-048-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  q3834321
NCBI GI
                   297
BLAST score
                   6.0e-27
E value
Match length
                   61
                   97
% identity
NCBI Description
                   (AC005679) Strong similarity to F13P17.9 gi 3337356
                   transport protein SEC61 alpha subunit homolog from
                  Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis
                  thaliana]
Seq. No.
                  214440
Seq. ID
                  LIB3146-048-Q1-K1-D8
Method
                  BLASTX
                   g4056488
NCBI GI
BLAST score
                   392
                   5.0e-38
E value
                   86
Match length
                   77
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214441
                  LIB3146-048-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3341681
BLAST score
                   567
E value
                   1.0e-58
Match length
                   129
                   89
% identity
NCBI Description
                   (AC003672) small GTP-binding protein [Arabidopsis thaliana]
                   >gi 741994 prf 2008312A GTP-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   214442
Seq. ID
                  LIB3146-048-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   q120673
BLAST score
                   544
                  7.0e-56
E value
Match length
                  134
% identity
                  78
```

29894

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia



65

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

% identity

>gi_20551_emb_CAA42904_ (X60346) glyceraldehyde
3-phosphate dehydrogenase [Petunia x hybrida]

```
214443
Seq. No.
                  LIB3146-048-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544404
BLAST score
                  226
                  1.0e-18
E value
                  125
Match length
% identity
NCBI Description
                  (AC007047) unknown protein [Arabidopsis thaliana]
                   214444
Seq. No.
                  LIB3146-048-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                   q399940
NCBI GI
BLAST score
                   532
                   2.0e-54
E value
                   136
Match length
                   78
% identity
                  MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
NCBI Description
                   >gi_100004_pir__S25005 heat shock protein, 70K - kidney
                   bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock
                   protein [Phaseolus vulgaris]
                   214445
Seq. No.
                   LIB3146-048-01-K1-E6
Seq. ID
Method
                   BLASTX
                   g4263703
NCBI GI
                   188
BLAST score
                   3.0e-14
E value
                   43
Match length
% identity
                   74
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214446
                   LIB3146-048-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2119045
BLAST score
                   211
                   5.0e-19
E value
Match length
                   79
                   62
% identity
                   small nuclear ribonucleoprotein U1A - potato
NCBI Description
                   >qi 1050840 emb CAA90282 (Z49990) UlsnRNP-specific
                   protein, U1A [Solanum tuberosum]
                   214447
Seq. No.
                   LIB3146-048-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q3023685
NCBI GI
BLAST score
                   358
E value
                   2.0e-40
                   131
Match length
```



(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)

>gi 1041245 emb CAA63121_ (X92377) enolase [Alnus

glutinosa]

214448 Seq. No.

LIB3146-048-Q1-K1-F11 Seq. ID

Method BLASTX NCBI GI g82426 683 BLAST score 3.0e-72 E value Match length 137 % identity 59

ubiquitin precursor - barley (fragment) NCBI Description

>gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor

(171 aa) [Hordeum vulgare]

214449 Seq. No.

LIB3146-048-Q1-K1-F6 Seq. ID

Method BLASTX NCBI GI g4559358 BLAST score 369 E value 2.0e-35 Match length 89 % identity 78

NCBI Description (AC006585) putative steroid binding protein [Arabidopsis

thaliana]

214450 Seq. No.

Seq. ID LIB3146-048-Q1-K1-F9

Method BLASTX q136739 NCBI GI BLAST score 662 E value 9.0e-70 Match length 138 93 % identity

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >qi 218001 dbj BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 214451

LIB3146-048-Q1-K1-G10 Seq. ID

Method BLASTX g4538927 NCBI GI 238 BLAST score E value 5.0e-20 Match length 80 % identity 56

(AL049483) putative peroxidase [Arabidopsis thaliana] NCBI Description

214452 Seq. No.

Seq. ID LIB3146-048-Q1-K1-G11

BLASTXMethod NCBI GI g1657950 BLAST score 627 E value 1.0e-65



```
Match length
% identity
                  89
NCBI Description (U73467) MipE [Mesembryanthemum crystallinum]
Seq. No.
                  214453
Seq. ID
                  LIB3146-048-Q1-K1-G3
Method
                  BLASTX
                  g3478700
NCBI GI
BLAST score
                  390
                  8.0e-38
E value
                  89
Match length
                  84
% identity
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
                  214454
Seq. No.
Seq. ID
                  LIB3146-048-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g100226
                  249
BLAST score
                  3.0e-21
E value
                  129
Match length
% identity
                  42
NCBI Description
                  hypothetical protein - tomato >gi 19275 emb CAA78112
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                  214455
Seq. ID
                  LIB3146-048-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3738309
BLAST score
                  338
                  1.0e-31
E value
                  93
Match length
                  70
% identity
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  214456
Seq. ID
                  LIB3146-048-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g577503
BLAST score
                  376
                  4.0e-36
E value
Match length
                  134
                  57
% identity
NCBI Description (L37790) cationic peroxidase [Stylosanthes humilis]
Seq. No.
                  214457
Seq. ID
                  LIB3146-048-Q1-K1-H12
Method
                  BLASTX
                  g3319882
NCBI GI
BLAST score
                  616
E value
                  2.0e-64
                  130
Match length
                  92
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
```

New Parks

29897

arietinum]



Seq. No. 214458 Seq. ID LIB3146-048-Q1-K1-H4 Method BLASTX NCBI GI g1008904 BLAST score 718 E value 3.0e-76 Match length 136 % identity 96 (L43094) xyloglucan endotransglycosylase [Tropaeolum majus] NCBI Description Seq. No. 214459 Seq. ID LIB3146-048-Q1-K1-H6 Method BLASTX NCBI GI a217855 BLAST score 498 2.0e-50 E value Match length 134 % identity 75 NCBI Description (D00710) heat-shock protein [Arabidopsis thaliana] Seq. No. 214460 Seq. ID LIB3146-048-Q1-K1-H9 Method BLASTX NCBI GI g2894601 BLAST score 177 E value 8.0e-13 Match length . 97 % identity 41 (AL021889) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 214461 Seq. ID LIB3146-049-Q1-K1-A1 Method BLASTX NCBI GI q99749 BLAST score 364 E value 7.0e-35 Match length 106 75 % identity probable serine/threonine-specific protein kinase ATPK64 NCBI Description (EC 2.7.1.-) - Arabidopsis thaliana >gi_217843_dbj_BAA01731_ (D10937) protein kinase [Arabidopsis thaliana] Seq. No. 214462 Seq. ID LIB3146-049-Q1-K1-A4 Method BLASTX NCBI GI q1086252 BLAST score 335 E value 2.0e-31 Match length 125 % identity 54 NCBI Description sucrose cleavage protein - Potato >gi 707001 bbs 157931

29898

[Solanum tuberosum]

(\$74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]



Seq. No. 214463

Seq. ID LIB3146-049-Q1-K1-A5

Method BLASTX
NCBI GI g118514
BLAST score 243
E value 1.0e-20
Match length 45
% identity 100

NCBI Description TURGOR-RESPONSIVE PROTEIN 26G >gi 100051 pir S11863

aldehyde dehydrogenase homolog - garden pea

>gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum

satīvum]

Seq. No. 214464

Seq. ID LIB3146-049-Q1-K1-A8

Method BLASTX
NCBI GI g1619946
BLAST score 203
E value 7.0e-16
Match length 89
% identity 46

NEBI Description (U71300) snRNA activating protein complex 50kD subunit

[Homo sapiens] >gi_4097682 (U66413) proximal sequence element-binding transcription factor beta subunit [Homo sapiens] >gi 4507105 ref NP 003075.1 pSNAPC3 small nuclear

RNA activating complex, polypeptide 3, 50kD

Seq. No. 214465

Seq. ID LIB3146-049-Q1-K1-B1

Method BLASTX
NCBI GI g3122258
BLAST score 371
E value 1.0e-35
Match length 90
% identity 81

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) (B4

INTEGRIN INTERACTOR) (CAB) >gi_2809383 (AF022229)
translation initiation factor 6 [Homo sapiens]

>gi_2910997_emb_CAA72243_ (Y11435) b4 integrin interactor
[Homo sapiens] >gi_3335506 (AF047433) b(2)gcn homolog [Homo sapiens] >gi_4504771 ref_NP_002203.1_pITGB4BP_ integrin

beta 4 binding protein

Seq. No. 214466

Seq. ID LIB3146-049-Q1-K1-B10

Method BLASTX
NCBI GI g3236235
BLAST score 490
E value 1.0e-49
Match length 127
% identity 72

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

>gi 4056501 (AC005896) unknown protein [Arabidopsis

thaliana]

Seq. No. 214467

Seq. ID LIB3146-049-Q1-K1-B11

Method

BLASTX



```
BLASTX
Method
                  q488571
NCBI GI
BLAST score
                   246
                   6.0e-21
E value
Match length
                   52
% identity
                  92
                  (U09462) histone H3.2 [Medicago sativa]
NCBI Description
Seq. No.
                   214468
Seq. ID
                  LIB3146-049-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1019946
BLAST score
                   545
E value
                   5.0e-56
Match length
                   128
                   80
% identity
NCBI Description
                  (U37060) ascorbate peroxidase [Gossypium hirsutum]
Seq. No.
                   214469
Seq. ID
                   LIB3146-049-Q1-K1-B3
Method
                   BLASTN
NCBI GI
                   q3335331
BLAST score
                   76
E value
                   1.0e-34
Match length
                   156
                   87
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   214470
Seq. ID
                   LIB3146-049-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g3334115
BLAST score
                   666
E value
                   3.0e-70
Match length
                   138
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
Seq. No.
                   214471
Seq. ID
                   LIB3146-049-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g2135893
BLAST score
                   230
                   4.0e-19
E value
                   86
Match length
% identity
                   53
                  peptidylprolyl isomerase (EC 5.2.1.8) A - human
NCBI Description
                   >gi 4406227 gb AAD19906 (AF104012) peptidyl-prolyl
                   cis-trans isomerase E [Homo sapiens]
                   214472
Seq. No.
Seq. ID
                   LIB3146-049-Q1-K1-B9
```



```
q4455129
NCBI GI
                  160
BLAST score
                  7.0e-11
E value
                  60
Match length
% identity
                  53
NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
                  214473
Seq. No.
                  LIB3146-049-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2943792
BLAST score
                  665
E value
                  4.0e-70
Match length
                  134
% identity
                  83
NCBI Description (AB006809) PV72 [Cucurbita sp.]
Seq. No.
                  214474
                  LIB3146-049-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3402758
BLAST score
                  157
E value
                  2.0e-10
Match length
                   93
                   43
% identity
                   (AL031187) serine/threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214475
Seq. ID
                  LIB3146-049-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3721926
BLAST score
                   333
                   4.0e-31
E value
Match length
                   81
% identity
                   83
                  (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
NCBI Description
Seq. No.
                   214476
                   LIB3146-049-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3193314
NCBI GI
                   379
BLAST score
                   2.0e-36
E value
Match length
                   136
% identity
                   55
                   (AF069299) contains similarity to Arabidopsis scarecrow
NCBI Description
                   (GB:U62798) [Arabidopsis thaliana]
Seq. No.
                   214477
Seq. ID
                   LIB3146-049-Q1-K1-C5
                   BLASTX
Method
                   g4406780
NCBI GI
                   527
BLAST score
                   6.0e-54
E value
Match length
                   128
```

29901

81

% identity



```
(AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  214478
Seq. No.
Seq. ID
                  LIB3146-049-Q1-K1-C6
Method
                  BLASTN
                  g18058
NCBI GI
BLAST score
                  65
                  4.0e-28
E value
Match length
                  77
                  96
% identity
                  Citrus limon cistron for 26S ribosomal RNA
NCBI Description
                  214479
Seq. No.
                  LIB3146-049-Q1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204575
                  270
BLAST score
                  9.0e-24
E value
                   90
Match length
                   63
% identity
MCBI Description
                  (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
Seq. No.
                   214480
                  LIB3146-049-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2662415
BLAST score
                   173
                   2.0e-12
E value
Match length
                   56
% identity
                   54
                  (U97494) metallothionein-like protein [Prunus armeniaca]
NCBI Description
                   214481
Seq. No.
Seq. ID
                   LIB3146-049-Q1-K1-D10
                  BLASTX
Method
                   q3334405
NCBI GI
BLAST score
                   438
                   1.0e-43
E value
                   117
Match length
                   78
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                   >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
Seq. No.
                   214482
                   LIB3146-049-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                   q4335755
NCBI GI
BLAST score
                   231
                   3.0e-19
E value
```

115 Match length 48 % identity

(AC006284) putative hydroxyproline-rich glycoprotein NCBI Description

[Arabidopsis thaliana]

214483 Seq. No.

E value

Match length

8.0e-33

89



```
LIB3146-049-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2894610
BLAST score
                  318
                  2.0e-29
E value
                  78
Match length
                  72
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  214484
Seq. ID
                  LIB3146-049-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2262113
BLAST score
                  318
                  2.0e-29
E value
Match length
                  84
% identity
                  70
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                  214485
Seq. No.
Seq. ID
                  LIB3146-049-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3643608
BLAST score
                  391
E value
                  6.0e-38
Match length
                  127
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                  214486
Seq. No.
Seq. ID
                  LIB3146-049-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q99600
BLAST score
                  674
                  3.0e-71
E value
Match length
                  126
                  99
% identity
NCBI Description chlorophyll a/b-binding protein - upland cotton
Seq. No.
                  214487
Seq. ID
                  LIB3146-049-Q1-K1-E10
Method
                  BLASTN
NCBI GI
                  g2865522
BLAST score
                  34
                  1.0e-09
E value
Match length
                  42
                  95
% identity
NCBI Description Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
                  complete cds
Seq. No.
                  214488
Seq. ID
                  LIB3146-049-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  347
```

Match length % identity

87

```
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   214489
Seq. ID
                  LIB3146-049-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4490295
BLAST score
                  207
                   2.0e-16
E value
Match length
                   92
% identity
                   37
NCBI Description
                  (AL035678) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   214490
Seq. ID
                  LIB3146-049-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1169128
BLAST score
                   325
E value
                   3.0e-30
Match length
                   88
% identity
                   72
                  SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789)
NCBI Description
                  protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                   214491
Seq. ID
                  LIB3146-049-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4102600
BLAST score
                  374
E value
                   6.0e-36
Match length
                  93
% identity
                  82
NCBI Description
                  (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                  214492
Seq. ID
                  LIB3146-049-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3695061
BLAST score
                  267
E value
                  2.0e-23
Match length
                  136
% identity
                  51
NCBI Description
                   (AF064788) rac GTPase activating protein 2 [Lotus
                  japonicus]
Seq. No.
                  214493
Seq. ID
                  LIB3146-049-Q1-K1-F6
                  BLASTN
Method
NCBI GI
                  g2656028
BLAST score
                  35
E value
                  3.0e-10
                  75
```

29904

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



214494 Seq. No. Seq. ID LIB3146-049-Q1-K1-G1 ${\tt BLASTX}$ Method NCBI GI g2813966 BLAST score 149 E value 1.0e-09 94 Match length % identity 38 (Z97053) placental protein Diff33 [Homo sapiens] NCBI Description >qi 4545219 gb AAD22448.1 (AF112227) TDE homolog [Homo sapiens] Seq. No. 214495 Seq. ID LIB3146-049-Q1-K1-G2 Method BLASTX NCBI GI g3033384 294 BLAST score 1.0e-26 E value 77 Match length % identity 69 NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana] Seq. No. 214496 Seq. ID LIB3146-049-Q1-K1-G3 Method BLASTX NCBI GI q3980378 BLAST score 630 5.0e-66 E value Match length 131 87 % identity NCBI Description (AC004561) putative RNA binding protein [Arabidopsis thaliana] 214497 Seq. No. Seq. ID LIB3146-049-Q1-K1-G4 Method BLASTX NCBI GI g2507443 262 BLAST score 6.0e-23 E value Match length 95 79 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) (23 NCBI Description KD CALLUS PROTEIN) (P23) >gi 1675196 (L47968) callus protein P23 [Pisum sativum] Seq. No. 214498 Seq. ID LIB3146-049-Q1-K1-G7 Method BLASTX NCBI GI g2911068 BLAST score 411 E value

2.0e-40 Match length 85 % identity

NCBI Description (AL021960) G10 - like protein [Arabidopsis thaliana]



```
214499
Seq. No.
                  LIB3146-049-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                  q3327271
NCBI GI
BLAST score
                  422
                  1.0e-41
E value
Match length
                  109
% identity
                  70
                  (AB016000) PKn2 [Ipomoea nil]
NCBI Description
                  214500
Seq. No.
                  LIB3146-049-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  q1161167
NCBI GI
BLAST score
                  314
E value
                  7.0e-29
                  101
Match length
                  53
% identity
                  (L42466) ethylene-forming enzyme [Picea glauca]
NCBI Description
                  214501
Seq. No.
                  LIB3146-049-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4455351
NCBI GI
BLAST score
                  172
                  3.0e-12
E value
                  48
Match length
                   65
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   214502
Seq. No.
                  LIB3146-049-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3024126
BLAST score
                   631
E value
                   4.0e-66
Match length
                   139
                   89
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi 1655576 emb CAA95856 (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
Seq. No.
                   214503
                   LIB3146-049-Q1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g125887
BLAST score
                   168
E value
                   8.0e-12
Match length
                   93
% identity
                   37
```

ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR NCBI Description

> >qi 82092 pir S04765 LAT52 protein precursor - tomato >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 214504

Seq. No.

Seq. ID

214509

LIB3146-050-Q1-K1-A4



```
LIB3146-049-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2623618
BLAST score
                  145
E value
                   4.0e-09
                   123
Match length
% identity
                   32
NCBI Description
                   (AF028243) GTPase activating protein RanGAP1
                   [Strongylocentrotus purpuratus]
                   214505
Seq. No.
Seq. ID
                  LIB3146-050-Q1-K1-A10
Method
                  BLASTN
NCBI GI
                   g18644
BLAST score
                   41
                   6.0e-14
E value
Match length
                   71
% identity
                   90
NCBI Description Soybean mRNA for HMG-1 like protein
Seq. No.
                   214506
Seq. ID
                   LIB3146-050-Q1-K1-A11
Method
                   BLASTX
                   g4455349
NCBI GI
BLAST score
                   238
E value
                   3.0e-20
Match length
                   100
% identity
                   56
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   214507
Seq. ID
                   LIB3146-050-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g122070
BLAST score
                   291
                   2.0e-26
E value
                   79
Match length
                   77
% identity
                  HISTONE H3 >gi 82483 pir A25564 histone H3 - rice
NCBI Description
                   >gi 169793 (M1\overline{5}664) \overline{h}istone 3 [Oryza sativa] >gi_940018
                   (U25664) histone H3 [Oryza sativa]
Seq. No.
                   214508
Seq. ID
                   LIB3146-050-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                   g2493321
BLAST score
                   248
                   1.0e-21
E value
Match length
                   53
                   83
% identity
                  L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)
NCBI Description
                   >gi 2129952 pir S66353 L-ascorbate oxidase (EC 1.10.3.3)
                   precursor - common tobacco >gi_599594_dbj_BAA07734
                   (D43624) ascorbate oxidase precursor [Nicotiana tabacum]
```

BLAST score

Match length

% identity

E value

179

42

76

2.0e-13



```
BLASTX
Method
NCBI GI
                  g2335100
BLAST score
                  352
                  1.0e-33
E value
Match length
                  87
                  72
% identity
                  (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
                  214510
Seq. No.
                  LIB3146-050-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g4510377
NCBI GI
                   409
BLAST score
                   2.0e-40
E value
                  95
Match length
% identity
                   82
                  (AC007017) putative RNA helicase A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214511
Seq. ID
                  LIB3146-050-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                   43821780
BLAST score
                   36
                   2.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   214512
Seq. ID
                   LIB3146-050-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                   g4098126
BLAST score
                   70
E value
                   1.0e-31
Match length
                   70
                   100
% identity
                  Gossypium hirsutum sucrose synthase mRNA, partial cds
NCBI Description
Seq. No.
                   214513
Seq. ID
                  LIB3146-050-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                   g3367568
BLAST score
                  515
E value
                   1.0e-52
Match length
                   107
                   87
% identity
                   (ALO31135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214514
Seq. ID
                   LIB3146-050-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                   g1052956
```

Seq. No.

Seq. ID

214520

LIB3146-050-Q1-K1-C8



```
(U39747) high mobility group protein 2 HMG2 [Ipomoea nil]
NCBI Description
Seq. No.
                   214515
Seq. ID
                   LIB3146-050-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g3935169
BLAST score
                   250
                   1.0e-21
E value
                   55
Match length
% identity
                   89
                   (AC004557) F17L21.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214516
Seq. ID
                   LIB3146-050-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g4335750
BLAST score
                   178
                   3.0e-13
E value
Match length
                   52
% identity
                   58
NCBI Description
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
                   thalianal
Seq. No.
                   214517
Seq. ID
                   LIB3146-050-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q1332579
BLAST score
                   377
                   1.0e-36
E value
Match length
                   80
% identity
NCBI Description
                   (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   214518
Seq. ID
                   LIB3146-050-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   q4138581
BLAST score
                   284
                   1.0e-25
E value
Match length
                   96
                   55
% identity
NCBI Description
                   (X98474) mitochondrial energy transfer protein [Solanum
                   tuberosum]
Seq. No.
                   214519
Seq. ID
                   LIB3146-050-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2244993
BLAST score
                   217
E value
                   8.0e-18
Match length
                   87
                   55
% identity
NCBI Description
                   (Z97341) similarity to AMP-activated protein kinase beta
                   [Arabidopsis thaliana]
```



```
Method
NCBI GI
                  q3643090
BLAST score
                  306
E value
                  1.0e-28
Match length
                  94
% identity
                  64
NCBI Description
                  (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum
                  crystallinum]
Seq. No.
                  214521
Seq. ID
                  LIB3146-050-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  253
E value
                  6.0e-22
Match length
                  105
% identity
                  45
NCBI Description
                  (AC005967) unknown protein [Arabidopsis thaliana]
                  214522
Seq. No.
                  LIB3146-050-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462763
BLAST score
                  140
                  7.0e-09
E value
Match length
                  89
% identity
                  40
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  214523
Seq. ID
                  LIB3146-050-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q130720
BLAST score
                  210
E value
                  4.0e-17
Match length
                  85
                  47
% identity
NCBI Description
                  PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable
                  H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein
                  - yeast (Saccharomyces cerevisiae) >gi 172221 (M35294)
                  proteolipid protein of proton ATPase [Saccharomyces
                  cerevisiae] >gi_500700 (U10399) Ppalp: Proteolipid protein
                  of proton ATPase [Saccharomyces cerevisiae]
Seq. No.
                  214524
Seq. ID
                  LIB3146-050-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3249084
BLAST score
                  411
```

E value 2.0e-40 Match length 105 % identity 31

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene

gb X92750 from Mus musculus. ESTs qb AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. ID

Method



```
214525
Seq. No.
                  LIB3146-050-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g3063471
NCBI GI
BLAST score
                  301
                  1.0e-27
E value
                  82
Match length
                  67
% identity
                  (AC003981) F22013.33 [Arabidopsis thaliana]
NCBI Description
                  214526
Seq. No.
                  LIB3146-050-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  387
                   8.0e-38
E value
Match length
                  75
% identity
                   51
                  CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
NCBI Description
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                   214527
Seq. ID
                  LIB3146-050-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                   q3882171
BLAST score
                   148
E value
                   9.0e-10
Match length
                   51
% identity
                   49
                  (AB018268) KIAA0725 protein [Homo sapiens]
NCBI Description
                   214528
Seq. No.
Seq. ID
                   LIB3146-050-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   g3894171
                   357
BLAST score
                   3.0e-34
E value
Match length
                   87
% identity
                   72
                   (AC005312) putative glutathione s-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   214529
Seq. No.
Seq. ID
                   LIB3146-050-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g452357
BLAST score
                   165
                   9.0e-12
E value
                   44
Match length
% identity
                   82
                   (Z29591) quanine nucleotide regulatory protein [Vicia faba]
NCBI Description
                   >gi 1098294 prf 2115367B small GTP-binding protein [Vicia
                   faba]
                   214530
Seq. No.
```

29911

LIB3146-050-Q1-K1-E11

BLASTX



```
q2760326
NCBI GI
BLAST score
                  154
                  2.0e-10
E value
                  78
Match length
                  41
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.
                  214531
                  LIB3146-050-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2809326
                  365
BLAST score
E value
                  4.0e-35
Match length
                  92
                  79
% identity
NCBI Description (U72663) uricase II [Phaseolus vulgaris]
                  214532
Seq. No.
                  LIB3146-050-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g303742
MLAST score
                  263
                  3.0e-23
E value
                  55
Match length
% identity
                  96
                  (D12544) GTP-binding protein [Pisum sativum]
NCBI Description
                  >gi 738936 prf 2001457D GTP-binding protein [Pisum
                  sativum]
Seq. No.
                  214533
                  LIB3146-050-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  g2980793
NCBI GI
BLAST score
                  349
                  3.0e-33
E value
Match length
                  85
% identity
                  73
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214534
                  LIB3146-050-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g1778093
NCBI GI
                   341
BLAST score
E value
                   3.0e-32
Match length
                   83
                   77
% identity
                   (U64902) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   214535
Seq. No.
Seq. ID
                   LIB3146-050-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                   g1706107
BLAST score
                   166
```

29912

8.0e-12

E value



```
Match length
   % identity
                      CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
   NCBI Description
                      >gi 1143709 (U13630) chloroplast phosphate/triose-phosphate
                      translocator precursor [Brassica oleracea]
   Seq. No.
                      214536
                      LIB3146-050-Q1-K1-G12
   Seq. ID
   Method
                      BLASTN
   NCBI GI
                      q2980787
   BLAST score
                      39
   E value
                      1.0e-12
   Match length
                      75
   % identity
                      88
                      Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
   NCBI Description
                      (ESSAII project)
                      214537
   Seq. No.
                      LIB3146-050-Q1-K1-G2
   Seq. ID
   Method
                      BLASTX
  .NCBI GI
                      g3004560
BLAST score
                      271
                      4.0e-24
   E value
   Match length
                      67
   % identity
                      76
                      (AC003673) putative ATP binding protein [Arabidopsis
   NCBI Description
                      thaliana]
   Seq. No.
                      214538
                      LIB3146-050-Q1-K1-G6
   Seq. ID
                      BLASTX
   Method
   NCBI GI
                      q4406759
   BLAST score
                      188
   E value
                      4.0e-16
                      90
   Match length
    % identity
                      62
   NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                      214539
                      LIB3146-050-Q1-K1-G9
    Seq. ID
   Method
                      BLASTX
    NCBI GI
                      g4467147
   BLAST score
                      260
   E value
                      8.0e-23
   Match length
                      92
                      55
    % identity
    NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
    Seq. No.
                      214540
                      LIB3146-050-Q1-K1-H10
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      q4262149
    BLAST score
                      334
                      2.0e-31
    E value
    Match length
                      83
                      75
    % identity
```

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29913

NCBI Description (AC005275) putative xyloglucan endotransglycosylase

NCBI Description



[Arabidopsis thaliana]

```
214541
Seq. No.
Seq. ID
                  LIB3146-050-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  g2244993
                  189
BLAST score
                  1.0e-14
E value
                  74
Match length
% identity
                  57
                   (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  214542
Seq. ID
                  LIB3146-050-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2642157
BLAST score
                  401
                  2.0e-39
E value
Match length
                  84
% identity
                  83
NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  214543
                  LIB3146-050-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643090
BLAST score
                  372
                  5.0e-36
E value
Match length
                   94
                  74
% identity
                   (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  214544
Seq. ID
                  LIB3146-050-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                  g122070
BLAST score
                   394
                  1.0e-38
E value
Match length
                   79
                   100
% identity
                  HISTONE H3 >gi_82483_pir__A25564 histone H3 - rice
NCBI Description
                  >gi 169793 (M15664) histone 3 [Oryza sativa] >gi 940018
                   (U2\overline{5}664) histone H3 [Oryza sativa]
Seq. No.
                   214545
Seq. ID
                  LIB3146-051-Q1-K1-A1
                  BLASTX
Method
NCBI GI
                   g4210504
BLAST score
                   469
E value
                   4.0e-47
Match length
                   134
                   69
% identity
                   (AC002392) putative cadmium-transporting ATPase
```

[Arabidopsis thaliana]

```
Seq. No.
                   214546
Seq. ID
                   LIB3146-051-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   q1856971
BLAST score
                   249
E value
                   2.0e-21
Match length
                   53
                   92
% identity
                  (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
Seq. No.
                   214547
Seq. ID
                   LIB3146-051-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   a3264828
BLAST score
                   624
```

E value 3.0e-65 Match length 124 % identity

NCBI Description (AF072404) cotton fiber expressed protein 1 [Gossypium

hirsutum]

Seq. No. 214548 LIB3146-051-Q1-K1-A5 Seq. ID Method BLASTX g4467095 NCBI GI BLAST score 280 E value 6.0e-25 Match length 132

% identity 43

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 214549

Seq. ID LIB3146-051-Q1-K1-A7

Method BLASTX NCBI GI q3947448 BLAST score 158 E value 9.0e-11 Match length 117 % identity

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3

comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 214550

Seq. ID LIB3146-051-Q1-K1-B1

Method BLASTX NCBI GI g1666173 BLAST score 443 E value 4.0e-44



```
Match length 94 % identity 94
```

NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No. 214551

Seq. ID LIB3146-051-Q1-K1-B12

Method BLASTX
NCBI GI g4115940
BLAST score 242
E value 2.0e-20
Match length 101
% identity 44

NCBI Description (AF118223) contains similarity to sugar (and other) transporters (Pfam: PF00083, score=20.4, E=2.6e-06, N=1

[Arabidopsis thaliana]

Seq. No. 214552

Seq. ID LIB3146-051-Q1-K1-B4

Method BLASTX
NCBI GI g3297819
BLAST score 654
E value 8.0e-69
Match length 130
% identity 94

NCBI Description (AL031032) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 214553

Seq. ID LIB3146-051-Q1-K1-B7

Method BLASTN
NCBI GI g2062705
BLAST score 37
E value 2.0e-11
Match length 50
% identity 40

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 214554

Seq. ID LIB3146-051-Q1-K1-B9

Method BLASTX
NCBI GI g4406766
BLAST score 181
E value 2.0e-13
Match length 71
% identity 49

NCBI Description (AC006836) putative flavonol sulfotransferase [Arabidopsis

thaliana]

Seq. No. 214555

Seq. ID LIB3146-051-Q1-K1-C12

Method BLASTX
NCBI GI g2738998
BLAST score 507
E value 2.0e-51
Match length 134
% identity 76

NCBI Description (AF022458) CYP98A2p [Glycine max]



```
214556
 Seq. No.
                    LIB3146-051-Q1-K1-C4
  Seq. ID
 Method
                    BLASTX
                    g1351856
 NCBI GI
                    332
 BLAST score
                    2.0e-31
 E value
                    69
 Match length
                    91
  % identity
                    ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
 NCBI Description
                    (ACONITASE) >gi 868003 dbj BAA06108_ (D29629) aconitase
                    [Cucurbita sp.]
                    214557
  Seq. No.
                    LIB3146-051-Q1-K1-C5
  Seq. ID
  Method
                    BLASTX
                    q441457
  NCBI GI
                    624
  BLAST score
                    2.0e-65
  E value
                    116
 Match length
                    97
  % identity
NCBI Description
                    (X73419) ubiquitin conjugating enzyme E2 [Lýcopersicon
                    esculentum]
                    214558
  Seq. No.
                    LIB3146-051-Q1-K1-C6
  Seq. ID
                    BLASTX
  Method
                    g119355
  NCBI GI
  BLAST score
                    301
                    2.0e-27
  E value
                    71
  Match length
  % identity
                     85
                    ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
  NCBI Description
                     (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                     >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                     4.2.1.11) - maize >gi 22273_emb_CAA39454_ (X55981) enolase
                     [Zea mays]
                     214559
  Seq. No.
                     LIB3146-051-Q1-K1-C8
  Seq. ID
                     BLASTX
  Method
                     q4006827
  NCBI GI
                     346
  BLAST score
  E value
                     1.0e-32
                     94
  Match length
                     69
  % identity
  NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]
                     214560
  Seq. No.
                     LIB3146-051-Q1-K1-D10
  Seq. ID
  Method
                     BLASTX
                     g2286153
  NCBI GI
                     657
  BLAST score
                     4.0e-69
  E value
                     133
  Match length
                     97
  % identity
  NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
```

NCBI Description



```
214561
  Seq. No.
                      LIB3146-051-Q1-K1-D12
  Seq. ID
  Method
                      BLASTX
                      g3540184
  NCBI GI
                      513
  BLAST score
                      3.0e-52
  E value
                      133
  Match length
                      72
  % identity
                      (AC004122) Similar to endoxylanases [Arabidopsis thaliana]
  NCBI Description
                      214562
  Seq. No.
                      LIB3146-051-Q1-K1-D2
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      g3413424
  BLAST score
                       274
                       3.0e-24
  E value
                       113
  Match length
                       43
  % identity
                      (AJ006309) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
Seq. No.
                       214563
                       LIB3146-051-Q1-K1-D3
  Seq. ID
                       BLASTX
  Method
                       q1702983
  NCBI GI
  BLAST score
                       233
                       3.0e-24
  E value
  Match length
                       98
                       59
   % identity
                       AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855_pir__S11850
   NCBI Description
                      hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein
                       [Fragaria ananassa]
                       214564
   Seq. No.
                       LIB3146-051-Q1-K1-D4
   Seq. ID
                       BLASTX
   Method
                       g2271477
   NCBI GI
   BLAST score
                       587
   E value
                       6.0e-61
                       124
   Match length
   % identity
                       91
                      (AF009631) AP47/50p [Arabidopsis thaliana]
   NCBI Description
                       214565
   Seq. No.
                       LIB3146-051-Q1-K1-D5
   Seq. ID
   Method
                       BLASTX
   NCBI GI
                       g3023713
   BLAST score
                       444
   E value
                       2.0e-44
   Match length
                       94
                       90
   % identity
```

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372

ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(U09450) enolase [Oryza sativa]



```
214566
Seq. No.
                  LIB3146-051-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g4218187
NCBI GI
BLAST score
                  251
E value
                  1.0e-21
                  82
Match length
% identity
                  39
                  (AJ010165) leghemoglobin activating factor [Glycine max]
NCBI Description
Seq. No.
Seq. ID
                  LIB3146-051-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2995990
BLAST score
                  244
E value
                   6.0e-21
Match length
                  82
% identity
                   60
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
Seq. No.
                   214568
Seq. ID
                  LIB3146-051-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                   q3641868
BLAST score
                   348
E value
                   5.0e-33
Match length
                   95
                   72
% identity
                  (AJ011012) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                   214569
                   LIB3146-051-Q1-K1-E5
Seq. ID
Method
                   BLASTX
                   g1709970
NCBI GI
BLAST score
                   371
                   1.0e-35
E value
Match length
                   109
% identity
                   68
                   60S RIBOSOMAL PROTEIN L10A
NCBI Description
                   214570
Seq. No.
                   LIB3146-051-Q1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1707021
BLAST score
                   235
                   9.0e-20
E value
                   62
Match length
                   73
% identity
                   (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214571
Seq. ID
                   LIB3146-051-Q1-K1-E7
```

29919

BLASTX

g464840

Method NCBI GI



BLAST score E value 2.0e-59 111 Match length 97 % identity

TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin NCBI Description

alpha-1 chain - fern (Anemia phyllitidis)

>gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia

phyllitidis]

214572 Seq. No.

LIB3146-051-Q1-K1-E9 Seq. ID

Method BLASTX NCBI GI g4337175 BLAST score 464 2.0e-46 E value Match length 132 % identity

(AC006416) ESTs qb T20589, qb T04648, qb AA597906, NCBI Description

gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

214573 Seq. No.

LIB3146-051-Q1-K1-F10 Seq. ID

Method BLASTX NCBI GI g1351271 BLAST score 613 E value 6.0e-64 Match length 127 91 % identity

TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) NCBI Description

>gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

Seq. No. 214574

LIB3146-051-Q1-K1-F7 Seq. ID

BLASTX Method NCBI GI q3953463 310 BLAST score 4.0e-29 E value 109 Match length % identity 60

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

214575 Seq. No.

LIB3146-051-Q1-K1-F8 Seq. ID

Method BLASTX NCBI GI q4097569 BLAST score 348 6.0e-33 E value 103 Match length % identity

NCBI Description (U64915) GMFP4 [Glycine max]

214576 Seq. No.

Seq. ID

Method



```
LIB3146-051-01-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2131505
BLAST score
                  173
                  1.0e-12
E value
                  108
Match length
% identity
                  34
                  hypothetical protein YDR457w - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_927738 (U33050) Tom1p; CAI: 0.16
                  [Saccharomyces cerevisiae]
Seq. No.
                  214577
Seq. ID
                  LIB3146-051-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3757521
BLAST score
                  198
E value
                  3.0e-15
Match length
                  61
% identity
                  66
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                  214578
Seq. No. 5
                  LIB3146-051-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g1209703
NCBI GI
BLAST score
                  402
E value
                  3.0e-39
Match length
                  107
% identity
                  68
NCBI Description (U40489) maize gl1 homolog [Arabidopsis thaliana]
Seq. No.
                  214579
                  LIB3146-051-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g464981
NCBI GI
BLAST score
                  724
E value
                  5.0e-77
Match length
                  138
% identity
                  96
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  214580
                  LIB3146-051-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585241
BLAST score
                  241
E value
                  2.0e-20
Match length
                  63
% identity
                  76
NCBI Description
                  HISTONE H1 >gi_629668_pir__S45662 histone H1 - tomato
                  >gi 424100 (U03391) histone H1 [Lycopersicon esculentum]
Seq. No.
                  214581
```

29921

LIB3146-051-Q1-K1-H5

BLASTX

Seq. No.

Seq. ID

214586

LIB3146-052-Q1-K1-B4

```
q3212116
NCBI GI
BLAST score
                   226
                   1.0e-18
E value
                   96
Match length
                   46
% identity
NCBI Description (Y17393) prefoldin subunit 2 [Mus musculus]
Seq. No.
                   214582
                   LIB3146-051-Q1-K1-H8
Seq. ID
Method
                   BLASTX
                   g3355474
NCBI GI
                   610
BLAST score
                   1.0e-63
E value
Match length
                   130
% identity
                   89
                   (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                   214583
Seq. No.
                   LIB3146-051-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   g1169534
NCBI GI
                  618
BLAST score
                   1.0e-64
E value
                   129
Match length
% identity
                   91
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                   >gi 433609 emb CAA82232_ (Z28386) enolase [Ricinus
                   communis]
                   214584
Seq. No.
                   LIB3146-052-Q1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2274859
BLAST score
                   396
                   8.0e-39
E value
Match length
                   73
% identity
                   97
                    (AJ000016) Cksl protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510420_gb_AAD21506.1_ (AC006929) putative
                    cyclin-dependent kinase regulatory subunit [Arabidopsis
                   thaliana]
                    214585
Seq. No.
                   LIB3146-052-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                    q4567232
NCBI GI
BLAST score
                    267
                    1.0e-23
E value
Match length
                    65
                    80
% identity
                    (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                    thaliana]
```



```
BLASTX
Method
NCBI GI
                  g2191136
                  222
BLAST score
                  2.0e-18
E value
                  91
Match length
                   57
% identity
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                  coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                  214587
Seq. No.
                  LIB3146-052-Q1-K1-B7
Seq. ID
Method
                  BLASTN
                  g2687434
NCBI GI
BLAST score
                   246
                   1.0e-136
E value
                   294
Match length
% identity
                   96
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   214588
Seq. No.
                   LIB3146-052-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2996096
                   420
BLAST score
                   1.0e-41
E value
                   92
Match length
                   89
% identity
                  (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                   alpha [Oryza sativa]
                   214589
Seq. No.
                   LIB3146-052-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3135258
                   152
BLAST score
E value
                   3.0e-10
Match length
                   92
% identity
                   15
                   (AC003058) salt inducible protein-like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214590
                   LIB3146-052-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   q125887
NCBI GI
```

BLAST score 145 2.0e-09 E value Match length 79 % identity 47

ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR NCBI Description

>gi_82092_pir__S04765_LAT52_protein_precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon

esculentum]

BLAST score

E value

276 1.0e-24



```
Seq. No.
                  214591
                  LIB3146-052-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1019946
                  358
BLAST score
                  2.0e-34
E value
Match length
                  89
                  78
% identity
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
Seq. No.
                  214592
Seq. ID
                  LIB3146-052-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q1944216
BLAST score
                  455
                  1.0e-45
E value
Match length
                  96
                  88
% identity
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
                  214593
Seq. No.
                  LIB3146-052-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3953466
BLAST score
                  167
E value
                  6.0e-12
                  55
Match length
                  58
% identity
NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]
                  214594
Seq. No.
                  LIB3146-052-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                  284
                  1.0e-25
E value
Match length
                  57
                  93
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  214595
Seq. No.
                  LIB3146-052-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3617770
BLAST score
                   413
E value
                   9.0e-41
Match length
                  92
% identity
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   214596
Seq. No.
                  LIB3146-052-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                   g2129622
NCBI GI
```

NCBI GI BLAST score

E value

Match length

% identity



```
Match length
                  85
% identity
                  immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
NCBI Description
                  (U52046) immunophilin [Arabidopsis thaliana]
                  214597
Seq. No.
                  LIB3146-052-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244990
BLAST score
                  349
E value
                  3.0e-33
Match length
                  87
% identity
                  83
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
                  Caenorhabditis [Arabidopsis thaliana]
                  214598
Seq. No.
Seq. ID
                  LIB3146-052-Q1-K1-F6
                  BLASTX
Method
                  g3337356
NCBI GI
                  445
BLAST score
                  1.0e-44
E value
Match length
                  91
% identity
                  98
                  (ACO04481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  214599
Seq. No.
Seq. ID
                  LIB3146-052-Q1-K1-F8
Method
                  BLASTX
                  q4106515
NCBI GI
                  401
BLAST score
                  2.0e-39
E value
Match length
                  85
% identity
                  (AF092743) CAK associated cyclinH homolog [Populus tremula
NCBI Description
                  x Populus tremuloides]
Seq. No.
                   214600
                  LIB3146-052-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3242720
BLAST score
                   301
E value
                   1.0e-27
                   91
Match length
                   58
% identity
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214601
                  LIB3146-052-Q1-K1-H4
Seq. ID
                  BLASTX
Method
```

29925

g1277164

1.0e-13 70

182



```
(U51853) cysteine proteinase inhibitor [Glycine max]
NCBI Description
                   214602
Seq. No.
Seq. ID
                   LIB3146-053-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g4063007
BLAST score
                   262
                   8.0e-23
E value
Match length
                   66
% identity
                   70
NCBI Description
                   (AB021706) uncoupling protein [Arabidopsis thaliana]
Seq. No.
                   LIB3146-053-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q169363
BLAST score
                   245
E value
                   8.0e-21
Match length
                   63
% identity
                   62
NCBI Description
                   (M75856) PVPR3 [Phaseolus vulgaris]
Seq. No.
                   214604
Seq. ID
                   LIB3146-053-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   q488573
BLAST score
                   472
                   1.0e-47
E value
Match length
                   98
                   97
% identity
NCBI Description
                   (U09463) histone H3.2 [Medicago sativa]
Seq. No.
                   214605
Seq. ID
                   LIB3146-053-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   q548774
BLAST score
                   147
E value
                   1.0e-09
Match length
                   72
% identity
                    44
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__ S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   214606
Seq. ID
                   LIB3146-053-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   q4539543
```

BLAST score 629 E value 6.0e-66 Match length 127 % identity 97

(AJ133422) glyceraldehyde-3-phosphate dehydrogenase NCBI Description

[Nicotiana tabacum]

Seq. No. 214607

LIB3146-053-Q1-K1-A6 Seq. ID

Seq. No.

Seq. ID

Method

214612

BLASTX

LIB3146-053-Q1-K1-B3



```
BLASTX
Method
NCBI GI
                  q2062167
BLAST score
                  415
                  8.0e-41
E value
Match length
                  124
                  65
% identity
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  214608
Seq. No.
                  LIB3146-053-Q1-K1-B1
Seq. ID
Method
                  BLASTX
                  g2623310
NCBI GI
BLAST score
                  252
                  8.0e-22
E value
                  97
Match length
                  52
% identity
                  (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                  214609
Seq. No.
                  LIB3146-053-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2935416
BLAST score
                  277
                  1.0e-24
E value
                  123
Match length
                  45
% identity
                  (AF047896) isoflavone reductase homolog [Betula pendula]
NCBI Description
                  214610
Seq. No.
                  LIB3146-053-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2144271
BLAST score
                   540
E value
                  2.0e-55
Match length
                  115
% identity
                   88
NCBI Description
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus
                   kitakamiensis (fragment) >gi 1777372 dbj BAA11578 (D82814)
                   cinnamic acid 4-hydroxylase [Populus kitakamiensis]
                   214611
Seq. No.
Seq. ID
                  LIB3146-053-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                   q3738257
BLAST score
                   251
E value
                   1.0e-21
Match length
                   55
% identity
                   95
NCBI Description
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                  nigra]
```



```
q4049349
NCBI GI
BLAST score
                  294
E value
                  1.0e-26
Match length
                   90
                   63
% identity
                   (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  214613
Seq. No.
                  LIB3146-053-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2688820
BLAST score
                   276
                   1.0e-24
E value
                   112
Match length
                   48
% identity
NCBI Description (U93271) enoyl-CoA hydratase [Prunus armeniaca]
                   214614
Seq. No.
                  LIB3146-053-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2431769
                   204
BLAST score
                   4.0e-16
E value
Match length
                   56
                   73
% identity
                  (U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
                   214615
Seq. No.
                   LIB3146-053-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                   q3901014
NCBI GI
                   232
BLAST score
E value
                   1.0e-19
                   56
Match length
% identity
                   77
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
Seq. No.
                   214616
                   LIB3146-053-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g114176
BLAST score
                   409
                   3.0e-40
E value
Match length
                   90
                   89
% identity
                   3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR
NCBI Description
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP
                   SYNTHASE) >qi 66620 pir XUPJVS 3-phosphoshikimate
                   1-carboxyvinyltransferase (EC 2.5.1.19) precursor - garden
                   petunia >gi 169191 (M21084)
                   5-enolpyruvylshikimate-3-phosphate synthase precursor
                   [Petunia hybrida]
```

Seq. No. 214617

Seq. ID LIB3146-053-Q1-K1-C1

Seq. ID

Method



```
Method
                  BLASTX
NCBI GI
                  q1168470
BLAST score
                  532
                  2.0e-54
E value
                  128
Match length
                  80
% identity
                  PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase,
NCBI Description
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi_217829_dbj_BAA02092_
                                                                  (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
                   214618
Seq. No.
                  LIB3146-053-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                   g4544434
NCBI GI
                   375
BLAST score
                   4.0e-36
E value
                   130
Match length
% identity
                   63
                  (AC006955) putative DNA-directed RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214619
                   LIB3146-053-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g4469025
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
Match length
                   62
                   56
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214620
                   LIB3146-053-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4210334
                   300
BLAST score
                   2.0e-27
E value
Match length
                   63
                   92
% identity
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214621
                   LIB3146-053-Q1-K1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   38
E value
                   6.0e-12
Match length
                   38
                   38
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   214622
```

29929

LIB3146-053-Q1-K1-C3

BLASTX



```
q4337175
NCBI GI
BLAST score
                   318
E value
                   2.0e-29
Match length
                   99
                   64
% identity
                   (AC006416) ESTs gb T20589, gb T04648, gb_AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                   gb AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   214623
                   LIB3146-053-Q1-K1-C4
Seq. ID
Method
                   BLASTX
                   g3668082
NCBI GI
                   187
BLAST score
                   4.0e-14
E value
                   38
Match length
                   92
% identity
                   (AC004667) putative DAL1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214624
                   LIB3146-053-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1708313
BLAST score
                   143
E value
                   7.0e-09
Match length
                   47
                   72
% identity
                   HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396_bbs_163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                   thaliana]
                   214625
Seq. No.
                   LIB3146-053-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   g548774
NCBI GI
BLAST score
                   322
                   6.0e-30
E value
Match length
                   87
% identity
                   71
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   214626
Seq. ID
                   LIB3146-053-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   q3281868
BLAST score
                   472
E value
                   1.0e-47
Match length
                   115
% identity
```

Seq. No. 214627

NCBI Description

Seq. ID LIB3146-053-Q1-K1-D1

(AL031004) putative protein [Arabidopsis thaliana]



```
BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  33
E value
                  5.0e-09
Match length
                  57
                  44
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  214628
Seq. No.
                  LIB3146-053-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g416662
BLAST score
                  346
                  1.0e-32
E value
Match length
                  128
                  55
% identity
                  21 KD SEED PROTEIN PRECURSOR >gi 99954 pir S16252 trypsin
NCBI Description
                  inhibitor homolog - soybean >gi 21909 emb CAA39860
                  (X56509) 21 kDa seed protein [Theobroma cacao]
Seq. No.
                  214629
                  LIB3146-053-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g4099092
NCBI GI
BLAST score
                  281
E value
                  4.0e-25
Match length
                  76
% identity
                  68
NCBI Description
                  (U83179) unknown [Arabidopsis thaliana]
Seq. No.
                  214630
                  LIB3146-053-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4099090
BLAST score
                  369
E value
                  2.0e-35
Match length
                  132
% identity
                  51
NCBI Description
                  (U83178) unknown [Arabidopsis thaliana]
Seq. No.
                  214631
                  LIB3146-053-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2118220
BLAST score
                  262
E value
                  6.0e-23
Match length
                  83
% identity
                  67
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
NCBI Description
                   (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16
```

kDa proteolipid [Arabidopsis thaliana]

>gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi 4539311 emb CAB38812.1 (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]

% identity



```
214632
Seq. No.
                  LIB3146-053-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3153902
BLAST score
                  461
                  2.0e-46
E value
Match length
                  98
                  92
% identity
NCBI Description
                  (AF066076) 14-3-3-like protein [Helianthus annuus]
                  214633
Seq. No.
                  LIB3146-053-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g629561
NCBI GI
BLAST score
                  114
                  3.0e-12
E value
                  95
Match length
                  45
% identity
NCBI Description
                  SRG1 protein - Arabidopsis thaliana
                  >gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                  thaliana]
Seq. No.
                  214634
Seq. ID
                  LIB3146-053-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2435511
BLAST score
                  302
                  2.0e-27
E value
Match length
                  111
% identity
                  55
                  (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  214635
Seq. ID
                  LIB3146-053-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g466160
BLAST score
                  365
E value
                  6.0e-35
Match length
                  84
                  82
% identity
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                  >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis
                  elegans >gi 289769 (L14429) putative [Caenorhabditis
                  elegans]
Seq. No.
                  214636
Seq. ID
                  LIB3146-053-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2739000
BLAST score
                  403
E value
                  2.0e-39
Match length
                  135
```

29932

NCBI Description (AF022459) CYP71D10p [Glycine max]

```
214637
Seq. No.
                  LIB3146-053-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135693
BLAST score
                  357
                  4.0e-34
E value
Match length
                  101
                  65
% identity
NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum]
Seq. No.
                  214638
Seq. ID
                  LIB3146-053-Q1-K1-E8
                  BLASTX
Method
                  q3873807
NCBI GI
BLAST score
                  192
E value
                   1.0e-14
Match length
                   95
% identity
NCBI Description (Z49907) B0491.1 [Caenorhabditis elegans]
                   214639
Seq. No.
                  LIB3146-053-Q1-K1-E9
Seq. ID
                   BLASTN
Method
                   g531828
NCBI GI
                   36
BLAST score
                   1.0e-11
E value
Match length
                   44
                   95
% identity
NCBI Description Cloning vector pSport1, complete cds
                   214640
Seq. No.
Seq. ID
                   LIB3146-053-Q1-K1-F1
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
                   9.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   214641
                   LIB3146-053-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   q224293
NCBI GI
                   407
BLAST score
                   8.0e-40
E value
                   82
Match length
                   99
% identity
NCBI Description histone H4 [Triticum aestivum]
                   214642
Seq. No.
                   LIB3146-053-Q1-K1-F12
Seq. ID
Method
                   BLASTX
```

29933

g1169534

3.0e-09

141

35

NCBI GI

E value

BLAST score

Match length

Match length

% identity



```
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                   >gi 433609 emb_CAA82232_ (Z28386) enolase [Ricinus
                   communis]
Seq. No.
                   214643
                   LIB3146-053-Q1-K1-F3
Seq. ID
Method
                   BLASTN
                   q3821780
NCBI GI
                   36
BLAST score
                   7.0e-11
E value
Match length
                   42
                   64
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   214644
Seq. No.
                   LIB3146-053-Q1-K1-F4
Seq. ID
Method
                   BLASTN
                   g4102722
NCBI GI
                   46
BLAST score
                   1.0e-16
E value
                   78
Match length
% identity
                   90
NCBI Description Phaseolus vulgaris TATA-box binding protein (PVTBP1) mRNA,
                   complete cds
                   214645
Seq. No.
                   LIB3146-053-Q1-K1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1350956
BLAST score
                   282
E value
                   3.0e-25
                   62
Match length
% identity
                   92
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
                   214646
Seq. No.
Seq. ID
                   LIB3146-053-Q1-K1-G1
                   BLASTX
Method
                   q4309698
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
Match length
                   122
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214647
                   LIB3146-053-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2583123
BLAST score
                   600
E value
                   2.0e-62
```



```
(AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
                  214648
Seq. No.
                  LIB3146-053-01-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341684
BLAST score
                  315
                  4.0e-29
E value
                  106
Match length
% identity
NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  214649
                  LIB3146-053-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g4101574
NCBI GI
                  203
BLAST score
                  7.0e-16
E value
Match length
                  136
% identity
                  38
NCBI Description (AF004876) 54TMp [Homo sapiens]
                  214650
Seq. No.
                  LIB3146-053-Q1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2506139
                  217
BLAST score
                  1.0e-17
E value
                  61
Match length
% identity
                  69
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
                  214651
Seq. No.
                  LIB3146-053-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3915037
NCBI GI
BLAST score
                  635
E value
                  1.0e-66
                  128
Match length
                  88
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                  >gi 2570067 emb CAA04512 (AJ001071) second sucrose
                  synthase [Pisum sativum]
                  214652
Seq. No.
                  LIB3146-053-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g3901268
NCBI GI
BLAST score
                  161
E value
                  4.0e-11
                  100
Match length
                   38
% identity
```

NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]



```
Seq. No.
                  214653
                  LIB3146-053-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3355483
BLAST score
                  199
                  2.0e-15
E value
Match length
                  44
                  73
% identity
                  (AC004218) gibberellin-regulated protein (GASA5)-like
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  214654
Seq. ID
                  LIB3146-053-Q1-K1-H11
Method
                  BLASTX
                  q4309972
NCBI GI
                  216
BLAST score
                  1.0e-17
E value
Match length
                  91
                  57
% identity
                  (AC002983) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214655
Seq. ID
                  LIB3146-053-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g116908
                  440
BLAST score
                  6.0e-44
E value
                  87
Match length
% identity
                  89
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_166420 (M63853)
                  S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase
                   [Medicago sativa]
Seq. No.
                  214656
Seq. ID
                  LIB3146-053-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q445612
BLAST score
                  141
                  7.0e-09
E value
Match length
                  72
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   214657
Seq. ID
                  LIB3146-053-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q4220462
BLAST score
                  291
                  3.0e-26
E value
```

Match length 61 % identity

(AC006216) Strong similarity to gb Z50851 HD-zip (athb-8) NCBI Description gene from Arabidopsis thaliana containing Homeobox PF 00046

and bZIP PF 00170 domains. [Arabidopsis thaliana]

BLAST score

E value

688

8.0e-73



```
214658
Seq. No.
Seq. ID
                  LIB3146-053-Q1-K1-H6
Method
                  BLASTX
                  q4467147
NCBI GI
                   349
BLAST score
                   5.0e-33
E value
Match length
                  95
% identity
                  75
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                  214659
Seq. No.
                  LIB3146-053-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                   g4455349
NCBI GI
BLAST score
                  183
                   2.0e-16
E value
                   55
Match length
                   85
% identity
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                  214660
Seq. No.
                  LIB3146-054-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455349
BLAST score
                   226
                   8.0e-19
E value
Match length
                   99
                   55
% identity
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                   214661
Seq. No.
                   LIB3146-054-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539348
BLAST score
                   409
E value
                   4.0e-40
Match length
                   101
% identity
                   69
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   214662
                   LIB3146-054-Q1-K1-A4
Seq. ID
Method
                   BLASTX
                   g1256259
NCBI GI
BLAST score
                   273
                   1.0e-25
E value
Match length
                   84
                   74
% identity
NCBI Description
                   (U50900) voltage-dependent anion channel protein [Spinacia
                   oleracea]
Seq. No.
                   214663
Seq. ID
                   LIB3146-054-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   g3046693
```



```
Match length
% identity
                  92
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  214664
Seq. ID
                  LIB3146-054-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4454043
                  543
BLAST score
E value
                  8.0e-56
Match length
                  130
% identity
                  (AL035394) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214665
Seq. ID
                  LIB3146-054-Q1-K1-A9
Method
                  BLASTX
                  g3420733
NCBI GI
                  148
BLAST score
E value
                  5.0e-10
Match length
                  29
                                      4.
% identity
                  97
NCBI Description (AF076335) chalcone synthase B1 [Brassica napus]
Seq. No.
                  214666
                  LIB3146-054-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173624
BLAST score
                  182
                  2.0e-13
E value
Match length
                  119
% identity
NCBI Description
                  (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
                  SM9108']
Seq. No.
                  214667
Seq. ID
                  LIB3146-054-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q1839578
BLAST score
                  457
E value
                  1.0e-45
Match length
                  132
                  64
% identity
                  vacuolar invertase 1, GIN1 [Vitis vinifera=grape berries,
NCBI Description
                  Sultana, berries, Peptide, 642 aa]
Seq. No.
                  214668
Seq. ID
                  LIB3146-054-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3367574
                  170
BLAST score
```

5.0e-12 E value Match length 48 % identity 73

(AL031135) hypothetical protein [Arabidopsis thaliana] NCBI Description



```
214669
Seq. No.
                  LIB3146-054-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4566614
BLAST score
                  476
                  6.0e-48
E value
                  97
Match length
                  92
% identity
                  (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                  Populus tremula]
                  214670
Seq. No.
                  LIB3146-054-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539335
BLAST score
                  152
E value
                  4.0e-10
Match length
                   43
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214671
                  LIB3146-054-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g417103
BLAST score
                   247
E value
                   3.0e-21
                   50
Match length
% identity
                   HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
                   [Arabidopsis thaliana] >gi 404825_emb_CAA42958_ (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                   (U09458) histone H3.2 [Medicago sativa] >gi_488567 (\overline{U}09460)
                   histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
                   H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
                   [Medicago sativa] >gi_4885\overline{7}7 (U09465) histone H3.2
                   [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
                   H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_
                   histone H3 variant H3.3 [Lycopersicon esculentum]
                   >qi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                   >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
                   tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa]
                   >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                   coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone
                   H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
                   (AL035708) Histon H3 [Arabidopsis thaliana]
```

 Seq. No.
 214672

 Seq. ID
 LIB3146-054-Q1-K1-C3

 Method
 BLASTX

NCBI GI g3915031 BLAST score 652 E value 1.0e-68 Match length 134 % identity 96



NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232 (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum] 214673 Seq. No. LIB3146-054-Q1-K1-C4 Seq. ID BLASTX Method g3915031 NCBI GI 469 BLAST score 3.0e-50 E value 113 Match length % identity ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR NCBI Description (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232 (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum] 214674 Seq. No. LIB3146-054-Q1-K1-C6 Sea. ID Method BLASTX q585565 NCBI GI 171 BLAST score 3.0e-12 E value Match length 40 80 % identity RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN NCBI Description D2) >gi_629661_pir__S32716 nuclear protein - carrot >qi 297891 emb CAA51077 (X72384) nuclear located protein [Daucus carota] 214675 Seq. No. LIB3146-054-Q1-K1-C8 Seq. ID BLASTX Method g3935169 NCBI GI BLAST score 216 2.0e-17 E value 43 Match length 95 % identity (AC004557) F17L21.12 [Arabidopsis thaliana] NCBI Description 214676 Seq. No. LIB3146-054-Q1-K1-C9 Seq. ID BLASTX Method g2500376 NCBI GI 449 BLAST score 6.0e-45 E value

89 Match length 96 % identity

60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494_ NCBI Description

(AC005508) 23552 [Arabidopsis thaliana]

214677 Seq. No.

Seq. ID LIB3146-054-Q1-K1-D11

BLASTX Method NCBI GI g2191171 BLAST score 152

E value

Match length

5.0e-16

80



```
3.0e-10
E value
Match length
% identity
                  45
                   (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110)
NCBI Description
                   [Arabidopsis thaliana]
                   214678
Seq. No.
                  LIB3146-054-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                  g1708025
NCBI GI
                   238
BLAST score
                   3.0e-20
E value
                   56
Match length
% identity
                   82
                  GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]
NCBI Description
                   >gi 840731 emb CAA56125_ (X79677) glycerol-3-phosphate
                   dehydrogenase (NAD+) [Cuphea lanceolata]
                   214679
Seq. No.
                   LIB3146-054-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g4559334
NCBI GI
                   397
BLAST score
                   1.0e-38
E value
Match length
                   102
% identity
                   65
                   (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                   214680
Seq. No.
                   LIB3146-054-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3128228
NCBI GI
                   334
BLAST score
                   2.0e-31
E value
                   102
Match length
                   65
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   214681
Seq. No.
                   LIB3146-054-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g2465406
NCBI GI
BLAST score
                   245
E value
                   2.0e-21
                   64
Match length
                   75
% identity
                   (AF020709) chalcone synthase [Vitis vinifera]
NCBI Description
Seq. No.
                   214682
                   LIB3146-054-Q1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3461817
BLAST score
                   204
```



% identity 50 (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No. 214683
Seq. ID LIB3146-054-Q1-K1-E10

Method BLASTX
NCBI GI g1170507
BLAST score 230
E value 2.0e-19
Match length 47
% identity 96

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi_100276_pir__S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 214684

Seq. ID LIB3146-054-Q1-K1-E2

Method BLASTX
NCBI GI g3935167
BLAST score 146
E value 3.0e-09
Match length 45
% identity 62

NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No. 214685

Seq. ID LIB3146-054-Q1-K1-E6

Method BLASTX
NCBI GI g3047125
BLAST score 214
E value 3.0e-17
Match length 82
% identity 49

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 214686

Seq. ID LIB3146-054-Q1-K1-E8

Method BLASTX
NCBI GI g3176684
BLAST score 352
E value 2.0e-33
Match length 128
% identity 55

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb U81375 from Homo sapiens. ESTs gb_N65317,

gb_T20785, gb_AA586285 and gb_AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 214687

Seq. ID LIB3146-054-Q1-K1-E9

Method BLASTX
NCBI GI g4008446
BLAST score 148
E value 6.0e-10
Match length 51



% identity (AL034488) predicted using Genefinder; cDNA EST EMBL:C08771 NCBI Description comes from this gene; cDNA EST EMBL: C07412 comes from this gene [Caenorhabditis elegans] 214688 Seq. No. Seq. ID LIB3146-054-Q1-K1-F12 Method BLASTX NCBI GI g3367521 235 BLAST score 7.0e-20 E value Match length 68 % identity (AC004392) Similar to gb U08285 membrane-associated NCBI Description salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana] 214689 Seq. No. LIB3146-054-Q1-K1-F2 Seq. ID Method BLASTX g4263771 NCBI GI BLAST score 339 E value 6.0e-32 Match length 114 % identity 59 NCBI Description (AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] Seq. No. 214690 LIB3146-054-Q1-K1-F6 Seq. ID Method BLASTX g4204575 NCBI GI BLAST score 366 4.0e-35 E value Match length 112 % identity (AF098510) cytochrome b5 DIF-F [Petunia x hybrida] NCBI Description Seq. No. 214691 LIB3146-054-Q1-K1-F8 Seq. ID Method BLASTX NCBI GI q2499570 344 BLAST score E value 2.0e-32 96 Match length % identity

NCBI Description PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE

(PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN

L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN

CARBOXYL METHYLTRANSFERASE) >gi 414332 (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]

214692 Seq. No.

Seq. ID LIB3146-054-Q1-K1-G11

Method BLASTX g3176669 NCBI GI



```
BLAST score
                  2.0e-45
E value
                  104
Match length
                  75
% identity
NCBI Description (AC004393) End is cut off. [Arabidopsis thaliana]
Seq. No.
                  214693
                  LIB3146-054-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  q1785621
NCBI GI
BLAST score
                  380
E value
                  1.0e-36
Match length
                  124
% identity
                  64
                  (Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927
NCBI Description
                  (AF024650) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana] >gi 4249408 (AC006072) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
                  214694
Seq. No.
                  LIB3146-054-Q1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  33
                  5.0e-09
E value
Match length
                  38
                  37
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  214695
Seq. No.
                  LIB3146-054-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076715
                  282
BLAST score
                  3.0e-25
E value
Match length
                  85
                  56
% identity
                  abscisic acid-induced protein HVA22 - barley >gi_404589
NCBI Description
                   (L19119) A22 [Hordeum vulgare]
Seq. No.
                  214696
Seq. ID
                  LIB3146-054-Q1-K1-H2
                  BLASTX
Method
                  g1655653
NCBI GI
BLAST score
                  198
E value
                  2.0e-15
Match length
                  129
                  36
% identity
                  (Z81368) hypothetical protein Rv2406c [Mycobacterium
NCBI Description
                  tuberculosis]
                  214697
Seq. No.
Seq. ID
                  LIB3146-054-Q1-K1-H3
Method
                  BLASTX
```

11 N.F

q2765081

629 7.0e-66

NCBI GI BLAST score

E value

NCBI Description

Seq. No.

214703



```
Match length
                  90
% identity
                  (Y10557) g5bf [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214698
                  LIB3146-054-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262182
BLAST score
                  172
                   3.0e-12
E value
Match length
                  73
% identity
                   (AC005508) 44123 [Arabidopsis thaliana]
NCBI Description
                   214699
Seq. No.
Seq. ID
                   LIB3146-054-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   q927428
                   636
BLAST score
                   1.0e-66
E value
                   131
Match length
% identity
                   (X86733) fis1 [Linum usitatissimum]
NCBI Description
                   214700
Seq. No.
                   LIB3146-055-Q1-K1-A1
Seq. ID
Method
                   BLASTX
                   q1008904
NCBI GI
                   430
BLAST score
E value
                   1.0e-42
                   114
Match length
                   75
% identity
                   (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
                   214701
Seq. No.
                   LIB3146-055-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   g282963
NCBI GI
                   417
BLAST score
                   5.0e-41
E value
Match length
                   89
% identity
                   80
                   transforming protein (myb) homolog (clone myb.Ph2) - garden
NCBI Description
                   petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
                   x hybrida]
                   214702
Seq. No.
                   LIB3146-055-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g2746719
NCBI GI
                   234
BLAST score
                   1.0e-19
E value
Match length
                   49
                   98
 % identity
                   (AF038386) histone H2B [Capsicum annuum]
```



```
LIB3146-055-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  q124429
NCBI GI
                  254
BLAST score
                  2.0e-22
E value
                  67
Match length
                  75
% identity
                  37 KD CHLOROPLAST INNER ENVELOPE MEMBRANE PROTEIN PRECURSOR
NCBI Description
                  (E37) >gi 99543_pir S14409 membrane protein, 37K,
                  precursor, chloroplast inner envelope - spinach
                  >gi_21228_emb_CAA40283_ (X56963) 37 kD inner envelope
                  membrane polypeptide [Spinacia oleracea]
Seq. No.
                  214704
                  LIB3146-055-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  g2738998
NCBI GI
                  581
BLAST score
                  3.0e-60
E value
                  122
Match length
                  89
% identity
NCBI Description (AF022458) CYP98A2p [Glycine max]
                  214705
Seq. No.
                  LIB3146-055-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g2765093
NCBI GI
                   485
BLAST score
                   6.0e-49
E value
Match length
                   143
% identity
NCBI Description (Y10983) putative cytochrome P450 [Glycine max]
                   214706
Seq. No.
                   LIB3146-055-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   q19611
NCBI GI
                   385
BLAST score
                   2.0e-37
E value
Match length
                   98
                   80
% identity
                   (X13675) histone H3 (AA 1-123) [Medicago sativa]
NCBI Description
                   >gi 2916748 emb_CAA05554_ (AJ002555) histone H3 [Pisum
                   sativum]
                   214707
Seq. No.
                   LIB3146-055-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455207
BLAST score
                   405
                   1.0e-39
E value
Match length
                   88
% identity
                   91
                   (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
```

214708 LIB3146-055-Q1-K1-B5 Seq. ID

Seq. No.



```
BLASTX
Method
                  g1702983
NCBI GI
                  351
BLAST score
                  3.0e-33
E value
                  110
Match length
                  59
% identity
                  AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855_pir__S11850
NCBI Description
                  hypothetical protein - garden strawberry
                  >gi 22573 emb CAA36676 (X52429) 12.5 kDa protein [Fragaria
                  x ananassa] >gi 927034 (L44142) auxin-repressed protein
                  [Fragaria ananassa]
                  214709
Seq. No.
                  LIB3146-055-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g4455800
NCBI GI
                  189
BLAST score
                  1.0e-14
E value
                  81
Match length
                  51
% identity
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214710
                  LIB3146-055-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3550440
BLAST score
                  370
                  1.0e-35
E value
                  99
Match length
                  76
% identity
                  (AF085816) alcohol dehydrogenase A [Gossypium barbadense]
NCBI Description
                  214711
Seq. No.
                  LIB3146-055-Q1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455192
BLAST score
                  311
                  1.0e-28
E value
Match length
                  121
% identity
                   54
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   214712
Seq. No.
                  LIB3146-055-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g462195
BLAST score
                   261
E value
                   1.0e-22
Match length
                   67
% identity
                   79
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 100682 pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
```

Seq. No. 214713

satīva]



```
LIB3146-055-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  q4220481
NCBI GI
BLAST score
                  258
                  2.0e-22
E value
Match length
                  130
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  214714
Seq. No.
                  LIB3146-055-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4240385
BLAST score
                  184
                  8.0e-14
E value
Match length
                  48
                  71
% identity
NCBI Description
                   (AF061027) omega-3 fatty acid desaturase precursor
                   [Vernicia fordii]
                  214715
Seq. No.
                  LIB3146-055-Q1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2244741
                   34
BLAST score
                  2.0e-09
E value
                   54
Match length
                   91
% identity
NCBI Description
                  Antirrhinum majus mRNA for bZIP DNA-binding protein, 1095
Seq. No.
                   214716
Seq. ID
                  LIB3146-055-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                   q3738290
BLAST score
                   207
                   2.0e-16
E value
Match length
                   81
% identity
                   49
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                   214717
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-C8
Method
                  BLASTX
                   g4538903
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
Match length
                   49
                   94
% identity
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
                   214718
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                   g4510350
```

243

9.0e-21

BLAST score E value

% identity

Seq. No.

55

214724

```
Match length
% identity
                   75
NCBI Description
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
                   214719
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                   q2495092
BLAST score
                   300
E value
                   2.0e-27
Match length
                   124
% identity
                   45
NCBI Description
                  GRPE PROTEIN >gi 1001149 dbj BAA10291 (D64001) heat shock
                  protein GrpE [Synechocystis sp.]
Seq. No.
                   214720
                  LIB3146-055-01-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4467134
BLAST score
                   374
E value
                   5.0e-36
Match length
                   104
% identity
                   67
NCBI Description
                   (AL035540) protein kinase like protein [Arabidopsis
                  thaliana]
Seq. No.
                   214721
Seq. ID
                  LIB3146-055-Q1-K1-D5
Method
                   BLASTX
                   g556409
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
Match length
                   69
% identity
                   52
NCBI Description
                  (L34551) transcriptional activator protein [Oryza sativa]
Seq. No.
                   214722
Seq. ID
                   LIB3146-055-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   q3252868
BLAST score
                   235
E value
                   1.0e-19
Match length
                   90
                   50
% identity
NCBI Description
                  (AF033536) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                   214723
Seq. ID
                   LIB3146-055-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g3493172
BLAST score
                   366
E value
                   4.0e-35
Match length
                   74
```

29949

NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Method

NCBI GI

BLAST score

BLASTX

188

g465898



```
LIB3146-055-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g2995990
NCBI GI
                  374
BLAST score
                  5.0e-36
E value
Match length
                  115
% identity
                  63
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  214725
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-E10
Method
                  BLASTX
                  g3877252
NCBI GI
BLAST score
                  332
E value
                  5.0e-31
                  107
Match length
% identity
                  56
                  (Z93382) F45G2.10 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                  214726
Seq. ID
                  LIB3146-055-Q1-K1-E12
Method
                  BLASTN
NCBI GI
                  q3241920
BLAST score
                  58
                  6.0e-24
E value
Match length
                  278
                  80
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  214727
                  LIB3146-055-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2865175
BLAST score
                  321
E value
                  8.0e-30
                  69
Match length
                  80
% identity
NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana]
Seq. No.
                  214728
Seq. ID
                  LIB3146-055-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4103243
BLAST score
                  592
E value
                  2.0e-61
Match length
                  140
                  80
% identity
NCBI Description (AF022368) BIPOSTO [Arabidopsis thaliana]
Seq. No.
                  214729
Seq. ID
                  LIB3146-055-Q1-K1-E8
```



```
E value
                  4.0e-14
Match length
                  104
                  44
% identity
                  HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III
NCBI Description
                  >gi 630692 pir S44849 K12H4.8 protein - Caenorhabditis
                  elegans >gi 289703 (L14331) homology with eukaryotic
                  initiation factor-4A (eIF-4A) and E. coli Ribonuclease III;
                  coded for by C. elegans cDNA GenBank: T02268; putative
                  [Caenorhabditis elegans]
Seq. No.
                  214730
Seq. ID
                  LIB3146-055-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1362054
BLAST score
                  309
                  2.0e-28
E value
Match length
                  75
                  79
% identity
NCBI Description mitotic cyclin group III - alfalfa >gi 780267 emb CAA55272
                  (X78504) B-like cyclin [Medicago sativa]
                  214731
Seq. No.
                  LIB3146-055-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244804
                  282
BLAST score
                  2.0e-25
E value
                  102
Match length
% identity
NCBI Description (Z97336) Ste20-like kinase homolog [Arabidopsis thaliana]
Seq. No.
                  214732
Seq. ID
                  LIB3146-055-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3281846
BLAST score
                  174
E value
                  1.0e-12
                  70
Match length
% identity
NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
Seq. No.
                  214733
                  LIB3146-055-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076316
BLAST score
                  360
E value
                  3.0e-34
Match length
                  111
% identity
NCBI Description drought-induced protein Di19 - Arabidopsis thaliana
                  >gi_469110_emb_CAA55321 (X78584) Di19 [Arabidopsis
```

Seq. No. 214734

Seq. ID LIB3146-055-Q1-K1-F3

thaliana]

Method BLASTN NCBI GI g3821780



```
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  214735
Seq. No.
Seg. ID
                  LIB3146-055-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1174600
BLAST score
                  734
E value
                  4.0e-78
Match length
                  142
                  97
% identity
NCBI Description TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717)
                  beta-tubulin [Oryza sativa]
Seq. No.
                  214736
Seq. ID
                  LIB3146-055-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q4376763
BLAST score
                  210
E value
                  1.0e-16
Match length
                  142
% identity
                  39
NCBI Description (AE001633) GTP Binding Protein [Chlamydia pneumoniae]
                  214737
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g4104931
BLAST score
                  515
E value
                  2.0e-52
Match length
                  139
                  72
% identity
NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]
Seq. No.
                  214738
Seq. ID
                  LIB3146-055-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3668097
BLAST score
                  439
                  1.0e-43
E value
Match length
                  107
% identity
                  80
NCBI Description (AC004667) putative glycine cleavage system protein H
                  precursor [Arabidopsis thaliana]
Seq. No.
                  214739
Seq. ID
                  LIB3146-055-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1173638
BLAST score
                  438
E value
                  2.0e-43
Match length
                  129
% identity
NCBI Description (U35779) 1-aminocyclopropane-1-carboxylate synthase
```

Seq. No.

Seq. ID

Method

214745

BLASTX

LIB3146-055-Q1-K1-H2



[Triticum aestivum]

214740 Seq. No. Seq. ID LIB3146-055-Q1-K1-G4 Method BLASTX NCBI GI q3023931 BLAST score 493 E value 7.0e-50 Match length 128 % identity 66 NCBI Description HISTONE DEACETYLASE 2 (HD2) >gi 2791686 (AF039752) histone deacetylase-2; HD-2 [Gallus gallus] 214741 Seq. No. Seq. ID LIB3146-055-Q1-K1-G6 Method BLASTX NCBI GI q4415912 254 BLAST score 7.0e-22 E value Match length 132 37 % identity NCBI Description (AC006282) putative protease [Arabidopsis thaliana] Seq. No. 214742 LIB3146-055-Q1-K1-G7 Seq. ID Method BLASTX q2443329 NCBI GI 334 BLAST score E value 3.0e-31 Match length 76 % identity 79 NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana] Seq. No. 214743 Seq. ID LIB3146-055-Q1-K1-G8 Method BLASTX NCBI GI g2160166 BLAST score 308 3.0e-28 E value Match length 135 % identity 47 (AC000132) No definition line found [Arabidopsis thaliana] NCBI Description Seq. No. 214744 Seq. ID LIB3146-055-Q1-K1-G9 Method BLASTX NCBI GI q4467157 BLAST score 198 3.0e-15 E value Match length 104 % identity 42 NCBI Description (AL035540) disease resistance response like protein [Arabidopsis thaliana]



```
NCBI GI
                  g2924520
BLAST score
                  640
                  4.0e-67
E value
                  137
Match length
                  88
% identity
NCBI Description
                 (AL022023) plasma membrane intrinsic protein (SIMIP)
                  [Arabidopsis thaliana]
                  214746
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2911062
BLAST score
                  167
E value
                  1.0e-11
Match length
                  45
% identity
                  78
NCBI Description (AL021961) bZIP transcription factor - like protein
                  (fragment) [Arabidopsis thaliana]
Seq. No.
                  214747
                  LIB3146-055-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3540201
BLAST score
                  300
                  3.0e-27
E value
                  91
Match length
% identity
NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]
                  214748
Seq. No.
Seq. ID
                  LIB3146-055-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1172872
BLAST score
                  495
E value
                  4.0e-50
Match length
                  132
% identity
                  72
NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi 435618 dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi 4539328 emb CAB38829.1 (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  214749
                  LIB3146-056-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133940
BLAST score
                  276
E value
                  2.0e-24
Match length
                  74
% identity
                  74
NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >qi 70851 pir R3XL3A
```

[Xenopus laevis]

ribosomal protein S3a - African clawed frog

>gi_65091 emb CAA40592 (X57322) ribosomal protein S1a

BLAST score

E value

354

1.0e-33



```
Seq. No.
                  214750
Seq. ID
                  LIB3146-056-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4140598
BLAST score
                  519
E value
                  5.0e-53
                  119
Match length
% identity
                  84
NCBI Description (AF090148) alcohol dehydrogenase A [Gossypium hirsutum]
Seq. No.
                  214751
                  LIB3146-056-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g1542941
NCBI GI
BLAST score
                  278
                  1.0e-24
E value
Match length
                  65
% identity
                  83
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                  214752
Seq. No.
                  LIB3146-056-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  426
                  5.0e-42
E value
                  88
Match length
                  89
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                  214753
Seq. No.
Seq. ID
                  LIB3146-056-Q1-K1-A6
Method
                  BLASTX
                  g2196466
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
Match length
                  123
% identity
                  64
NCBI Description (Y13673) TATA binding protein-associated factor
                  [Arabidopsis thaliana]
Seq. No.
                  214754
                  LIB3146-056-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2780194
BLAST score
                  382
                  5.0e-37
E value
                  81
Match length
% identity
NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]
Seq. No.
                  214755
Seq. ID
                  LIB3146-056-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3687251
```



```
Match length
                   72
% identity
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
                   214756
Seq. No.
                  LIB3146-056-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   g1363742
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
                   107
Match length
                   50
% identity
                   probable membrane protein YLR243w - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_662338 (U20865) Ylr243wp [Saccharomyces
                   cerevisiae]
                   214757
Seq. No.
                   LIB3146-056-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   q4309738
NCBI GI
                   177
BLAST score
                   4.0e-13
E value
                   81
Match length
                   51
% identity
                   (AC006439) putative tubby protein [Arabidopsis thaliana]
NCBI Description
                   214758
Seq. No.
                   LIB3146-056-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g2388575
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   125
Match length
                   42
% identity
                   (AC000098) YUP8H12.18 [Arabidopsis thaliana]
NCBI Description
                   214759
 Seq. No.
                   LIB3146-056-Q1-K1-B8
 Seq. ID
                   BLASTX
Method
                   g3242709
NCBI GI
                   185
BLAST score
                   9.0e-14
 E value
                   107
Match length
                   39
 % identity
                   (AC003040) putative guanine nucleotide-binding protein
 NCBI Description
                    [Arabidopsis thaliana]
                    214760
 Seq. No.
                   LIB3146-056-Q1-K1-B9
```

Seq. ID

BLASTX Method NCBI GI q3122673 447 BLAST score 2.0e-44 E value 114 Match length % identity 75

60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb_CAB10447_ NCBI Description (Z97341) ribosomal protein [Arabidopsis thaliana]



```
214761
Seq. No.
Seq. ID
                  LIB3146-056-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q4126471
BLAST score
                  268
                  1.0e-23
E value
                  105
Match length
% identity
NCBI Description (AB014722) rSALT-1(806) [Rattus norvegicus]
                  214762
Seq. No.
                  LIB3146-056-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850579
BLAST score
                  272
E value
                  5.0e-24
Match length
                  115
% identity
                  47
                  (AC005278) Strong similarity to gb D14550 extracellular
NCBI Description
                  dermal glycoprotein (EDGP) precursor from Daucus carota.
                  ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470,
                  gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373,
                  gb Z34678 an
                  214763
Seq. No.
                  LIB3146-056-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628471
                  233
BLAST score
                  2.0e-19
E value
Match length
                  71
% identity
                  61
NCBI Description
                  (Y08780) Men-8 [Silene latifolia]
Seq. No.
                  214764
                  LIB3146-056-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687245
                  436
BLAST score
                  3.0e-43
E value
                  125
Match length
                  63
% identity
                  (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214765
Seq. ID
                  LIB3146-056-Q1-K1-D1
                  BLASTX
Method
NCBI GI
                  g114734
BLAST score
                  181
E value
                  3.0e-13
Match length
                  54
                  70
% identity
NCBI Description AUXIN-INDUCED PROTEIN AUX28 >gi 81759 pir A28993 aux28
```

protein (Aux28) [Glycine max]

protein - soybean >gi_169921 (JO3919) auxin-regulated



```
214766
Seq. No.
                  LIB3146-056-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g3763933
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
                  125
Match length
                  42
% identity
                  (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  214767
Seq. No.
                  LIB3146-056-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g2369714
NCBI GI
                   493
BLAST score
                   7.0e-50
E value
                   106
Match length
                   88
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   214768
Seq. No.
                   LIB3146-056-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g4510412
NCBI GI
BLAST score
                   262
                   7.0e-23
E value
                   117
Match length
                   45
% identity
                   (AC006929) putative chloroplast nucleoid DNA binding
NCBI Description
                   protein [Arabidopsis thaliana]
                   214769
 Seq. No.
                   LIB3146-056-Q1-K1-D9
 Seq. ID
                   BLASTX
 Method
                   q2252863
 NCBI GI
                    326
 BLAST score
                    3.0e-30
 E value
                    137
 Match length
                    23
 % identity
                   (AF013294) similar to nucleolin protein [Arabidopsis
 NCBI Description
                    thaliana]
                    214770
 Seq. No.
                    LIB3146-056-Q1-K1-E1
 Seq. ID
                    BLASTX
 Method
                    q2982251
 NCBI GI
                    173
 BLAST score
                    2.0e-12
 E value
                    44
 Match length
 % identity
                    77
 NCBI Description (AF051208) putative RNA-binding protein [Picea mariana]
                    214771
 Seq. No.
                    LIB3146-056-Q1-K1-E10
 Seq. ID
 Method
                    BLASTX
```

g4115371

NCBI GI



```
BLAST score
                  2.0e-15
E value
                  109
Match length
                  50
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  214772
Seq. No.
                  LIB3146-056-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                  g4467113
NCBI GI
                  113
BLAST score
                  7.0e-11
E value
                  115
Match length
                  14
% identity
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]
                  214773
Seq. No.
                  LIB3146-056-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                                1.5
                  g82734
NCBI GI
                   489
BLAST score
                   2.0e-49
E value
                   98
Match length
                   29
% identity
                  ubiquitin precursor - maize (fragment)
NCBI Description
                   >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
                   214774
Seq. No.
                   LIB3146-056-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g1705826
NCBI GI
                   213
BLAST score
                   4.0e-17
E value
                   44
Match length
% identity
                   CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                   >gi 437708 (M91193) chalcone synthase [Trifolium
                   subterraneum] >gi_741008_prf__2006270A chalcone synthase
                   [Trifolium subterraneum]
                   214775
Seq. No.
                   LIB3146-056-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   q1170898
NCBI GI
                   469
BLAST score
                   4.0e-47
E value
                   121
Match length
 % identity
                   MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
 NCBI Description
                   >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial
                   - cider tree >gi 473206 emb CAA55383 (X78800)
                   mitochondrial malate dehydrogenase [Eucalyptus gunnii]
                   214776
 Seq. No.
```

LIB3146-056-Q1-K1-E9 Seq. ID

Method BLASTX NCBI GI g2695925



```
BLAST score
                  204
E value
                  3.0e-16
Match length
                  46
% identity
                  80
NCBI Description (AJ222776) hypothetical protein [Hordeum vulgare]
                  214777
Seq. No.
                  LIB3146-056-Q1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  33
E value
                  4.0e-09
Match length
                  38
% identity
                  37
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  214778
Seq. No.
                  LIB3146-056-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467156
BLAST score
                  522
                  3.0e-53
E value
Match length
                  133
% identity
                  71
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                  214779
Seq. ID
                  LIB3146-056-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g417073
BLAST score
                  543
E value
                  7.0e-56
Match length
                  122
                  85
% identity
NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
                  >gi_484529_pir__JQ1977_glutamate synthase (NADH) (EC
                  1.4.1.14) - alfalfa >gi 166412 (L01660) NADH-glutamate
                  synthase [Medicago sativa]
Seq. No.
                  214780
Seq. ID
                  LIB3146-056-Q1-K1-F4
Method
                  BLASTN
NCBI GI
                  g4210572
BLAST score
                  43
E value
                  6.0e-15
                  55
Match length
                  95
% identity
NCBI Description Tilia kiusiana chloroplast matK gene for maturase, partial
                  cds
Seq. No.
                  214781
                  LIB3146-056-Q1-K1-F5
Seq. ID
```

Method BLASTX q4455275 NCBI GI BLAST score 216 E value 2.0e-17 Match length 68

Match length

108



```
% identity
NCBI Description (AL035527) putative protein [Arabidopsis thaliana]
                  214782
Seq. No.
Seq. ID
                  LIB3146-056-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q82188
BLAST score
                  444
E value
                  4.0e-44
                  123
Match length
% identity
                  73
NCBI Description photosystem II oxygen-evolving complex protein 2 precursor
                  - common tobacco (fragment) >gi 19896 emb CAA41713
                  (X58910) photosystem II 23 kDa polypeptide [Nicotiana
                  tabacum]
                  214783
Seq. No.
                  LIB3146-056-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244833
BLAST score
                  147
E value
                  2.0e-09
Match length
                  74
% identity
                  47
NCBI Description (297337) centromere protein homolog [Arabidopsis thaliana]
Seq. No.
                  214784
Seq. ID
                  LIB3146-056-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2827559
BLAST score
                  196
E value
                  4.0e-15
                  59
Match length
% identity
                  66
NCBI Description
                  (AL021635) predicted protein [Arabidopsis thaliana]
                  >gi 3292808 emb CAA19798 (AL031018) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  214785
Seq. ID
                  LIB3146-056-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4063751
BLAST score
                  257
E value
                  3.0e-22
Match length
                  138
% identity
                  36
NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]
                  >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
Seq. No.
                  214786
Seq. ID
                  LIB3146-056-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1136432
BLAST score
                  165
E value
                  2.0e-11
```

Seq. ID



```
% identity
                  (D80008) KIAA0186 [Homo sapiens]
NCBI Description
                  214787
                  LIB3146-056-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g2911067
NCBI GI
                  150
BLAST score
                   6.0e-10
E value
                  74
Match length
                   43
% identity
                  (AL021960) UV-damaged DNA-binding protein- like
NCBI Description
                   [Arabidopsis thaliana]
                   214788
Seq. No.
                   LIB3146-056-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g3184285
NCBI GI
                   245
BLAST score
                   9.0e-21
E value
                   79
Match length
                   56
% identity
NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]
                   214789
Seq. No.
                   LIB3146-056-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g2244866
NCBI GI
                   272
BLAST score
                   5.0e-24
E value
                   133
Match length
                   41
 % identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   214790
 Seq. No.
                   LIB3146-056-Q1-K1-G4
 Seq. ID
                   BLASTX
 Method
                   g2104529
 NCBI GI
                   589
 BLAST score
                   4.0e-61
 E value
                   140
 Match length
                    81
 % identity
                   (AF001308) putative hexose transporter [Arabidopsis
 NCBI Description
                    thaliana]
                    214791
 Seq. No.
                    LIB3146-056-Q1-K1-G5
 Seq. ID
                    BLASTX
 Method
                    g2695711
 NCBI GI
                    255
 BLAST score
                    5.0e-22
 E value
                    61
 Match length
 % identity
                    79
                   (AJ001370) cytochome b5 [Olea europaea]
 NCBI Description
                    214792
 Seq. No.
```

29962

LIB3146-056-Q1-K1-G7



```
Method
                  BLASTX
NCBI GI
                  q3901014
BLAST score
                  234
E value
                  1.0e-19
Match length
                  55
% identity
                  76
                 (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                  214793
Seq. ID
                  LIB3146-056-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1346156
BLAST score
                  636
E value
                  1.0e-66
Match length
                  140
% identity
                  86
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR
                  (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                  (SHMT) >gi 481943 pir S40213 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                  >gi 437997 emb CAA81079 (Z25860) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
Seq. No.
                  214794
Seq. ID
                  LIB3146-056-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3023858
BLAST score
                  209
E value
                  5.0e-17
Match length
                  64
% identity
                  59
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN >gi_1256608 (U44850) G protein beta subunit
                  [Glycine max]
Seq. No.
                  214795
Seq. ID
                  LIB3146-056-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g584794
BLAST score
                  463
E value
                  2.0e-49
Match length
                  138
                  75
% identity
NCBI Description PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                  >gi 282953 pir A41779 H+-transporting ATPase (EC 3.6.1.35)
                  - curled-leaved tobacco >gi 170289 (M80489) plasma membrane
                  H+ ATPase [Nicotiana plumbaginifolia]
                  214796
Seq. No.
Seq. ID
                  LIB3146-056-Q1-K1-H5
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3885334
BLAST score 312
E value 3.0e-29
Match length 72
% identity 79

(AC005623) putative argonaute protein [Arabidopsis NCBI Description thaliana] 214797 Seq. No. LIB3146-056-Q1-K1-H9 Seq. ID BLASTX Method g3355490 NCBI GI 309 BLAST score 2.0e-28 E value Match length 72 78 % identity (AC004218) putative dolichyl-phosphate NCBI Description beta-glucosyltransferase [Arabidopsis thaliana] 214798 Seq. No. LIB3146-057-Q1-K1-A1 Seq. ID BLASTN Method g2264302 NCBI GI 47 BLAST score 2.0e-17 E value 59 Match length 95 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MAC12, complete sequence [Arabidopsis thaliana] 214799 Seq. No. LIB3146-057-Q1-K1-A10 Seq. ID BLASTX Method g2529721 NCBI GI 225 BLAST score 2.0e-18 E value 105 Match length 44 % identity

(AF001891) unknown [Homo sapiens] NCBI Description

214800 Seq. No.

LIB3146-057-Q1-K1-A2 Seq. ID

BLASTX Method g3786011 NCBI GI 427 BLAST score 4.0e-42 E value 100 Match length 89 % identity

(AC005499) putative elongation factor [Arabidopsis NCBI Description

thaliana]

214801 Seq. No.

LIB3146-057-Q1-K1-A3 Seq. ID

BLASTX Method q1945611 NCBI GI BLAST score 197 3.0e-15 E value 87 Match length 46 % identity

(AB003103) 26S proteasome subunit p55 [Homo sapiens] NCBI Description

>gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome,

macropain) 26S subunit, non-ATPase,



```
214802
Seq. No.
                  LIB3146-057-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q529353
NCBI GI
                  241
BLAST score
                  2.0e-20
E value
                  129
Match length
% identity
                  41
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
                  214803
Seq. No.
                  LIB3146-057-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g2911280
NCBI GI
                  450
BLAST score
                  6.0e-45
E value
                  121
Match length
                  70
% identity
                  (U73937) PK12 protein kinase [Nicotiana tabacum]
NCBI Description
                  214804
Seq. No.
                  LIB3146-057-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                   g3482967
NCBI GI
                   602
BLAST score
                   1.0e-62
E value
                   137
Match length
                   80
% identity
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                   protein phosphatase 2C [Arabidopsis thaliana]
                   214805
Seq. No.
                   LIB3146-057-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   q3860250
NCBI GI
                   383
BLAST score
                   5.0e-37
E value
                   123
Match length
                   59
% identity
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   214806
Seq. No.
                   LIB3146-057-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   q1928991
NCBI GI
BLAST score
                   554
                   1.0e-62
E value
Match length
                   132
 % identity
                   (U92815) heat shock protein 70 precursor [Citrullus
NCBI Description
                   lanatus]
```

214807

LIB3146-057-Q1-K1-B5

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  q2464852
                  191
BLAST score
                  1.0e-14
E value
                  114
Match length
                  43
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  214808
Seq. No.
                  LIB3146-057-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g3319208
NCBI GI
BLAST score
                   423
                  1.0e-41
E value
                   112
Match length
% identity
NCBI Description (U68751) ubiquitin-carboxyl extension [Daucus carota]
                   214809
Seq. No.
                   LIB3146-057-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g2388577
NCBI GI
                   436
BLAST score
                   3.0e-43
E value
Match length
                   118
                   75
% identity
                   (AC000098) Similar to Arabidopsis putative ion-channel
NCBI Description
                   PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]
                   214810
Seq. No.
                   LIB3146-057-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g1652860
NCBI GI
BLAST score
                   167
                   1.0e-11
E value
Match length
                   80
 % identity
                   (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
                   214811
Seq. No.
                   LIB3146-057-Q1-K1-C2
 Seq. ID
                   BLASTX
Method
                   g2558962
NCBI GI
                   382
 BLAST score
                   6.0e-37
 E value
 Match length
                   77
                   100
 % identity
                   (AF025667) histone H2B1 [Gossypium hirsutum]
 NCBI Description
                   214812
 Seq. No.
                   LIB3146-057-Q1-K1-C4
 Seq. ID
                   BLASTX
 Method
                   g3024871
 NCBI GI
                   148
 BLAST score
                   2.0e-09
 E value
```

123

33

Match length

% identity



```
HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                  >gi 1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
                  sp.]
Seq. No.
                  214813
Seq. ID
                  LIB3146-057-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q543905
BLAST score
                  672
E value
                  7.0e-71
Match length
                  133
% identity
                  92
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                  214814
                  LIB3146-057-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543565
BLAST score
                  288
                  7.0e-26
E value
                  90
Match length
                  58
% identity
                 hypothetical 10.0K protein - Zinnia elegans
NCBI Description
                  >gi 493721 dbj BAA06462 (D30802) TED4 [Zinnia elegans]
                  >gi_641903 (U19266) putative nonspecific lipid transfer;
                  auxin induced gene [Zinnia elegans]
Seq. No.
                  214815
Seq. ID
                  LIB3146-057-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2342682
BLAST score
                  157
                  1.0e-10
E value
                  58
Match length
                  62
% identity
                 (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                  protein kinase (gb X95577). [Arabidopsis thaliana]
Seq. No.
                  214816
Seq. ID
                  LIB3146-057-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2194137
                  272
BLAST score
                  5.0e-24
E value
Match length
                  107
% identity
NCBI Description
                  (AC002062) ESTs gb R29947, gb H76702 come from this gene.
                  [Arabidopsis thaliana]
```

Seq. No. 214817

LIB3146-057-Q1-K1-D12 Seq. ID

Method BLASTX NCBI GI g2842480 BLAST score 612 E value 7.0e-64 Match length 129



% identity 91
NCBI Description (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]

Seq. No. 214818
Seq. ID LIB3146-057-Q1-K1-D5
Method BLASTX
NCBI GI g3510260

NCBI GI g3510260
BLAST score 297
E value 7.0e-27
Match length 107
% identity 59

NCBI Description (AC005310) putative AP2 domain containing protein

[Arabidopsis thaliana] >gi 3522951 (AC004411) putative AP2

domain containing protein [Arabidopsis thaliana]

Seq. No. 214819

Seq. ID LIB3146-057-Q1-K1-D6

Method BLASTX
NCBI GI g3334144
BLAST score 343
E value 2.0e-32
Match length 90
% identity 73

NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_

(D86925) C-type cyclin [Oryza sativa]

Seq. No. 214820

Seq. ID LIB3146-057-Q1-K1-D7

Method BLASTX
NCBI GI g1931638
BLAST score 182
E value 2.0e-13
Match length 111
% identity 44

NCBI Description (U95973) transcription factor RUSH-lalpha isolog

[Arabidopsis thaliana]

Seq. No. 214821

Seq. ID LIB3146-057-Q1-K1-E10

Method BLASTX
NCBI GI g3334244
BLAST score 396
E value 2.0e-38
Match length 82
% identity 87

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica

juncea]

Seq. No. 214822

Seq. ID LIB3146-057-Q1-K1-E12

Method BLASTX NCBI GI g4126401 BLAST score 638



```
E value
                  7.0e-67
Match length
                  142
% identity
NCBI Description
                 (AB011795) flavanone 3-hydroxylase [Citrus sinensis]
Seq. No.
                  214823
Seq. ID
                  LIB3146-057-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2833389
BLAST score
                  271
                  7.0e-24
E value
Match length
                  54
% identity
                  85
                  SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III)
NCBI Description
                  >gi 1200154 emb CAA65065 (X95759) glycogen (starch)
                  synthase [Solanum tuberosum]
                  214824
Seq. No.
                  LIB3146-057-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432860
BLAST score
                  320
E value
                  9.0e-30
Match length
                  106
% identity
                  27
NCBI Description
                  (AC006300) putative glucose-induced repressor protein
                  [Arabidopsis thaliana]
Seq. No.
                  214825
Seq. ID
                  LIB3146-057-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1742965
BLAST score
                  347
E value
                  9.0e-33
Match length
                  123
                  55
% identity
NCBI Description (Y09562) HAPp48,5 protein [Arabidopsis thaliana]
Seq. No.
                  214826
Seq. ID
                  LIB3146-057-Q1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4105130
BLAST score
                  35
                  3.0e-10
E value
                  91
Match length
% identity
                  86
NCBI Description
                  Spinacia oleracea ClpC protease (clpC) mRNA, chloroplast
                  gene encoding chloroplast protein, complete cds
Seq. No.
                  214827
Seq. ID
                  LIB3146-057-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4567225
BLAST score
                  257
E value
                  3.0e-22
```

77

66

Match length % identity



NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 214828

Seq. ID LIB3146-057-Q1-K1-F12

Method BLASTX
NCBI GI g431164
BLAST score 177
E value 2.0e-13
Match length 44
% identity 73

NCBI Description (D21823) ORF [Lilium longiflorum]

Seq. No. 214829

Seq. ID LIB3146-057-Q1-K1-F2

Method BLASTX
NCBI GI g3894168
BLAST score 234
E value 2.0e-19
Match length 136
% identity 35

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 214830

Seq. ID LIB3146-057-Q1-K1-F4

Method BLASTX
NCBI GI g120668
BLAST score 558
E value 1.0e-57
Match length 121
% identity 93

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_82399_pir__A24159 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>qi 167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var.

distichum]

Seq. No. 214831

Seq. ID LIB3146-057-Q1-K1-F5

Method BLASTX
NCBI GI g3924609
BLAST score 405
E value 1.0e-39
Match length 140
% identity 54

NCBI Description (AF069442) putative polyprotein of LTR transposon

[Arabidopsis thaliana]

Seq. No. 214832

Seq. ID LIB3146-057-Q1-K1-F8

Method BLASTX
NCBI GI g3894168
BLAST score 227
E value 1.0e-18
Match length 133



```
% identity
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                   thaliana]
                   214833
Seq. No.
                   LIB3146-057-Q1-K1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3341687
                   154
BLAST score
                   3.0e-10
E value
                   58
Match length
                   57
% identity
NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]
Seq. No.
                   214834
                   LIB3146-057-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g1771780
NCBI GI
                   407
BLAST score
                   7.0e-40
E value
                   109
Match length
                   79
% identity
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
                   214835
Seq. No.
                   LIB3146-057-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g3152606
NCBI GI
                   172
BLAST score
                   2.0e-12
E value
                   94
Match length
                   44
% identity
                  (AC004482) putative ring zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   214836
Seq. No.
                   LIB3146-057-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g464621
NCBI GI
                   275
BLAST score
E value
                   2.0e-24
Match length
                   119
                   54
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539 emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                    214837
Seq. No.
                   LIB3146-057-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                    q2104675
NCBI GI
BLAST score
                    320
                    9.0e-30
E value
                    107
Match length
% identity
                    58
NCBI Description (X97903) transcription factor [Vicia faba]
```



```
Seq. No.
                  214838
                  LIB3146-057-Q1-K1-H5
Seq. ID
Method
                  BLASTX
                  q4512671
NCBI GI
                  217
BLAST score
E value
                  1.0e-17
Match length
                  56
                  70
% identity
NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
                  214839
Seq. No.
Seq. ID
                  LIB3146-057-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3927831
BLAST score
                  507
E value
                  1.0e-51
                  124
Match length
                  76
% identity
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                  thaliana]
                  214840
Seq. No.
                  LIB3146-057-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3183088
BLAST score
                  209
                  1.0e-16
E value
Match length
                  71
                  56
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                   cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                   like protein [Vigna unguiculata]
Seq. No.
                   214841
Seq. ID
                  LIB3146-057-Q1-K1-H9
Method
                  BLASTX
                  q3935184
NCBI GI
BLAST score
                   157
                   2.0e-10
E value
                   96
Match length
% identity
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]
                   214842
Seq. No.
                   LIB3146-058-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   q3914442
NCBI GI
BLAST score
                   442
                   6.0e-44
E value
                   127
Match length
% identity
                   71
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
```

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

NCBI Description



```
214843
Seq. No.
                  LIB3146-058-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2388689
                  317
BLAST score
                  3.0e-29
E value
                  135
Match length
                  50
% identity
NCBI Description (AF016633) GH1 protein [Glycine max]
                  214844
Seq. No.
                  LIB3146-058-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                  g115813
NCBI GI
                  336
BLAST score
                  2.0e-31
E value
Match length
                  101
% identity
                  67
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                   (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  214845
                  LIB3146-058-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g548770
NCBI GI
BLAST score
                  417
                  2.0e-41
E value
                  83
Match length
                  92
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  214846
Seq. No.
                  LIB3146-058-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q548770
                   350
BLAST score
E value
                   5.0e-33
Match length
                   132
                   58
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                   ribosomal protein L3 [Oryza sativa]
                   214847
Seq. No.
                   LIB3146-058-Q1-K1-B4
Seq. ID
Method
                   BLASTX
                   q548770
NCBI GI
BLAST score
                   433
                   6.0e-43
E value
                   128
Match length
                   66
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi 481228_pir__S38359 ribosomal
```

29973

ribosomal protein L3 [Oryza sativa]

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)



```
Seq. No.
                  214848
Seq. ID
                  LIB3146-058-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  163
E value
                  8.0e-12
Match length
                  51
% identity
                  65
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  214849
Seq. No.
Seq. ID
                  LIB3146-058-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1125691
                  205
BLAST score
E value
                  4.0e-16
Match length
                  56
% identity
                 - 82
NCBI Description (X94301) DnaJ protein [Solanum tuberosum]
                  214850
Seq. No.
Seq. ID
                  LIB3146-058-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q3913420
                  156
BLAST score
E value
                  2.0e-10
Match length
                  67
                  49
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine
                  decarboxylase [Pisum sativum]
Seq. No.
                  214851
Seq. ID
                  LIB3146-058-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  501
E value
                  7.0e-51
Match length
                  108
% identity
                  91
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  214852
Seq. ID
                  LIB3146-058-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2462929
BLAST score
                  426
E value
                  4.0e-42
Match length
                  117
% identity
                  64
```

Seq. ID LIB3146-058-Q1-K1-C2

214853

Seq. No.

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]



```
BLASTX
Method
                  g3914740
NCBI GI
                  450
BLAST score
                  7.0e-45
E value
                  114
Match length
                  75
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941
                  (D78495) ribosomal protein [Brassica rapa]
                  214854
Seq. No.
                  LIB3146-058-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g4512671
NCBI GI
BLAST score
                  229
                  6.0e-19
E value
Match length
                  58
% identity
                  71
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                   214855
Seq. No.
                  LIB3146-058-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                   g1710587
NCBI GI
BLAST score
                   567
                   1.0e-58
E value
                   129
Match length
% identity
                   88
                   60S ACIDIC RIBOSOMAL PROTEIN PO >gi_1196897 (L46848) acidic
NCBI Description
                   ribosomal protein PO [Glycine max]
                   214856
Seq. No.
                   LIB3146-058-Q1-K1-C8
Seq. ID
                   BLASTN
Method
                   g2264305
NCBI GI
BLAST score
                   35
                   4.0e-10
E value
                   51
Match length
                   92
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBK23, complete sequence [Arabidopsis thaliana]
                   214857
 Seq. No.
                   LIB3146-058-Q1-K1-D1
 Seq. ID
                   BLASTX
Method
                   q4455246
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   92
Match length
                   54
 % identity
                   (AL035523) putative protein [Arabidopsis thaliana]
 NCBI Description
                   214858
 Seq. No.
                   LIB3146-058-Q1-K1-D12
 Seq. ID
                   BLASTX
 Method
                   g3184285
 NCBI GI
```

225

2.0e-18

BLAST score

E value



Match length 63 % identity 65 NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 214859

Seq. ID LIB3146-058-Q1-K1-D2

Method BLASTX
NCBI GI g122106
BLAST score 410
E value 3.0e-40
Match length 82
% identity 100

NCBI Description HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize

>gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana

>gi_2119028_pir__S60475 histone H4 - garden pea

>gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 (H4C13) [700 m

thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi_168501 (MI3370) histone H4 [Zea mays] >gi_168503

 $(M1\overline{3}377)$ histone H4 [Zea mays] >gi_498898 (U1 $\overline{0}042$) histone

H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4

[Arabidopsis thaliana]

Seq. No. 214860

Seq. ID LIB3146-058-Q1-K1-D4

Method BLASTX
NCBI GI 9464851
BLAST score 172
E value 3.0e-12
Match length 43
% identity 77

NCBI Description TUBULIN BETA-2 CHAIN >gi 421784 pir S32669 tubulin beta-2

chain - fern (Anemia phyllitidis) (fragment)

>gi 296500 emb CAA48930 (X69186) beta tubulin 2 [Anemia

phyllitidis]

Seq. No. 214861

Seq. ID LIB3146-058-Q1-K1-D7

Method BLASTX
NCBI GI g3850587
BLAST score 328
E value 1.0e-30
Match length 118
% identity 59

NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical

protein from Arabidopsis thaliana chromosome 4 contig

gb_Z97335. [Arabidopsis thaliana]

Seq. No. 214862

Seq. ID LIB3146-058-Q1-K1-D8

Method BLASTX NCBI GI g3859606



```
BLAST score
                  1.0e-21
E value
                  101
Match length
                  51
% identity
                  (AF104919) contains similarity to cysteine proteases (Pfam:
NCBI Description
                  PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                  214863
Seq. No.
                  LIB3146-058-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g3549291
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
Match length
                  82
                  50
% identity
                  (AF074923) endo-1,4-beta-glucanase precursor [Fragaria x
NCBI Description
                  ananassa]
                  214864
Seq. No.
                  LIB3146-058-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g4335719
NCBI GI
                   160
BLAST score
                   7.0e-11
E value
Match length
                   50
                   56
% identity
                   (AC006248) putative RING-H2 finger protein RHG1a
NCBI Description
                   [Arabidopsis thaliana]
                   214865
Seq. No.
                   LIB3146-058-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g3746069
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
                   91
Match length
% identity
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   214866
Seq. No.
                   LIB3146-058-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g232031
NCBI GI
BLAST score
                   215
E value
                   3.0e-17
                   67
Match length
                   58
 % identity
                   ELONGATION FACTOR 1 BETA' >gi_322851_pir__$29224
 NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi 218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza satīva]
```

Seq. ID LIB3146-058-Q1-K1-E6

Method BLASTX NCBI GI g3176684



BLAST score 143 E value 7.0e-09 Match length 80 % identity 38

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317, gb_T20785, gb_AA586285 and gb_AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 214868

Seq. ID LIB3146-058-Q1-K1-E7

Method BLASTX
NCBI GI g3915826
BLAST score 568
E value 1.0e-58
Match length 132
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 214869

Seq. ID LIB3146-058-Q1-K1-E8

Method BLASTX
NCBI GI g4417280
BLAST score 337
E value 1.0e-31
Match length 88
% identity 75

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 214870

Seq. ID LIB3146-058-Q1-K1-F11

Method BLASTX
NCBI GI g2244990
BLAST score 239
E value 9.0e-22
Match length 93
% identity 56

NCBI Description (Z97340) similarity to LIM homeobox protein -

Caenorhabditis [Arabidopsis thaliana]

Seq. No. 214871

Seq. ID LIB3146-058-Q1-K1-F12

Method BLASTX
NCBI GI g2738949
BLAST score 554
E value 3.0e-57
Match length 112
% identity 90

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 214872

Seq. ID LIB3146-058-Q1-K1-F2

Method BLASTX
NCBI GI g1172556
BLAST score 390
E value 8.0e-38



```
Match length
% identity
                    90
                    36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                    (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir_B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin
                    II [Solanum tuberosum]
                    214873
Seq. No.
                    LIB3146-058-Q1-K1-F4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3152618
                    380
BLAST score
                    1.0e-36
E value
Match length
                    108
% identity
                    (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                    >gi 3242724 (AC003040) putative pectinesterase [Arabidopsis
                    thaliana]
                    214874
Seq. No.
                    LIB3146-058-Q1-K1-F5
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2264312
                    33
BLAST score
                    6.0e-09
E value
                    45
Match length
                    93
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MOK16, complete sequence [Arabidopsis thaliana]
                    214875
Seq. No.
                    LIB3146-058-Q1-K1-G1
Seq. ID
Method
                    BLASTX
                    g137460
NCBI GI
BLAST score
                    141
                    5.0e-16
E value
                    110
Match length
                    56
% identity
                    VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                    SUBUNIT) >gi_67952_pir__PXPZV9 H+-transporting ATPase (EC
                    3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)
                    vacular H+-ATPase [Daucus carota]
                    214876
Seq. No.
                    LIB3146-058-Q1-K1-G10
Seq. ID
                    BLASTX
Method
NCBI GI
                    q3386609
                     157
BLAST score
```

E value 1.0e-10 100 Match length % identity

(AC004665) putative DNA-binding protein [Arabidopsis NCBI Description

thaliana]

214877 Seq. No.

Seq. ID

Method



```
LIB3146-058-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g2688824
NCBI GI
                  265
BLAST score
                  2.0e-23
E value
                   66
Match length
                  80
% identity
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   214878
Seq. No.
                  LIB3146-058-Q1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3024127
BLAST score
                   687
                   1.0e-72
E value
                   136
Match length
                   93
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
                   214879
Seq. No.
                   LIB3146-058-Q1-K1-G5
Seq. ID
Method
                   BLASTX
                   q3618320
NCBI GI
BLAST score
                   242
                   2.0e-20
E value
                   55
Match length
                   84
% identity
                   (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                   214880
Seq. No.
                   LIB3146-058-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g4539292
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
                   59
Match length
                   88
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   214881
Seq. No.
                   LIB3146-058-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   g2677830
NCBI GI
BLAST score
                   550
E value
                   1.0e-56
Match length
                   117
% identity
                   93
                   (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                   214882
Seq. No.
```

29980

LIB3146-058-Q1-K1-H4

BLASTX



```
q3461884
NCBI GI
BLAST score
                    351
                    3.0e-33
E value
Match length
                    105
% identity
                    (AB006082) phosphoribosyl-ATP pyrophosphohydrolase
NCBI Description
                    [Arabidopsis thaliana] >gi_3461886_dbj_BAA32529_ (AB006083)
                    phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis
                    thaliana]
                    214883
Seq. No.
Seq. ID
                    LIB3146-058-Q1-K1-H8
Method
                    BLASTX
NCBI GI
                    q3868758
BLAST score
                    350
E value
                    4.0e-33
Match length
                    102
% identity
                    62
                   (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                    214884
Seq. No.
                    LIB3146-059-Q1-K1-A1
Seq. ID
Method
                    BLASTX
                    g2104536
NCBI GI
BLAST score
                    301
E value
                    2.0e-27
Match length
                    61
                    80
% identity
                    (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                    thalianal
Seq. No.
                    214885
                    LIB3146-059-Q1-K1-A10
Seq. ID
Method
                    BLASTN
                    g2564048
NCBI GI
BLAST score
                    35
E value
                    3.0e-10
                    134
Match length
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                    214886
Seq. ID
                    LIB3146-059-Q1-K1-A4
Method
                    BLASTX
NCBI GI
                    g122085
BLAST score
                    345
E value
                    1.0e-32
Match length
                    90
% identity
                    81
                    HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis
NCBI Description
                    thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136)
                    [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3
```

(AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]



>gi_168497 (M13379) histone H3 [Zea mays] >gi_168506
(M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone
H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3
[Petroselinum crispum] >gi_169659 (M77495) histone H3
[Petroselinum crispum] >gi_387565 (M17130) histone H3
[Arabidopsis thaliana] >gi_387567 (M17131) histone H3
[Arabidopsis thaliana] >gi_886738 emb_CAA59111 (X84377)
histone 3 [Zea mays] >gi_1040764 (M35387) histone H3
[Arabidopsis thaliana] >gi_1314779 (U54827) histone H3
homolog [Brassica napus] >gi_1531754 emb_CAA57811 (X82414)
Histone H3 [Asparagus officinalis] >gi_1667592 (U77296)
histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to
histone H3 gene gb_M17131 and gb_M35387 from A. thaliana.
ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and
gb_T42306 come from this gene. [Arabidopsis thaliana]
>gi_225459_prf__1303352A histone H3 [Helicoverpa zea]
>gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 214887 LIB3146-059-Q1-K1-A8 Seq. ID Method BLASTX g2833388 NCBI GI BLAST score 547 3.0e-56 E value Match length 121 % identity 82 NCBI Description

escription GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi_629660_pir__S43341_ADPglucose--starch

glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042 emb_CAA52273 (X74160) starch (bacterial

glycogen) synthase [Manihot esculenta]

Seq. No. 214888

Seq. ID LIB3146-059-Q1-K1-A9

Method BLASTX
NCBI GI g2245136
BLAST score 498
E value 2.0e-50
Match length 134
% identity 69

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 214889

Seq. ID LIB3146-059-Q1-K1-B1

Method BLASTX
NCBI GI g1171866
BLAST score 256
E value 1.0e-22
Match length 49
% identity 94

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild

29982

cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. ID

NCBI GI

Method

```
21
```

```
214890
Seq. No.
                  LIB3146-059-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g4371290
NCBI GI
                  199
BLAST score
                  2.0e-15
E value
                  51
Match length
                  67
% identity
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]
                  214891
Seq. No.
                  LIB3146-059-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4529972
                   447
BLAST score
                   9.0e-45
E value
                   100
Match length
                   82
% identity
                  (AC002330) putative chloroplast outer envelope 86-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   214892
Seq. No.
                   LIB3146-059-Q1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2443836
                   229
BLAST score
                   2.0e-19
E value
                   60
Match length
                   68
% identity
                   (AF020793) tonoplast intrinsic protein homolog MSMCP1
NCBI Description
                   [Medicago sativa]
                   214893
Seq. No.
                   LIB3146-059-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4455244
BLAST score
                   265
                   2.0e-23
E value
                   96
Match length
                   55
% identity
                   (AL035523) MtN3-like protein [Arabidopsis thaliana]
NCBI Description
                   214894
 Seq. No.
                   LIB3146-059-Q1-K1-C11
 Seq. ID
Method
                   BLASTX
                   g4160402
 NCBI GI
 BLAST score
                   242
                   2.0e-20
 E value
Match length
                   115
                   50
 % identity
                   (AJ132240) eukaryotic translation initiation factor 5 [Zea
 NCBI Description
                   mays]
                   214895
 Seq. No.
```

29983

LIB3146-059-Q1-K1-C6

BLASTX

g3128173

Seq. ID Method

NCBI GI

BLAST score



```
BLAST score
                  5.0e-11
E value
                  38
Match length
                  74
% identity
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  214896
Seq. No.
                  LIB3146-059-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g3702121
NCBI GI
                  195
BLAST score
                  2.0e-15
E value
                  71
Match length
                  61
% identity
                  (AJ011681) retinoblastoma-related protein [Chenopodium
NCBI Description
                  rubrum]
                   214897
Seq. No.
                  LIB3146-059-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                   g2760323
NCBI GI
                   193
BLAST score
                   1.0e-14
E value
                   111
Match length
                   31
% identity
                  (AC002130) F1N21.8 [Arabidopsis thaliana]
NCBI Description
                   214898
Seq. No.
                   LIB3146-059-Q1-K1-D3
Seq. ID
Method
                   BLASTX
                   q2499614
NCBI GI
                   315
BLAST score
                   4.0e-29
E value
                   80
Match length
                   75
% identity
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
NCBI Description
                   >gi_481830_pir__S39559 mitogen-activated protein kinase 3
                   homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_
                   (X69971) NTF3 [Nicotiana tabacum]
                   214899
Seq. No.
                   LIB3146-059-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   q3548802
NCBI GI
BLAST score
                   193
                   8.0e-15
E value
                   75
Match length
                   48
% identity
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4335769 gb AAD17446 (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   214900
Seq. No.
```

29984

LIB3146-059-Q1-K1-D6

BLASTX

g2746515 230



```
E value
                  3.0e-25
Match length
                  104
% identity
NCBI Description (AF037558) alcohol dehydrogenase 2 [Leavenworthia stylosa]
                  214901
Seq. No.
Seq. ID
                  LIB3146-059-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3176667
                  353
BLAST score
E value
                  1.0e-33
Match length
                  104
% identity
                  (ACO04393) Similar to hypothetical 41.9KD protein
NCBI Description
                  gb 1001369 from sequence of Synechocystis sp. gb_D64006.
                  [Arabidopsis thaliana]
Seq. No.
                  214902
                  LIB3146-059-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  q3063448
NCBI GI
                  414
BLAST score
E value
                  1.0e-40
Match length
                  121
% identity
                  60
                  (AC003981) F22013.10 [Arabidopsis thaliana]
NCBI Description
                  214903
Seq. No.
Seq. ID
                  LIB3146-059-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2462837
BLAST score
                  187
E value
                  3.0e-14
Match length
                  64
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  214904
Seq. ID
                  LIB3146-059-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q2961345
BLAST score
                  406
E value
                  1.0e-39
Match length
                  93
                  76
% identity
NCBI Description (AL022140) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  214905
Seq. ID
                  LIB3146-059-Q1-K1-F11
Method
                  BLASTX
                  g2529678
NCBI GI
                  205
BLAST score
                  3.0e-16
E value
                  74
Match length
% identity
                  64
```

NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]

% identity

NCBI Description

31

pombe]



```
214906
Seq. No.
Seq. ID
                  LIB3146-059-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q1174470
BLAST score
                  340
                  5.0e-32
E value
Match length
                  116
% identity
                  59
NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
                  (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A
                  integral membrane protein [Mus musculus]
Seq. No.
                  214907
                  LIB3146-059-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927830
                  268
BLAST score
E value
                  1.0e-23
Match length
                  116
                  23
% identity
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  214908
Seq. ID
                  LIB3146-059-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  621
                  5.0e-65
E value
Match length
                  115
                  100
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                  214909
Seq. ID
                  LIB3146-059-Q1-K1-G1
Method
                  BLASTX
                  q1408471
NCBI GI
BLAST score
                   505
E value
                  3.0e-51
                  113
Match length
% identity
                   81
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
Seq. No.
                   214910
Seq. ID
                  LIB3146-059-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3618214
BLAST score
                   147
                   2.0e-09
E value
Match length
                   102
```

29986

(AL031579) dihydrofolate reductase [Schizosaccharomyces

BLAST score

Match length

E value

240 3.0e-20

50



```
214911
Seq. No.
                  LIB3146-059-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023751
BLAST score
                  328
E value
                  8.0e-31
Match length
                  106
                  59
% identity
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                  >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
                  [Triticum aestivum]
                  214912
Seq. No.
                  LIB3146-059-Q1-K1-G4
Seq. ID
Method
                  BLASTX
                  g3319882
NCBI GI
                  164
BLAST score
                  7.0e-12
E value
Match length
                  41
% identity
                  80
NCBI Description
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
Seq. No.
                  214913
                  LIB3146-059-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q3087888
NCBI GI
BLAST score
                  163
                  3.0e-11
E value
Match length
                  55
% identity
                  58
                  (X94302) hexokinase [Solanum tuberosum]
NCBI Description
Seq. No.
                  214914
Seq. ID
                  LIB3146-059-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q729617
BLAST score
                  271
                  7.0e-24
E value
Match length
                  72
% identity
                  72
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 1 (GRP 78-1)
NCBI Description
                  (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 1) (BIP
                  1) >gi 100337 pir S21877 heat shock protein BiP homolog
                  blp1 - common tobacco (fragment) >gi 19805 emb CAA42662
                   (X60060) luminal binding protein (BiP) [Nicotiana tabacum]
Seq. No.
                  214915
Seq. ID
                  LIB3146-059-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q3335361
```

% identity

48



```
% identity
                  (AC003028) putative acyltransferase [Arabidopsis thaliana]
NCBI Description
                  214916
Seq. No.
                  LIB3146-059-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  g4539307
NCBI GI
                  173
BLAST score
                  8.0e-13
E value
Match length
                  46
                  72
% identity
                  (ALO49480) putative acidic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  214917
                  LIB3146-059-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  q2494416
NCBI GI
BLAST score
                  115
                  1.0e-09
E value
Match length
                  46
                  55
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >qi 166956 (M80597) fructose-1,6-bisphosphatase [Beta
                  vulgaris] >gi 444324 prf 1906373A cytosolic fructose
                  bisphosphatase [Beta vulgaris]
Seq. No.
                  214918
                  LIB3146-059-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                   g4160292
NCBI GI
                   315
BLAST score
                   4.0e-29
E value
                   91
Match length
% identity
                   69
                  (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
NCBI Description
                   214919
Seq. No.
                   LIB3146-059-Q1-K1-H8
Seq. ID
Method
                   BLASTX
                   g4263717
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
                   63
Match length
                   51
% identity
                   (AC006223) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   214920
Seq. ID
                   LIB3146-060-Q1-K1-A11
                   BLASTX
Method
NCBI GI
                   q2239089
BLAST score
                   256
                   4.0e-22
E value
Match length
                   102
```



(284386) anthranilate N-hydroxycinnamoyl/benzoyltransferase NCBI Description [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] 214921 Seq. No. LIB3146-060-Q1-K1-A2 Seq. ID Method BLASTX NCBI GI g3914002 BLAST score 340 6.0e-32 E value 80 Match length 85 % identity MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279 NCBI Description (AF033862) Lon protease [Arabidopsis thaliana] 214922 Seq. No. LIB3146-060-Q1-K1-A6 Seq. ID BLASTX Method NCBI GI q1806283 BLAST score 351 3.0e-33 E value 100 Match length 73 % identity (Z79637) Histone H4 homologue [Sesbania rostrata] NCBI Description Seq. No. 214923 LIB3146-060-Q1-K1-A8 Seq. ID BLASTX Method g400515 NCBI GI 178 BLAST score 6.0e-13 E value 66 Match length 48 % identity NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8) NCBI Description (CI-B8) >gi_346540_pir__S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine >gi_246_emb_CAA44904_ (X63219) NADH dehydrogenase [Bos taurus] Seq. No. 214924 Seq. ID LIB3146-060-Q1-K1-A9 Method BLASTX q3043428 NCBI GI BLAST score 502

5.0e-51 E value 106 Match length 95 % identity

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 214925

LIB3146-060-Q1-K1-B3 Seq. ID

Method BLASTX NCBI GI g2144271 BLAST score 344 2.0e-32 E value Match length 85

NCBI Description



```
% identity
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus
NCBI Description
                  kitakamiensis (fragment) >gi 1777372 dbj BAA11578 (D82814)
                  cinnamic acid 4-hydroxylase [Populus kitakamiensis]
                  214926
Seq. No.
Seq. ID
                  LIB3146-060-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4150974
                  369
BLAST score
E value
                  2.0e-35
Match length
                  95
% identity
                  69
                  (AJ224331) cystatin [Castanea sativa]
NCBI Description
                  214927
Seq. No.
Seq. ID
                  LIB3146-060-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q1297359
                  510
BLAST score
                  6.0e-52
E value
                  130
Match length
                  74
% identity
NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]
Seq. No.
                  214928
Seq. ID
                  LIB3146-060-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2815246
BLAST score
                  218
E value
                  9.0e-18
Match length
                  55
                  71
% identity
NCBI Description
                  (X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.
                  214929
Seq. ID
                  LIB3146-060-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q3386609
BLAST score
                  296
E value
                  8.0e-27
Match length
                  135
% identity
NCBI Description
                  (AC004665) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  214930
Seq. ID
                  LIB3146-060-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4263704
BLAST score
                  218
                  1.0e-17
E value
                  77
Match length
% identity
                  47
```

29990

[Arabidopsis thaliana]

(AC006223) putative sugar starvation-induced protein

الجملة

% identity

88



```
Seq. No.
Seq. ID
                   LIB3146-060-Q1-K1-
Method
                   BLASTX
NCBI GI
                   q548770
BLAST score
                   678
                   1.0e-71
E value
Match length
                   140
                   89
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
Seq. No.
                   214932
                   LIB3146-060-Q1-K1-C3
Seq. ID
Method
                   BLASTX
                   g2500047
NCBI GI
BLAST score
                   498
E value
                   2.0e-50
Match length
                   110
                   82
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi_534916_emb_CAA85362
                    (Z36894) soluble inorganic pyrophosphatase [Solanum
                   tuberosum]
Seq. No.
                   214933
                   LIB3146-060-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244775
                   201
BLAST score
                   1.0e-15
E value
                   112
Match length
% identity
                    42
NCBI Description
                    (Z97335) salt-inducible protein homolog [Arabidopsis
                   thaliana]
Seq. No.
                   214934
Seq. ID
                   LIB3146-060-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q2129918
BLAST score
                    471
E value
                    2.0e-47
Match length
                   134
% identity
                    63
                   BPF-1 protein - parsley >gi_396197_emb_CAA48413_ (X68337)
BPF-1 [Petroselinum crispum] >gi_441310_emb_CAA44518_
NCBI Description
                    (X62653) BPF-1 [Petroselinum crispum]
Seq. No.
                    214935
Seq. ID
                   LIB3146-060-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                    g4490330
BLAST score
                    636
                    1.0e-66
E value
Match length
                   129
```

29991

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis



thaliana]

```
214936
Seq. No.
                  LIB3146-060-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g4567304
NCBI GI
BLAST score
                  185
E value
                  8.0e-14
                  101
Match length
                  43
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                  214937
Seq. No.
Seq. ID
                  LIB3146-060-Q1-K1-E10
Method
                  BLASTX
                  g2746719
NCBI GI
BLAST score
                  133
                  4.0e-17
E value
                  53
Match length
% identity
                  93
                  (AF038386) histone H2B [Capsicum annuum]
NCBI Description
Seq. No.
                  214938
                  LIB3146-060-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707130
BLAST score
                  173
                  2.0e-12
E value
Match length
                  88
                  48
% identity
                  (U80455) coded for by C. elegans cDNA yk45f3.5; coded for
NCBI Description
                  by C. elegans cDNA yk9h4.5; coded for by C. elegans cDNA
                  yk104a4.5; coded for by C. elegans cDNA yk45f3.3; coded for
                  by C. elegans cDNA yk104a4.3; coded for by C. elegans cDNA
                  yk80d9
                  214939
Seq. No.
Seq. ID
                  LIB3146-060-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3738290
BLAST score
                   269
E value
                  1.0e-23
Match length
                  100
                  50
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  214940
Seq. No.
                  LIB3146-060-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729668
BLAST score
                   341
                   4.0e-32
E value
                   81
Match length
% identity
                   86
                  HISTONE H1 >gi_2147479_pir__S65059 histone H1,
NCBI Description
                  drought-inducible - Lycopersicon pennellii >gi 436823
```

(U01890) Solanum pennellii histone H1 [Solanum pennellii]



```
Seq. No.
                  214941
                  LIB3146-060-01-K1-E8
Seq. ID
Method
                  BLASTX
                  g1431629
NCBI GI
                  377
BLAST score
                  2.0e-36
E value
Match length
                  103
                  68
% identity
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  214942
Seq. No.
                  LIB3146-060-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g2980770
NCBI GI
                  346
BLAST score
                  1.0e-32
E value
                  121
Match length
                  62
% identity
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  214943
Seq. No.
                  LIB3146-060-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367591
BLAST score
                  264
                  5.0e-23
E value
                  95
Match length
                  56
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  214944
Seq. No.
                  LIB3146-060-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3135273
BLAST score
                   514
E value
                   2.0e-52
Match length
                   129
                   69
% identity
NCBI Description
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
                   >gi 4191773 (AC005917) putative WD-40 repeat protein
                   [Arabidopsis thaliana]
                   214945
Seq. No.
Seq. ID
                   LIB3146-060-Q1-K1-F4
Method
                   BLASTX
                   q3063396
NCBI GI
                   518
BLAST score
E value
                   7.0e-53
                   115
Match length
% identity
NCBI Description
                  (AB012947) vcCyP [Vicia faba]
```

Seq. ID LIB3146-060-Q1-K1-F6

Method BLASTX NCBI GI g2569938

29993



```
BLAST score
                  4.0e-30
E value
Match length
                  76
                  79
% identity
NCBI Description (Y15193) GAI [Arabidopsis thaliana]
                  214947
Seq. No.
Seq. ID
                  LIB3146-060-Q1-K1-F7
Method
                  BLASTN
                  g4376087
NCBI GI
BLAST score
                  47
                  3.0e-17
E value
                  119
Match length
% identity
                  85
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
                  214948
Seq. No.
                  LIB3146-060-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  g1563719
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
Match length
                  86
                   47
% identity
                  (Y08320) cyclophylin [Digitalis lanata]
NCBI Description
Seq. No.
                  214949
                  LIB3146-060-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4510363
BLAST score
                   436
                   3.0e-43
E value
                   106
Match length
                   75
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   214950
Seq. No.
                   LIB3146-060-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245005
BLAST score
                   277
E value
                   1.0e-24
Match length
                   75
% identity
                   41
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   214951
Seq. No.
Seq. ID
                   LIB3146-060-Q1-K1-G3
Method
                   BLASTX
                   q2583130
NCBI GI
BLAST score
                   145
E value
                   4.0e-09
Match length
                   97
% identity
                   31
NCBI Description (AC002387) putative reverse transcriptase [Arabidopsis
```



thaliana]

 Seq. No.
 214952

 Seq. ID
 LIB3146-060-Q1-K1-G7

 Method
 BLASTX

 NCBI GI
 g1352821

 BLAST score
 185

E value 5.0e-14
Match length 36
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 214953

Seq. ID LIB3146-060-Q1-K1-H1

Method BLASTX
NCBI GI g1707032
BLAST score 219
E value 8.0e-18
Match length 109
% identity 43

NCBI Description (U80445) coded for by C. elegans cDNA yk13g5.3; coded for

by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA

yk65h8

Seq. No. 214954

Seq. ID LIB3146-060-Q1-K1-H3

Method BLASTX
NCBI GI g3719211
BLAST score 490
E value 1.0e-49
Match length 118
% identity 82

NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 214955

Seq. ID LIB3146-060-Q1-K1-H4

Method BLASTX
NCBI GI g1311386
BLAST score 229
E value 3.0e-19
Match length 76
% identity 53

NCBI Description Cyanogenic Beta-Glucosidase Mol_id: 1; Molecule: Cyanogenic

Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21

Seq. No. 214956

Seq. ID LIB3146-060-Q1-K1-H5

Method BLASTX
NCBI GI g1946355
BLAST score 335
E value 2.0e-31



Match length 50 % identity (U93215) maize transposon MuDR mudrA protein isolog NCBI Description [Arabidopsis thaliana] >gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana] Seq. No. 214957 Seq. ID LIB3146-060-Q1-K1-H6 Method BLASTX NCBI GI q3954807 BLAST score 437 E value 2.0e-43 Match length 132 58 % identity (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus NCBI Description Seq. No. 214958 Seq. ID LIB3146-060-Q1-K1-H9 Method BLASTX NCBI GI q1698548 BLAST score 263 E value 4.0e-35 Match length 131 % identity NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum] Seq. No. 214959 Seq. ID LIB3146-061-Q1-K1-A1 Method BLASTX NCBI GI g122007 BLAST score 208 E value 8.0e-17 Match length 43 % identity 95 HISTONE H2A >gi 100161 pir S11498 histone H2A - parsley NCBI Description >gi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum] 214960 Seq. No. Seq. ID LIB3146-061-Q1-K1-A10 BLASTX Method NCBI GI g2498608 BLAST score 171 4.0e-12 E value 98 Match length 39 % identity NCBI Description L-ASPARTATE OXIDASE (QUINOLINATE SYNTHETASE B) >gi 608530 (U17232) L-aspartate oxidase [Pseudomonas aeruginosa] 214961 Seq. No. Seq. ID LIB3146-061-Q1-K1-A11

Method BLASTX

Method BLASTX
NCBI GI g466160
BLAST score 360
E value 2.0e-34
Match length 84



% identity HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III NCBI Description >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi 289769 (L14429) putative [Caenorhabditis elegans] Seq. No. 214962 Seq. ID LIB3146-061-Q1-K1-A12 Method BLASTX NCBI GI q4522005 BLAST score 159 E value 3.0e-11 Match length 71 % identity 45 (AC007069) putative reverse transcriptase [Arabidopsis NCBI Description thalianal Seq. No. 214963 LIB3146-061-Q1-K1-A2 Seq. ID Method BLASTX g2407800 NCBI GI 297 BLAST score E value 4.0e-27 Match length 68 % identity 88 NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana] 214964 Seq. No. Seq. ID LIB3146-061-Q1-K1-A6 Method BLASTX NCBI GI q1706377 BLAST score 583 E value 2.0e-60 Match length 134 79 % identity DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL NCBI Description 4-REDUCTASE) >gi 499018 emb CAA53578 (X75964) dihydroflavonol reductase [Vitis vinifera] Seq. No. 214965 Seq. ID LIB3146-061-Q1-K1-A7 Method BLASTX NCBI GI g2511541 BLAST score 437 E value 2.0e-43 Match length 101 % identity NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa] Seq. No. 214966 Seq. ID LIB3146-061-Q1-K1-B11 Method BLASTX

NCBI GI g3264769 BLAST score 159 9.0e-11 E value Match length 35 % identity 83





```
(AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                  armeniaca]
                  214967
Seq. No.
Seq. ID
                  LIB3146-061-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                  g3850778
                  431
BLAST score
                  1.0e-42
E value
                  104
Match length
                  79
% identity
NCBI Description (Y18346) gluaredoxin [Lycopersicon esculentum]
Seq. No.
                  214968
                  LIB3146-061-Q1-K1-B3
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  214969
Seq. No.
                  LIB3146-061-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                   q2738949
NCBI GI
BLAST score
                   627
                   1.0e-65
E value
                   132
Match length
                   88
% identity
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                   ananassa]
                   214970
Seq. No.
Seq. ID
                   LIB3146-061-Q1-K1-B5
Method
                   BLASTX
                   q3821280
NCBI GI
BLAST score
                   459
E value
                   6.0e-46
                   117
Match length
                   77
% identity
                  (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
                   214971
Seq. No.
                   LIB3146-061-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2462762
BLAST score
                   303
                   8.0e-28
E value
Match length
                   103
% identity
                   58
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
```

29998

214972

Seq. No.



```
LIB3146-061-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  g4539543
NCBI GI
BLAST score
                  516
                  1.0e-52
E value
                  127
Match length
% identity
                  84
                  (AJ133422) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                  [Nicotiana tabacum]
                  214973
Seq. No.
                  LIB3146-061-Q1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2495365
BLAST score
                  519
                  5.0e-53
E value
Match length
                  135
                  79
% identity
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  214974
Seq. No.
                  LIB3146-061-Q1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2191167
                  234
BLAST score
                  1.0e-19
E value
Match length
                  104
% identity
                  43
                   (AF007270) A IG002P16.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  214975
Seq. No.
                  LIB3146-061-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                   g2766715
NCBI GI
BLAST score
                   361
E value
                   2.0e-34
                   114
Match length
% identity
                   61
                   (AF039365) chromomethylase [Arabidopsis arenosa]
NCBI Description
                   >gi 2865435 (AF039375) chromomethylase [Arabidopsis
                   arenosa]
                   214976
Seq. No.
                   LIB3146-061-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g2370595
NCBI GI
BLAST score
                   164
E value
                   2.0e-11
Match length
                   131
% identity
                   27
NCBI Description (AJ001414) GTPase activating protein [Yarrowia lipolytica]
```

Seq. ID LIB3146-061-Q1-K1-C8

Method BLASTX



```
g2894598
NCBI GI
BLAST score
                  261
E value
                  1.0e-22
Match length
                  107
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                  214978
Seq. No.
Seq. ID
                  LIB3146-061-Q1-K1-D1
Method
                  BLASTX
                  g4105798
NCBI GI
BLAST score
                  334
                  3.0e-31
E value
                  76
Match length
                  74
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                  214979
                  LIB3146-061-Q1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548774
BLAST score
                  456
                  1.0e-45
E value
                   112
Match length
                   79
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi 542158 pir__S38360 ribosomal
NCBI Description
                   protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   214980
                   LIB3146-061-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   q3850778
NCBI GI
BLAST score
                   441
                   7.0e-44
E value
                   105
Match length
% identity
                   79
NCBI Description (Y18346) gluaredoxin [Lycopersicon esculentum]
                   214981
Seq. No.
                   LIB3146-061-Q1-K1-D3
Seq. ID
Method
                   BLASTX
                   q2266994
NCBI GI
                   346
BLAST score
                   1.0e-32
E value
                   104
Match length
                   62
% identity
                   (U77413) O-linked GlcNAc transferase [Homo sapiens]
NCBI Description
                   >gi 4505499 ref NP 003596.1_pOGT_ O-GlcNAc transferase
                   (uridine diphospho-N-acetylglucosamine:polypeptide
                   beta-N-acetylglucosaminyl transferase)
```

Seq. ID LIB3146-061-Q1-K1-D7

Method BLASTX
NCBI GI g2558962
BLAST score 313

```
E value
                   7.0e-29
Match length
                   63
                   100
% identity
NCBI Description
                  (AF025667) histone H2B1 [Gossypium hirsutum]
                  214983
Seq. No.
                  LIB3146-061-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3342211
BLAST score
                  183
E value
                  1.0e-13
Match length
                  51
% identity
                   67
NCBI Description
                  (U89255) Pti4 [Lycopersicon esculentum]
Seq. No.
                  214984
                  LIB3146-061-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3319357
BLAST score
                  255
E value
                   4.0e-22
Match length
                  84
                   60
% identity
NCBI Description
                  (AF077407) contains similarity to phosphoenolpyruxate
                  synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Sèq. No.
                  214985
                  LIB3146-061-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129472
BLAST score
                  452
                   4.0e-45
E value
Match length
                  105
                  82
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                  precursor - Scotch pine >gi_1100225 (L32561)
                  glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                  214986
Seq. No.
Seq. ID
                  LIB3146-061-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                  g3241926
BLAST score
                   61
E value
                   1.0e-25
                  213
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSG15, complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB3146-061-Q1-K1-E8

Method BLASTX
NCBI GI g2739010
BLAST score 236
E value 8.0e-20
Match length 132
% identity 35

Match length

NCBI Description

% identity

122

57



```
(AF022464) CYP77A3p [Glycine max]
NCBI Description
                  214988
Seq. No.
                  LIB3146-061-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  q3319357
NCBI GI
                   445
BLAST score
                   2.0e-44
E value
                  129
Match length
                   70
% identity
                   (AF077407) contains similarity to phosphoenolpyruvate
NCBI Description
                   synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
                   214989
Seq. No.
                  LIB3146-061-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                   q2501578
NCBI GI
BLAST score
                   584
                   1.0e-60
E value
                   124
Match length
                   96
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__$60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                   brasiliensis]
Seq. No.
                   214990
Seq. ID
                   LIB3146-061-Q1-K1-F11
                   BLASTX
Method:
                   g3421109
NCBI GI
                   595
BLAST score
                   7.0e-62
E value
                   124
Match length
                   90
% identity
                  (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   214991
                   LIB3146-061-Q1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1332579
BLAST score
                   626
                   1.0e-65
E value
Match length
                   128
% identity
                   10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   214992
Seq. ID
                   LIB3146-061-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q3548815
BLAST score
                   313
E value
                   8.0e-29
```

J. W. 34.

30002

[Arabidopsis thaliana]

(AC005313) similar to axoneme-associated protein mst101



```
214993
Seq. No.
                  LIB3146-061-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g2995990
NCBI GI
                  394
BLAST score
                  3.0e-38
E value
                  117
Match length
                   65
% identity
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  214994
Seq. No.
                  LIB3146-061-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                   g2829918
NCBI GI
BLAST score
                   380
                   1.0e-36
E value
Match length
                   115
                   72
% identity
                  (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                   214995
Seq. No.
                   LIB3146-061-Q1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3236252
                   447
BLAST score
                   2.0e-44
E value
                   135
Match length
                   61
% identity
                  (AC004684) CER1-like protein [Arabidopsis thaliana]
NCBI Description
                   214996
Seq. No.
                   LIB3146-061-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2431769
                   236
BLAST score
                   7.0e-20
E value
                   61
Match length
                   75
% identity
                  (U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
                   214997
Seq. No.
                   LIB3146-061-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3850587
BLAST score
                   249
E value
                   1.0e-21
```

68 Match length 75 % identity

(AC005278) Strong similarity to gi 2244780 hypothetical NCBI Description

protein from Arabidopsis thaliana chromosome 4 contig

gb Z97335. [Arabidopsis thaliana]

Seq. No. 214998

```
LIB3146-061-Q1-K1-G3.
Seq. ID
Method
                  BLASTX
                  g3264759
NCBI GI
                  343
BLAST score
                  2.0e-49
E value
Match length
                  112
                   92
% identity
                  (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
NCBI Description
                  214999
Seq. No.
                  LIB3146-061-Q1-K1-G4
Seq. ID
Method
                  BLASTX
                   g1931645
NCBI GI
                   188
BLAST score
                   2.0e-14
E value
Match length
                   61
                   67
% identity
                  (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
NCBI Description
                   215000
Seq. No.
                   LIB3146-061-Q1-K1-G5
Seq. ID
                   BLASTN
Method
                   g1220195
NCBI GI
                   38
BLAST score
                   2.0e-12
E value
                   74
Match length
                   88
% identity
                   Gossypium hirsutum alcohol dehydrogenase 2a mRNA, complete
NCBI Description
                   215001
Seq. No.
                   LIB3146-061-Q1-K1-G8
Seq. ID
Method
                   BLASTX
                   g3309170
NCBI GI
                   307
BLAST score
                   4.0e-28
E value
Match length
                   115
% identity
                   54
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]
                   215002
Seq. No.
                   LIB3146-061-Q1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1706738
                   197
BLAST score
                   3.0e-15
E value
Match length
                   83
% identity
                   51
NCBI Description FLAVONOL 3-SULFOTRANSFERASE (F3-ST) >gi 498645 (U10275)
                   flavonol 3-sulfotransferase [Flaveria bidentis]
                   215003
Seq. No.
Seq. ID
                   LIB3146-061-01-K1-H2
Method
                   BLASTX
                   g3738290
NCBI GI
                   313
BLAST score
                   8.0e-29
E value
```

```
129
Match length
                   50
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215004
Seq. No.
                                                                     . . . . .
                  LIB3146-061-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g4325355
NCBI GI
                   141
BLAST score
                   7.0e-14
E value
                   95
Match length
                   47
% identity
                  (AF128395) contains similarity to retrovirus-related
NCBI Description
                   polyproteins [Arabidopsis thaliana]
                   215005
Seq. No.
                   LIB3146-061-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   g4126401
NCBI GI
                   508
BLAST score
                   8.0e-52
E value
Match length
                   100
                   90
% identity
                  (AB011795) flavanone 3-hydroxylase [Citrus sinensis]
NCBI Description
                   215006
Seq. No.
                   LIB3147-001-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g2695861
NCBI GI
BLAST score
                   671
                   9.0e-71
E value
Match length
                   140
                   90
% identity
                  (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate
NCBI Description
                   synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273)
                   3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum
                   sativum]
                   215007
Seq. No.
Seq. ID
                   LIB3147-001-Q1-K1-A4
Method
                   BLASTN
NCBI GI
                   g12292
BLAST score
                   224
                   1.0e-123
E value
                   364
Match length
% identity
```

Spinach chloroplast DNA homologous to ARS and ARC elements NCBI Description

upstream of rDNA operon

215008 Seq. No.

Seq. ID LIB3147-001-Q1-K1-A5

Method BLASTN NCBI GI q12292 BLAST score 228 E value 1.0e-125 Match length 364 % identity 91

```
Spinach chloroplast DNA homologous to ARS and ARC elements
NCBI Description
                  upstream of rDNA operon
                  215009
Seq. No.
                  LIB3147-001-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                  g114682
NCBI GI
                  150
BLAST score
                  3.0e-10
E value
Match length
                  60
                  50
% identity
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi 168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                  215010
                  LIB3147-001-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710401
BLAST score
                  690
                  6.0e-73
E value
                  144
Match length
                  90
% identity
NCBI Description
                 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
                  (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                  >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                  R2 [Nicotiana tabacum]
Seq. No.
                  215011
                  LIB3147-001-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832898
BLAST score
                  609
                  2.0e-63
E value
Match length
                  141
                  78
% identity
                  (AJ000886) Tetrafunctional protein of glyoxysomal fatty
NCBI Description
                  acid beta-oxidation [Brassica napus]
                  215012
Seq. No.
                  LIB3147-001-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g872116
BLAST score
                  554
```

E value 4.0e-57 Match length 130 % identity

NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 215013

LIB3147-001-Q1-K1-C7 Seq. ID

Method BLASTN NCBI GI g2828187

BLAST score 32



1.0e-08 E value Match length 44 93

% identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K21C13, complete sequence [Arabidopsis thaliana]

215014 Seq. No.

LIB3147-001-Q1-K1-D2 Seq. ID

Method BLASTX NCBI GI g1076746 BLAST score 603 9.0e-63 E value 143 Match length 85 % identity

heat shock protein 70 - rice (fragment) NCBI Description

>gi 763160 emb CAA47948_ (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 215015

LIB3147-001-Q1-K1-D3 Seq. ID

Method BLASTX NCBI GI g2055374 BLAST score 142 8.0e-09 E value 60 Match length 55 % identity

NCBI Description (U29095) serine-threonine protein kinase [Triticum

aestivum]

215016 Seq. No.

LIB3147-001-Q1-K1-D4 Seq. ID

Method BLASTX NCBI GI g3183219 BLAST score 211 E value 8.0e-17 Match length 132

% identity 41

HYPOTHETICAL PROTEIN KIAA0112 (HA0609) NCBI Description

>gi_434779_dbj_BAA04948_ (D25218) KIAA0112 [Homo sapiens]

Seq. No. 215017

Seq. ID LIB3147-001-Q1-K1-D5

Method BLASTN NCBI GI g19396 BLAST score 59 E value 6.0e - 25Match length 107 % identity 89

NCBI Description Tomato ubi3 gene for ubiquitin

215018 Seq. No.

Seq. ID LIB3147-001-Q1-K1-D8

Method BLASTX NCBI GI g3913919 BLAST score 372 E value 1.0e-35 Match length 83



% identity 84

NCBI Description ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID

SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI) (VACUOLAR INVERTASE) >gi_2351827 (U92438) soluble acid

invertase [Phaseolus vulgaris]

Seq. No. 215019

Seq. ID LIB3147-001-Q1-K1-E1

Method BLASTX
NCBI GI g3024017
BLAST score 502
E value 6.0e-51
Match length 99
% identity 95

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)

(EIF-4C) >gi_2565421 (AF026804) eukaryotic translation

initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 215020

Seq. ID LIB3147-001-Q1-K1-E2

Method BLASTX
NCBI GI g3132472
BLAST score 143
E value 8.0e-09
Match length 56
% identity 50

NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 215021

Seq. ID LIB3147-001-Q1-K1-E3

Method BLASTX
NCBI GI g1835154
BLAST score 749
E value 7.0e-80
Match length 143
% identity 90

NCBI Description (Y10267) glutamine synthetase [Medicago truncatula]

Seq. No. 215022

Seq. ID LIB3147-001-Q1-K1-F1

Method BLASTX
NCBI GI g1052973
BLAST score 294
E value 2.0e-26
Match length 72
% identity 82

NCBI Description (U37838) fructokinase [Beta vulgaris]

Seq. No. 215023

Seq. ID LIB3147-001-Q1-K1-F2

Method BLASTX
NCBI GI g132939
BLAST score 404
E value 1.0e-39
Match length 108
% identity 71

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 81657 pir JQ0771 ribosomal



protein L3 (ARP1) - Arabidopsis thaliana >gi_166858

```
215024
Seq. No.
                   LIB3147-001-Q1-K1-F3
Seq. ID
Method
                   BLASTX
                   g508304
NCBI GI
                   350
BLAST score
                   4.0e-33
E value
                   79
Match length
                   80
% identity
                  (L22305) corC [Medicago sativa]
NCBI Description
                   215025
Seq. No.
                   LIB3147-001-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g4115377
NCBI GI
                   252
BLAST score
                   7.0e-22
E value
                   84
Match length
                   55
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   215026
Seq. No.
                   LIB3147-001-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   g2443757
NCBI GI
BLAST score
                   209
                   5.0e-17
E value
                   67
Match length
                   64
% identity
NCBI Description (AF020434) cyclophilin [Arabidopsis thaliana]
                   215027
Seq. No.
                   LIB3147-001-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924772
BLAST score
                   516
                   1.0e-52
E value
Match length
                   111
% identity
                   88
NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]
                   215028
Seq. No.
                   LIB3147-001-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q730463
BLAST score
                   322
E value
                   8.0e-30
                   105
Match length
                   59
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
                   >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
(Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                   protein L37 [Saccharomyces cerevisiae]
```

(M32654) ribosomal protein [Arabidopsis thaliana]

30009

[Saccharomyces cerevisiae]

>gi 1420537 emb CAA99454_ (Z75142) ORF YOR234c

```
215029
Seq. No.
Seq. ID
                   LIB3147-001-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1762939
BLAST score
                   286
                   1.0e-25
E value
Match length
                   91
% identity
                   59
                   (U66266) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   215030
                   LIB3147-001-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3377797
                   595
BLAST score
                   8.0e-62
E value
                   141
Match length
                   83
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
Seq. No.
                   215031
                   LIB3147-001-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3885515
BLAST score
                   414
                   1.0e-40
E value
Match length
                   96
                   80
 % identity
NCBI Description
                   (AF084202) similar to ribosomal protein S26 [Medicago
                   sativa]
                   215032
Seq. No.
                   LIB3147-001-Q1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710551
BLAST score
                   245
E value
                   8.0e-21
Match length
                   51
 % identity
                   88
NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728_
                   (X95458) ribosomal protein L3\overline{9} [Zea mays]
                   215033
Seq. No.
Seq. ID
                   LIB3147-001-Q1-K2-A10
Method
                   BLASTX
NCBI GI
                   g3334115
BLAST score
                   470
E value
                   4.0e-47
Match length
                   116
                   82
 % identity
```

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)





(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No. 215034

Seq. ID LIB3147-001-Q1-K2-A12

Method BLASTX
NCBI GI g2832664
BLAST score 195
E value 5.0e-15
Match length 98

% identity 44
NCBI Description (AL021710) pollen-specific protein - like [Arabidopsis

thaliana]

Seq. No. 215035

Seq. ID LIB3147-001-Q1-K2-A3

Method BLASTX
NCBI GI g2695861
BLAST score 616
E value 4.0e-67
Match length 150
% identity 80

NCBI Description (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate

synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum

sativum]

Seq. No. 215036

Seq. ID LIB3147-001-Q1-K2-A4

Method BLASTN
NCBI GI g559547
BLAST score 130
E value 7.0e-67
Match length 286
% identity 90

NCBI Description Transformation vector pPRV100B, plastid targeting segment

Seq. No. 215037

Seq. ID LIB3147-001-Q1-K2-A5

Method BLASTN
NCBI GI g12292
BLAST score 212
E value 1.0e-116

Match length 363 % identity 90

NCBI Description Spinach chloroplast DNA homologous to ARS and ARC elements

upstream of rDNA operon

Seq. No. 215038

Seq. ID LIB3147-001-Q1-K2-A8

Method BLASTX
NCBI GI g114682
BLAST score 160
E value 2.0e-11
Match length 55
% identity 60



NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
>gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

 Seq. No.
 215039

 Seq. ID
 LIB3147-001-Q1-K2-A9

 Method
 BLASTX

 NCBI GI
 g1174592

 BLAST score
 744

BLAST score 744 E value 2.0e-79 Match length 138 % identity 100

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 215040

Seq. ID LIB3147-001-Q1-K2-B1

Method BLASTX
NCBI GI g1710401
BLAST score 464
E value 1.0e-46
Match length 118
% identity 75

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

Seq. No. 215041

Seq. ID LIB3147-001-Q1-K2-B10

Method BLASTX
NCBI GI g81634
BLAST score 302
E value 2.0e-27
Match length 113
% identity 59

NCBI Description GTP-binding protein ara-5 - Arabidopsis thaliana (fragment)

Seq. No. 215042

Seq. ID LIB3147-001-Q1-K2-B11

Method BLASTX
NCBI GI g2213583
BLAST score 387
E value 1.0e-37
Match length 112
% identity 70

NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No. 215043

Seq. ID LIB3147-001-Q1-K2-B2

Method BLASTX
NCBI GI g2832898
BLAST score 570

```
7.0e-59
 E value
 Match length
                   141
 % identity
                    74
                   (AJ000886) Tetrafunctional protein of glyoxysomal fatty
 NCBI Description
                    acid beta-oxidation [Brassica napus]
 Seq. No.
                    215044
 Seq. ID
                    LIB3147-001-Q1-K2-B3
 Method
                    BLASTN
 NCBI GI
                    g296442
 BLAST score
                    33
 E value
                    6.0e-09
 Match length
                    65
                    88
% identity
 NCBI Description G.max ADR11 mRNA
                    215045
 Seq. No.
 Seq. ID
                    LIB3147-001-Q1-K2-B5
 Method
                    BLASTX
 NCBI GI
                    g1710401
 BLAST score
                    386
 E value
                    1.0e-37
 Match length
                    96
 % identity
                    78
 NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
                    (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                    >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                    R2 [Nicotiana tabacum]
 Seq. No.
                    215046
                    LIB3147-001-Q1-K2-B7
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g3046851
 BLAST score
                    34
 E value
                    2.0e-09
 Match length
                    89
                    23
 % identity
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MIJ24, complete sequence [Arabidopsis thaliana]
                    215047
 Seq. No.
 Seq. ID
                    LIB3147-001-Q1-K2-B8
 Method
                    BLASTX
 NCBI GI
                    g114682
 BLAST score
                    279
 E value
                    5.0e-25
                    98
 Match length
                    59
 % identity
 NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                    (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                    >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
```

Seq. No. 215048

Seq. ID LIB3147-001-Q1-K2-B9

precursor (EC 3.6.1.3) [Ipomoea batatas]

3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit



```
Method BLASTX

NCBI GI g131187

BLAST score 140

E value 9.0e-09

Match length 32
% identity 81

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi 72681 pir F1SP3 photosystem I chain III precurs
```

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
>gi_72681_pir__F1SP3 photosystem I chain III precursor spinach >gi_21303_emb_CAA31523_ (X13133) PSI subunit IV
preprotein (AA -77 to 154) [Spinacia oleracea]

>gi_226166_prf__1413236A photosystem I reaction center IV

[Spinacia oleracea]

 Seq. No.
 215049

 Seq. ID
 LIB3147-001-Q1-K2-C10

 Method
 BLASTX

 NCBI GI
 g2129675

 BLAST score
 363

 E value
 1.0e-34

 Match length
 76

% identity 88

NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana

>gi_972938 (U19382) putative chlorophyll synthetase
[Arabidopsis thaliana] >gi_3068709 (AF049236) putative

chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 215050

Seq. ID LIB3147-001-Q1-K2-C11

Method BLASTX
NCBI GI g2245064
BLAST score 142
E value 7.0e-09
Match length 63
% identity 54

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 215051

Seq. ID LIB3147-001-Q1-K2-C12

Method BLASTX
NCBI GI g3236261
BLAST score 363
E value 1.0e-34
Match length 128
% identity 52

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 215052

Seq. ID LIB3147-001-Q1-K2-C3

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 3.0e-09
Match length 49
% identity 41

NCBI Description Xenopus laevis cDNA clone 27A6-1

NCBI GI

E value

BLAST score

Match length

q3986110

603 1.0e-62

143



```
215053
Seq. No.
Seq. ID
                   LIB3147-001-Q1-K2-C5
Method
                   BLASTX
                   q2129844
NCBI GI
BLAST score
                   472
E value
                   2.0e-47
Match length
                   148
 % identity
                   43
                   stress-induced protein stil - soybean
NCBI Description
 Seq. No.
                   215054
                   LIB3147-001-Q1-K2-C6
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g2497733
 BLAST score
                   149
                   2.0e-11
E value
Match length
                   65
 % identity
                   55
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
 NCBI Description
                   >gi 1177796 (M80567) non-specific lipid transfer protein
                   [Arabidopsis thaliana] >gi 3786018 (AC005499) unknown
                   protein [Arabidopsis thaliana]
                   215055
Seq. No.
                   LIB3147-001-Q1-K2-C7
 Seq. ID
Method
                   BLASTN
 NCBI GI
                   g2828187
 BLAST score
                   36
                   1.0e-10
 E value
                   44
Match length
                   95
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                   K21C13, complete sequence [Arabidopsis thaliana]
                   215056
 Seq. No.
                   LIB3147-001-Q1-K2-D12
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g730463
                   302
 BLAST score
 E value
                   2.0e-27
                   105
 Match length
                   57
 % identity
                   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 NCBI Description
                   >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                   protein L37 [Saccharomyces cerevisiae]
                   >gi 1420537 emb CAA99454_ (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                   215057
 Seq. No.
                   LIB3147-001-Q1-K2-D2
 Seq. ID
 Method
                   BLASTX
```

```
% identity
NCBI Description
                   (AB012716) heat shock protein 70 cognate [Salix gilgiana]
                   215058
Seq. No.
                  LIB3147-001-Q1-K2-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2055374
BLAST score
                   142
                   8.0e-09
E value
Match length
                   60
                   55
% identity
NCBI Description
                   (U29095) serine-threonine protein kinase [Triticum
                   aestivum]
                   215059
Seq. No.
Seq. ID
                   LIB3147-001-Q1-K2-D4
                  BLASTX
                   g3183219
```

Method NCBI GI BLAST score 197 4.0e-15 E value

Match length 134 % identity 39

NCBI Description HYPOTHETICAL PROTEIN KIAA0112 (HA0609)

>gi 434779 dbj BAA04948 (D25218) KIAA0112 [Homo sapiens]

Seq. No. 215060

Seq. ID LIB3147-001-Q1-K2-D5

Method BLASTX NCBI GI g541954 BLAST score 448 1.0e-44 E value 132 Match length 70 % identity

ubiquitin extension protein - white lupine NCBI Description

>gi_438111_emb_CAA80334_ (Z22613) ubiquitin extension

protein [Lupinus albus]

Seq. No. 215061

LIB3147-001-Q1-K2-D6 Seq. ID

Method BLASTX g3273743 NCBI GI BLAST score 213 E value 5.0e-17 Match length 94 45 % identity

(AF057357) lipid transfer protein 2 precursor [Arabidopsis NCBI Description

thaliana] >gi_3786019 (AC005499) unknown protein

[Arabidopsis thaliana]

Seq. No. 215062

LIB3147-001-Q1-K2-D9 Seq. ID

Method BLASTX NCBI GI q2961346 BŁAST score 224 E value 3.0e-20 Match length 107 % identity 50



(AL022140) pectinesterase like protein [Arabidopsis NCBI Description thaliana] 215063 Seq. No. LIB3147-001-Q1-K2-E1 Seq. ID Method BLASTX NCBI GI q3024017 542 BLAST score 1.0e-55 E value 119 Match length 90 % identity EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) NCBI Description (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia] Seq. No. 215064 LIB3147-001-Q1-K2-E11 Seq. ID Method BLASTX q2144271 NCBI GI BLAST score 410 4.0e-40E value 134 Match length % identity 65 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus NCBI Description kitakamiensis (fragment) >gi_1777372_dbj_BAA11578_ (D82814) cinnamic acid 4-hydroxylase [Populus kitakamiensis] Seq. No. 215065 Seq. ID LIB3147-001-Q1-K2-E12 Method BLASTX NCBI GI q4539009 BLAST score 145 E value 4.0e-09 77 Match length 48 % identity (AL049481) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 215066 LIB3147-001-Q1-K2-E2 Seq. ID Method BLASTX g3132472 NCBI GI BLAST score 143 E value 8.0e-09 56 Match length 50 % identity NCBI Description (AC003096) unknown protein [Arabidopsis thaliana] 215067 Seq. No.

LIB3147-001-Q1-K2-E3 Seq. ID

Method BLASTX NCBI GI q585203 BLAST score 546 E value 3.0e-56 Match length 120 % identity 79

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 3 (GLUTAMATE--AMMONIA LIGASE) (GS112) >gi 481808 pir S39479 glutamate--ammonia



mays]

>gi 434328 emb CAA46721 (X65928) glutamine synthetase [Zea

```
215068
Seq. No.
                  LIB3147-001-Q1-K2-E5
Seq. ID
                  BLASTX
Method
                  g1771780
NCBI GI
                  151
BLAST score
                  7.0e-10
E value
                  92
Match length.
% identity
                  41
                  (Y10024) ubiquitin extension protein [Solanum tuberosum]
NCBI Description
Seq. No.
                  215069
                  LIB3147-001-Q1-K2-E8
Seq. ID
                  BLASTN
Method
                  g166857
NCBI GI
                  33
BLAST score
                  5.0e-09
E value
                  89
Match length
                  84
% identity
                  Arabidopsis thaliana cytoplasmic ribosomal protein mRNA,
NCBI Description
                  complete cds
                  215070
Seq. No.
                  LIB3147-001-Q1-K2-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2661840
BLAST score
                   426
                   4.0e-42
E value
Match length
                  117
                   68
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                   215071
Seq. No.
                  LIB3147-001-Q1-K2-F1
Seq. ID
Method
                  BLASTX
                  g1052973
NCBI GI
                   287
BLAST score
                   8.0e-26
E value
                  72
Match length
                   81
% identity
NCBI Description (U37838) fructokinase [Beta vulgaris]
                   215072
Seq. No.
                   LIB3147-001-Q1-K2-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2104712
BLAST score
                   227
E value
                   1.0e-18
Match length
                   121
                   41
% identity
NCBI Description (U95180) endosperm specific protein [Zea mays]
```

ligase (EC 6.3.1.2) 1-3, cytosolic - maize

30018

215073

LIB3147-001-Q1-K2-F2

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g132939
BLAST score
                  363
                  8.0e-35
E value
Match length
                  102
                   67
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81657. pir JQ0771 ribosomal
NCBI Description
                  protein L3 (ARP1) - Arabidopsis thaliana >gi_166858
                   (M32654) ribosomal protein [Arabidopsis thaliana]
                  215074
Seq. No.
                  LIB3147-001-Q1-K2-F3
Seq. ID
Method
                  BLASTX
                   q508304
NCBI GI
BLAST score
                   350
                   4.0e-33
E value
Match length
                  79
                   80
% identity
                  (L22305) corC [Medicago sativa]
NCBI Description
                   215075
Seq. No.
                   LIB3147-001-Q1-K2-F5
Seq. ID
Method
                   BLASTX
                   g4115377
NCBI GI
                   355
BLAST score
                   1.0e-33
E value
Match length
                   145
% identity
                   48
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215076
Seq. No.
Seq. ID
                   LIB3147-001-Q1-K2-F6
Method
                   BLASTX
                   g3063396
NCBI GI
BLAST score
                   349
                   5.0e-33
E value
Match length
                   113
% identity
                   64
                  (AB012947) vcCyP [Vicia faba]
NCBI Description
                   215077
Seq. No.
                   LIB3147-001-Q1-K2-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3618214
                   155
BLAST score
                   3.0e-10
E value
Match length
                   107
% identity
                   32
                  (AL031579) dihydrofolate reductase [Schizosaccharomyces
NCBI Description
                   pombe]
```

Seq. No. 215078

Seq. ID LIB3147-001-Q1-K2-G1

Method BLASTX
NCBI GI g730463
BLAST score 322
E value 8.0e-30



Match length 105 % identity 59

NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)

>gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast

(Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal

protein L37 [Saccharomyces cerevisiae]

>gi 1420537 emb CAA99454 (Z75142) ORF YOR234c

[Saccharomyces cerevisiae]

Seq. No. 215079

Seq. ID LIB3147-001-Q1-K2-G11

Method BLASTX
NCBI GI g2498464
BLAST score 243
E value 1.0e-20
Match length 87
% identity 57

NCBI Description 28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF

ASSOCIATED PROTEIN) >gi_1136584 (U41745) PDGF associated

protein [Homo sapiens] >gi_1589642_prf__2211382B

platelet-derived growth factor-associated protein [Homo

sapiens]

Seq. No. 215080

Seq. ID LIB3147-001-Q1-K2-G12

Method BLASTX
NCBI GI g549742
BLAST score 145
E value 3.0e-09
Match length 58
% identity 41

NCBI Description HYPOTHETICAL 47.4 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION

>gi 539215 pir S38032 hypothetical protein YKL195w - yeast

(Saccharomyces cerevisiae) >gi_486347_emb_CAA82039_(Z28195) ORF YKL195w [Saccharomyces cerevisiae]

Seq. No. 215081

Seq. ID LIB3147-001-Q1-K2-G3

Method BLASTX
NCBI GI g1762939
BLAST score 321
E value 1.0e-29
Match length 89
% identity 65

NCBI Description (U66266) ORF; able to induce HR-like lesions [Nicotiana

tabacum]

Seq. No. 215082

Seq. ID LIB3147-001-Q1-K2-G7

Method BLASTX
NCBI GI 94580398
BLAST score 165
E value 1.0e-11
Match length 101
% identity 46

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

E value

Match length

% identity

1.0e-35

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

86

86



```
Seq. No.
                  215083
                  LIB3147-001-Q1-K2-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377797
BLAST score
                  329
                  7.0e-55
E value
Match length
                  141
                  74
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  215084
                  LIB3147-001-Q1-K2-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583123
BLAST score
                  419
                  3.0e-41
E value
Match length
                  134
% identity
                  62
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  215085
Seq. ID
                  LIB3147-001-Q1-K2-H5
Method
                  BLASTX
NCBI GI
                  g1710551
BLAST score
                  273
E value
                  4.0e-24
Match length
                  51
                  98
% identity
                  60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728
NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                  215086
                  LIB3147-001-Q1-K2-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  32
                  4.0e-09
E value
Match length
                  37
                  59
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  215087
Seq. ID
                  LIB3147-002-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q1169534
BLAST score
                  372
```

30021

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 542019 pir \$39203

Match length

% identity

148 70

NCBI Description probable ATP synthase chain - soybean

```
phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                  >gi 433609 emb CAA82232 (Z28386) enolase [Ricinus
                  communis]
Seq. No.
                  215088
Seq. ID
                  LIB3147-002-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1729927
BLAST score
                  237
E value
                  7.0e-20
Match length
                  68
% identity
                  60
NCBI Description
                  QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi 940182
                  (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
                  215089
Seq. No.
                  LIB3147-002-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707008
                  257
BLAST score
E value
                  3.0e-22
Match length
                  57
                  89
% identity
NCBI Description (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
                  thaliana]
Seq. No.
                  215090
                  LIB3147-002-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1871185
BLAST score
                  611
E value
                  1.0e-63
Match length
                  137
% identity
NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]
Seq. No.
                  215091
Seq. ID
                  LIB3147-002-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4539435
BLAST score
                  286
E value
                  1.0e-25
Match length
                  63
                  78
% identity
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]
Seq. No.
                  215092
Seq. ID
                  LIB3147-002-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q421876
BLAST score
                  519
                  7.0e-53
E value
```

30022

>gi_396230_emb_CAA52349_ (X74296) putative ATP synthase

Method

NCBI GI

BLASTX

g3128173



subunit [Glycine max]

```
Seq. No.
                  215093
                  LIB3147-002-Q1-K1-C9
Seq. ID
Method
                  BLASTX
                  g4323640
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
Match length
                  71
                  51
% identity
                  (AF102805) Peter Pan [Drosophila melanogaster]
NCBI Description
Seq. No.
                  215094
                  LIB3147-002-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1495768
BLAST score
                  282
                  6.0e-45
E value
                  141
Match length
% identity
                  68
NCBI Description
                  (Z68506) chloroplast inner envelope protein, 110 kD
                   (IEP110) [Pisum sativum]
                  215095
Seq. No.
Seq. ID
                  LIB3147-002-Q1-K1-E10
Method
                  BLASTX
                  g3288883
NCBI GI
BLAST score
                  193
                  3.0e-15
E value
Match length
                   60
% identity
                   67
NCBI Description (AB015431) SAR DNA binding protein [Oryza sativa]
                  215096
Seq. No.
Seq. ID
                  LIB3147-002-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   q3158476
BLAST score
                   525
E value
                  1.0e-53
Match length
                  132
% identity
                  80
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  215097
Seq. ID
                  LIB3147-002-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                   q3158476
BLAST score
                   476
E value
                   7.0e-48
Match length
                  148
% identity
                   68
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  215098
Seq. ID
                  LIB3147-002-Q1-K1-E9
```



84

% identity

```
159
BLAST score
E value
                  6.0e-16
                  115
Match length
                  49
% identity
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215099
                  LIB3147-002-Q1-K1-F10
Seq. ID
Method
                  BLASTX
                  g167367
NCBI GI
                  703
BLAST score
                  2.0e-74
E value
                  149
Match length
% identity
                  91
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
Seq. No.
                  215100
                  LIB3147-002-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979542
BLAST score
                  209
                  1.0e-16
E value
                  52
Match length
                  71
% identity
                  (AC003680) putative Ser/Thr kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215101
                  LIB3147-002-Q1-K1-G11
Seq. ID
                  BLASTN
Method
                  g2369713
NCBI GI
BLAST score
                  43
E value
                  7.0e-15
Match length
                  47
                  98
% identity
NCBI Description Beta vulgaris cDNA for elongation factor
Seq. No.
                  215102
                  LIB3147-002-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4572669
                  540
BLAST score
E value
                  2.0e-55
Match length
                  146
% identity
                   68
                  (AC006954) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   215103
                  LIB3147-002-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                   233
E value
                   2.0e-19
                  51
Match length
```

NCBI Description (Y12013) RAD23, isoform I [Daucus carota]



215104

LIB3147-002-Q1-K1-H12

Seq. No.

Seq. ID

```
Method
                  BLASTX
NCBI GI
                   g2462925
BLAST score
                   564
E value
                   3.0e-58
                  127
Match length
                   85
% identity
                  (AJ000053) GTP cyclohydrolase II /
NCBI Description
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
                   215105
Seq. No.
                  LIB3147-002-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                   g2119353
NCBI GI
BLAST score
                   363
                  1.0e-34
E value
                  134
Match length
                   52
% identity
NCBI Description calmodulin - moss (Physcomitrella patens)
                   215106
Seq. No.
                   LIB3147-003-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3023180
BLAST score
                   325
                   2.0e-30
E value
                   86
Match length
                   78
% identity
NCBI Description 14-3-3-LIKE PROTEIN 10 >gi 1771166 emb CAA67374.1 (X98866)
                   14-3-3 protein [Lycopersicon esculentum]
                   215107
Seq. No.
                   LIB3147-003-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3451411
BLAST score
                   465
                   4.0e-62
E value
Match length
                   139
% identity
                   80
NCBI Description (Z98761) seryl-tRNA synthetase [Helianthus annuus]
Seq. No.
                   215108
                   LIB3147-003-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2160322
BLAST score
                   547
E value
                   3.0e-56
Match length
                   107
                   94
% identity
NCBI Description
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
                   sylvestris]
Seq. No.
                   215109
                   LIB3147-003-Q1-K1-A3
Seq. ID
Method
                   BLASTX
```



NCBI GI g3377797
BLAST score 594
E value 1.0e-61
Match length 145
% identity 80

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 215110

Seq. ID LIB3147-003-Q1-K1-A4

Method BLASTX
NCBI GI g585960
BLAST score 211
E value 6.0e-17
Match length 43
% identity 93

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT

>gi 433665 emb CAA81412 (Z26753) Sec61 beta-subunit

homolog [Arabidopsis thaliana]

Seq. No. 215111

Seq. ID LIB3147-003-Q1-K1-A8

Method BLASTX
NCBI GI g1350707
BLAST score 208
E value 2.0e-16
Match length 97
% identity 45

NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal

protein 17K - mouse >qi 404766 (L08651) ribosomal protein

[Mus musculus]

Seq. No. 215112

Seq. ID LIB3147-003-Q1-K1-B1

Method BLASTX
NCBI GI g2688830
BLAST score 209
E value 3.0e-19
Match length 74
% identity 74

NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No. 215113

Seq. ID LIB3147-003-Q1-K1-B5

Method BLASTX
NCBI GI g1399450
BLAST score 740
E value 8.0e-79
Match length 143
% identity 99

NCBI Description (U47660) beta-tubulin 2 [Lupinus albus]

Seq. No. 215114

Seq. ID LIB3147-003-Q1-K1-B6



Method BLASTX
NCBI GI g3377797
BLAST score 523
E value 2.0e-53
Match length 124
% identity 83

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 215115

Seq. ID LIB3147-003-Q1-K1-B7

Method BLASTX
NCBI GI g2245021
BLAST score 383
E value 5.0e-37
Match length 127
% identity 57

NCBI Description (Z97341) heat shock protein 110 homolog [Arabidopsis

thaliana]

Seq. No. 215116

Seq. ID LIB3147-003-Q1-K1-B8

Method BLASTX
NCBI GI g1297190
BLAST score 255
E value 2.0e-25
Match length 90
% identity 69

NCBI Description (U53501) Theoretical protein with similarity to GenBank

Accession Number L22302 serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 215117

Seq. ID LIB3147-003-Q1-K1-B9

Method BLASTX
NCBI GI g3334244
BLAST score 444
E value 2.0e-44
Match length 104

Match length 104 % identity 77

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica

juncea]

Seq. No. 215118

Seq. ID LIB3147-003-Q1-K1-C11

Method BLASTX
NCBI GI 94249403
BLAST score 347
E value 5.0e-33
Match length 101
% identity 66

Match length

NCBI Description

% identity

96 90



```
(AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                  215119
Seq. No.
                  LIB3147-003-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                  g1785615
NCBI GI
                  238
BLAST score
                  6.0e-20
E value
                  68
Match length
                  66
% identity
NCBI Description
                  (U83281) protein kinase homolog PsPK4 [Pisum sativum]
Seq. No.
                  215120
                  LIB3147-003-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490705
                  407
BLAST score
                  7.0e-40
E value
Match length
                  111
                  77
% identity
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  215121
Seq. No.
                  LIB3147-003-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g1173187
NCBI GI
BLAST score
                  531
                  2.0e-54
E value
                  105
Match length
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
                  215122
                  LIB3147-003-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                  g3510540
NCBI GI
BLAST score
                  668
E value
                  2.0e-70
                  143
Match length
% identity
                  84
NCBI Description (AF038815) expansin [Prunus armeniaca]
Seq. No.
                  215123
Seq. ID
                  LIB3147-003-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q1076386
BLAST score
                  311
E value
                   1.0e-28
```

30028

protein kinase ADK1 - Arabidopsis thaliana >gi 1216484

(U48779) dual specificity kinase 1 [Arabidopsis thaliana]



```
215124
Seq. No.
Seq. ID
                  LIB3147-003-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g126770
BLAST score
                  270
                  9.0e-24
E value
                  54
Match length
                  96
% identity
                  MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate
NCBI Description
                  synthase (EC 4.1.3.2) - upland cotton
                  >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
                   [Gossypium hirsutum]
                  215125
Seq. No.
                  LIB3147-003-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  g2809326
NCBI GI
                   377
BLAST score
                  3.0e - 36
E value
                  118
Match length
% identity
                   61
                 (U72663) uricase II [Phaseolus vulgaris]
NCBI Description
                  215126
Seq. No.
                  LIB3147-003-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2558962
                   393
BLAST score
E value
                   4.0e-38
Match length
                  93
                   87
% identity
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
                   215127
Seq. No.
                  LIB3147-003-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2500354
BLAST score
                   676
                   2.0e-71
E value
Match length
                   131
                   95
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   215128
Seq. No.
                   LIB3147-003-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115377
BLAST score
                   237
E value
                   5.0e-20
Match length
                   58
                   76
% identity
```

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 215129

Seq. ID LIB3147-003-Q1-K1-D6

Method BLASTX



g3024127 NCBI GI 465 BLAST score 1.0e-46 E value 112 Match length % identity 80 S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1655578 emb_CAA95857_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus] Seq. No. 215130 LIB3147-003-Q1-K1-D7 Seq. ID BLASTX Method NCBI GI g3603473 457 BLAST score 1.0e-45 E value Match length 126 % identity 66 (AF090698) elicitor-responsive gene-3 [Oryza sativa] NCBI Description 215131 Seq. No. LIB3147-003-Q1-K1-E12 Seq. ID Method BLASTX g4127850 NCBI GI 259 BLAST score E value 1.0e-24 Match length 122 % identity 51 NCBI Description (AJ011003) MLL protein [Gallus gallus] 215132 Seq. No. LIB3147-003-Q1-K1-E3 Seq. ID BLASTX Method g1723239 NCBI GI BLAST score 295 1.0e-26 E value Match length 104 % identity 52 NCBI Description HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi 1177358 emb CAA93234 (Z69240) putative amidohydrolase [Schizosaccharomyces pombe] Seq. No. 215133 LIB3147-003-Q1-K1-F11 Seq. ID Method BLASTX NCBI GI q3033381 BLAST score 437

E value 1.0e-43Match length 97 % identity

(AC004238) putative UDP-galactose-4-epimerase [Arabidopsis NCBI Description

thaliana]

215134 Seq. No.

Seq. ID LIB3147-003-Q1-K1-F12

Method BLASTX NCBI GI g3882183



```
BLAST score
E value
                  2.0e-39
Match length
                  143
% identity
                  43
NCBI Description (AB018274) KIAA0731 protein [Homo sapiens]
Seq. No.
                  215135
                  LIB3147-003-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2865523
BLAST score
                  170
                  5.0e-12
E value
Match length
                  51
% identity
                  35
NCBI Description (AF044584) cold regulated LTCOR18 [Lavatera thuringiaca]
Seq. No.
                  215136
                  LIB3147-003-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3694872
BLAST score
                  488
E value
                  3.0e-49
Match length
                  116
% identity
                  81
NCBI Description (AF092547) profilin [Ricinus communis]
Seq. No.
                  215137
                  LIB3147-003-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173234
BLAST score
                  240
E value
                  3.0e-20
Match length
                  53
% identity
                  89
NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal
                  protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                  >gi_1584836_prf__2123431A ribosomal protein S25
                   [Lycopersicon esculentum]
Seq. No.
                  215138
Seq. ID
                  LIB3147-003-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3093294
BLAST score
                  338
E value
                  1.0e-31
Match length
                  136
% identity
                  61
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
Seq. No.
                  215139
Seq. ID
                  LIB3147-003-Q1-K1-F7
```

Method BLASTX NCBI GI g167367 BLAST score 686 E value 1.0e-72 Match length 129



```
% identity
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  215140
                  LIB3147-003-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q231683
BLAST score
                  630
                  7.0e-66
E value
                  154
Match length
% identity
                  73
NCBI Description
                 CALNEXIN HOMOLOG PRECURSOR >gi 421825 pir JN0597
                  calnexin-like protein - Arabidopsis thaliana
                  >gi_16211 emb CAA79144 (Z18242) calnexin homolog
                  [Arabidopsis thaliana]
Seq. No.
                  215141
                  LIB3147-003-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132935
BLAST score
                  224
E value
                  2.0e-18
                  65
Match length
                  62
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
                  >gi 101568 pir S18431 ribosomal protein L35a.e.c16 - yeast
                  (Saccharomyces cerevisiae) >gi 4392 emb CAA41035 (X57969)
                  ribosomal protein L37a [Saccharomyces cerevisiae]
                  >gi_1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]
                  >gi_1370305_emb_CAA97847 (Z73499) ORF_YPL143w
                  [Saccharomyces cerevisiae]
Seq. No.
                  215142
                  LIB3147-003-Q1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  1.0e-11
Match length
                  49
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  215143
Seq. ID
                  LIB3147-003-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q267072
BLAST score
                  775
E value
                  6.0e-83
Match length
                  150
% identity
NCBI Description
                  TUBULIN BETA-1 CHAIN >gi 100072 pir S20868 tubulin beta-1
                  chain - garden pea >gi_20758_emb CAA38613 (X54844)
```

Seq. No. 215144

Seq. ID LIB3147-003-Q1-K1-G7

Method BLASTX

beta-tubulin 1 [Pisum sativum]



```
NCBI GI
                  g2245125
BLAST score
                  172
E value
                   3.0e-12
Match length
                  45
% identity
                  64
NCBI Description
                 (Z97343) hypothetical protein [Arabidopsis thaliana]
                  215145
Seq. No.
                  LIB3147-003-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  583
E value
                  2.0e-60
Match length
                  116
% identity
                  99
NCBI Description
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567 (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
Seq. No.
                  215146
                  LIB3147-003-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3355472
BLAST score
                  278
E value
                  6.0e-25
                  80
Match length
                  69
% identity
                  (AC004218) disease resistance response protein (206-d) like
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  215147
                  LIB3147-003-Q1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2564044
BLAST score
                  48
E value
                  6.0e-18
Match length
                  146
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  215148
Seq. ID
                  LIB3147-003-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4325370
BLAST score
                  353
E value
                  1.0e-33
                  99
Match length
% identity
NCBI Description
                  (AF128396) similar to human phosphotyrosyl phosphatase
```

Seq. No. 215149

Seq. ID LIB3147-003-Q1-K1-H2

Method BLASTX NCBI GI g2347194

30033

activator PTPA (GB:X73478) [Arabidopsis thaliana]



BLAST score 191 E value 2.0e-14 Match length 115 % identity 41

NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 215150

Seq. ID LIB3147-003-Q1-K1-H4

Method BLASTX
NCBI GI g2335099
BLAST score 476
E value 7.0e-48
Match length 143
% identity 63

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 215151

Seq. ID LIB3147-003-Q1-K1-H5

Method BLASTN
NCBI GI g2804257
BLAST score 38
E value 6.0e-12
Match length 194
% identity 80

NCBI Description Arabidopsis thaliana DNA for phosphoglycerate

dehydrogenase, complete cds

Seq. No. 215152

Seq. ID LIB3147-003-Q1-K1-H6

Method BLASTX
NCBI GI g1532168
BLAST score 231
E value 4.0e-19
Match length 66
% identity 64

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 215153

Seq. ID LIB3147-003-Q1-K1-H7

Method BLASTX
NCBI GI g1168258
BLAST score 594
E value 6.0e-62
Match length 146
% identity 83

NCBI Description ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR

(TRANSAMINASE A) >gi 693692 (U15034) aspartate

aminotransferase [Arabidopsis thaliana]

Seq. No. 215154

Seq. ID LIB3147-003-Q1-K1-H8

Method BLASTX NCBI GI q3033380



```
BLAST score
                   456
                   4.0e-49
E value
Match length
                  118
                  80
% identity
NCBI Description
                  (AC004238) putative coatomer epsilon subunit [Arabidopsis
                  thaliana]
                  215155
Seq. No.
                  LIB3147-004-Q1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2558943
                  57
BLAST score
E value
                  2.0e-23
                  69
Match length
                  96
% identity
NCBI Description Gossypium hirsutum histone 3 mRNA, complete cds
                  215156
Seq. No.
                  LIB3147-004-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982434
BLAST score
                  259
                  2.0e-22
E value
                  110
Match length
% identity
                  46
                 (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215157
                  LIB3147-004-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1762939
BLAST score
                  164
                  1.0e-11
E value
Match length
                   62
                   52
% identity
NCBI Description
                  (U66266) ORF; able to induce HR-like lesions [Nicotiana
                   tabacum]
Seq. No.
                   215158
Seq. ID
                  LIB3147-004-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2827710
BLAST score
                  285
E value
                   1.0e-25
Match length
                  70
                   71
% identity
NCBI Description
                   (ALO21684) lysosomal Pro-X carboxypeptidase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   215159
Seq. ID
                  LIB3147-004-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                   q4567259
BLAST score
                   53
E value
```

30035

6.0e-21

148

85

Match length

% identity



NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

215160 Seq. No.

Seq. ID LIB3147-004-Q1-K1-A9

Method BLASTX g3668086 NCBI GI BLAST score 376 4.0e-36 E value Match length 128 % identity 61

(AC004667) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 215161

LIB3147-004-Q1-K1-B1 Seq. ID

Method BLASTX NCBI GI g1168189 BLAST score 478 E value 3.0e-48Match length 126 83 % identity

NCBI Description 14-3-3-LIKE PROTEIN A (VFA-1433A) >gi_1076542_pir__S52899

14-3-3 brain protein homolog - fava bean

>gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein

homolog [Vicia faba]

Seq. No. 215162

LIB3147-004-Q1-K1-B12 Seq. ID

Method BLASTX NCBI GI g3980383 BLAST score 267 E value 2.0e-30 Match length 83

73 % identity

NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]

Seq. No. 215163

Seq. ID LIB3147-004-Q1-K1-B2

Method BLASTN NCBI GI q3821780 BLAST score 36 E value 8.0e-11 Match length 48 67 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 215164

Seq. ID LIB3147-004-Q1-K1-B4

Method BLASTX NCBI GI g3250675 BLAST score 401 E value 5.0e-39 Match length 138 % identity

(AL024486) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 215165



```
Seq. ID
                  LIB3147-004-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q4567279
BLAST score
                  151
E value
                  8.0e-10
Match length
                  48
% identity
                   58
                  (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  215166
Seq. ID
                  LIB3147-004-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3093294
BLAST score
                  200
                  2.0e-15
E value
Match length
                  66
% identity
                  64
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
Seq. No.
                  215167
Seq. ID
                  LIB3147-004-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q4240116
BLAST score
                  425
E value
                  6.0e-42
Match length
                  92
% identity
                  83
                  (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                  thaliana] >gi_4240118_dbj_BAA74838_ (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                  215168
Seq. ID
                  LIB3147-004-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3892051
BLAST score
                  427
E value
                  4.0e-42
Match length
                  119
                  73
% identity
NCBI Description
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
                   [Arabidopsis thaliana]
Seq. No.
                  215169
Seq. ID
                  LIB3147-004-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1346735
BLAST score
                  739
E value
                  1.0e-78
Match length
                  149
% identity
                  93
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                  (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
```

phosphoglycerate mutase [Ricinus communis]

>gi_1076562_pir__S49647 phosphoglycerate mutase (EC
5.4.2.1) - castor bean >gi 474170 emb CAA49995 (X70652)



```
Seq. No.
                   215170
Seq. ID
                   LIB3147-004-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2146732
BLAST score
                   465
E value
                   1.0e-46
Match length
                   123
% identity
                   76
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi 1373396
                   (U57838) rof1 [Arabidopsis thaliana]
Seq. No.
                   215171
Seq. ID
                  LIB3147-004-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   q1084389
BLAST score
                   104
E value
                   2.0e-11
Match length
                   110
% identity
                   48
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - castor bean
Seq. No.
                   215172
Seq. ID
                  LIB3147-004-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q1408471
BLAST score
                   394
E value
                   3.0e-57
Match length
                   131
% identity
                   83
NCBI Description
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                  215173
Seq. No.
Seq. ID
                  LIB3147-004-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q2244799
BLAST score
                   454
E value
                   3.0e-45
Match length
                  138
% identity
                   61
NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.
                  215174
Seq. ID
                  LIB3147-004-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  g2244733
BLAST score
                  46
E value
                  5.0e-17
Match length
                  115
% identity
                  84
NCBI Description Cotton mRNA for actin, clone CF456, partial cds
```

Seq. No. 215175

Seq. ID LIB3147-004-Q1-K1-D12

Method BLASTX NCBI GI g3660467



```
BLAST score
                   7.0e-25
E value
Match length
                  70
                   77
% identity
NCBI Description
                   (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
                   215176
Seq. No.
Seq. ID
                  LIB3147-004-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   g1173234
BLAST score
                   309
E value
                   3.0e-28
Match length
                   72
% identity
                   85
NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi 481909 pir S40089 ribosomal
                   protein S25 - tomato >gi 435679 emb \overline{CAA54132} (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                   >gi_1584836_prf__2123431A ribosomal protein S25
                   [Lycopersicon esculentum]
                  215177
Seq. No.
Seq. ID
                  LIB3147-004-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                   q3075391
BLAST score
                   319
E value
                   1.0e-29
Match length
                   69
% identity
                   88
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                  215178
Seq. ID
                  LIB3147-004-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   g2493146
BLAST score
                   485
E value
                   6.0e-49
Match length
                   135
                   76
% identity
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >qi 755148
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                   [Gossypium hirsutum] >gi 4519415 dbj BAA75542.1 (AB024275)
                   vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                   215179
Seq. ID
                  LIB3147-004-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2738248
```

BLAST score 421 E value 1.0e-41 84 Match length 93 % identity

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 215180

Seq. ID LIB3147-004-Q1-K1-E2



```
BLASTX
Method
NCBI GI
                   g4008159
BLAST score
                   573
E value
                   3.0e-59
Match length
                   118
% identity
                   87
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                   215181
Seq. ID
                   LIB3147-004-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g266945
BLAST score
                   635
E value
                   2.0e-66
Match length
                   147
% identity
                   85
NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                   >gi 100065 pir S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum] >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                    [Pisum sativum]
Seq. No.
                   215182
Seq. ID
                   LIB3147-004-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   q4558672
BLAST score
                   166
E value
                   7.0e-12
Match length
                   42
                   74
% identity
NCBI Description (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
                   thaliana]
Seq. No.
                   215183
Seq. ID
                   LIB3147-004-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g122106
BLAST score
                   284
E value
                   4.0e-33
                   78
Match length
% identity
                   94
NCBI Description HISTONE H4 >gi_70771_pir HSZM4 histone H4 - maize
                   >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                   >gi 2119028 pir S60475 histone H4 - garden pea
                   >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                   aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                   thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
                   >gi 168501 (M13370) histone H4 [Zea mays] >gi 168503
                    (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                   H4 homolog [Pisum sativum] >qi 1806285 emb CAB01914
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                   >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                   >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
```

[Arabidopsis thaliana]

[Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4



```
Seq. No.
                  215184
                  LIB3147-004-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3548801
BLAST score
                  207
E value
                  2.0e-29
Match length
                  110
% identity
NCBI Description
                  (AC005313) putative transmembrane protein [Arabidopsis
                  thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative
                  integral membrane protein [Arabidopsis thaliana]
                  215185
Seq. No.
Seq. ID
                  LIB3147-004-Q1-K1-F1
Method
                  BLASTX
                  q3093294
NCBI GI
BLAST score
                  282
                  4.0e-25
E value
                  63
Match length
                  83
% identity
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
Seq. No.
                  215186
Seq. ID
                  LIB3147-004-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1172835
BLAST score
                  547
                  3.0e-56
E value
Match length
                  109
% identity
                  94
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-A1 >gi 496268 (L16767)
                  GTP-binding protein [Nicotiana tabacum]
Seq. No.
                  215187
Seq. ID
                  LIB3147-004-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q973313
BLAST score
                  693
E value
                   3.0e-73
Match length
                  146
% identity
                   91
NCBI Description (U30250) myo-inositol 1-phosphate synthase isozyme-2
                   [Arabidopsis thaliana]
                  215188
Seq. No.
Seq. ID
                  LIB3147-004-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2146732
```

BLAST score 497 E value 3.0e-50Match length 130 75 % identity

NCBI Description FK506-binding protein - Arabidopsis thaliana >gi 1373396

(U57838) rof1 [Arabidopsis thaliana]

Seq. No. 215189

Seq. ID LIB3147-004-Q1-K1-F2

NCBI GI

E value

BLAST score

q973313

2.0e-74

702



```
Method
                    BLASTX
 NCBI GI
                    g3702368
 BLAST score
                    391
 E value
                    6.0e-38
 Match length
                    98
 % identity
                    76
 NCBI Description (AJ001855) alpha subunit of F-actin capping protein
                    [Arabidopsis thaliana]
 Seq. No.
                    215190
 Seq. ID
                   LIB3147-004-Q1-K1-F3
 Method
                   BLASTX
 NCBI GI
                    g3885515
 BLAST score
                    446
 E value
                    2.0e-44
 Match length
                    103
 % identity
                    81
 NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago
                    sativa]
 Seq. No.
                    215191
 Seq. ID
                    LIB3147-004-Q1-K1-F4
 Method
                   BLASTX
 NCBI GI
                    g2661840
. BLAST score
                   523
 E value
                    2.0e-53
 Match length
                   147
                    67
 % identity
 NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
 Seq. No.
                    215192
 Seq. ID
                   LIB3147-004-Q1-K1-F5
 Method
                   BLASTX
 NCBI GI
                    g1222552
 BLAST score
                    632
 E value
                    4.0e-66
 Match length
                   139
 % identity
                    83
 NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
 Seq. No.
                    215193
 Seq. ID
                    LIB3147-004-Q1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    g4191788
 BLAST score
                    556
                    3.0e-57
 E value
 Match length
                   129
                   78
 % identity
 NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate
                    oxidase [Arabidopsis thaliana]
 Seq. No.
                    215194
 Seq. ID
                   LIB3147-004-Q1-K1-F9
 Method
                   BLASTX
```



```
Match length
% identity
                   94
NCBI Description
                   (U30250) myo-inositol 1-phosphate synthase isozyme-2
                   [Arabidopsis thaliana]
Seq. No.
                   215195
Seq. ID
                  LIB3147-004-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                   q1708777
BLAST score
                   438
E value
                   1.0e-43
Match length
                   108
% identity
                   78
NCBI Description
                  (Z83202) potassium channel [Arabidopsis thaliana]
                  >gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel
                  protein [Arabidopsis thaliana] >gi_4090537 (U73325) K+
                  inward rectifying channel protein [Arabidopsis thaliana]
                   >gi 4098949 (U81239) K+ inward rectifying channel
                   [Arabidopsis thaliana]
Seq. No.
                  215196
Seq. ID
                  LIB3147-004-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2765366
BLAST score
                  187
E value
                   4.0e-14
Match length
                  100
% identity
                   40
NCBI Description (Y14038) putative Ole e 1 protein [Betula pendula]
Seq. No.
                  215197
Seq. ID
                  LIB3147-004-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g266989
BLAST score
                  464
E value
                  9.0e-47
Match length
                  89
% identity
                  98
NCBI Description
                  GTP-BINDING PROTEIN SAR1B >qi 322517 pir S28603
                  GTP-binding protein - Arabidopsis thaliana >gi 166734
                  (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  215198
Seq. ID
                  LIB3147-004-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1778372
BLAST score
                  161
E value
                  3.0e-11
Match length
                  57
% identity
```

NCBI Description (U77679) asparagine synthetase 1 [Glycine max]

Seq. No. 215199

Seq. ID LIB3147-004-Q1-K1-G4

Method BLASTX NCBI GI g115492 BLAST score 743



E value 3.0e-79 Match length 145 % identity 61

NCBI Description CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No. 215200

Seq. ID LIB3147-004-Q1-K1-G5

Method BLASTX
NCBI GI g2429280
BLAST score 532
E value 2.0e-63
Match length 136
% identity 88

NCBI Description (AF014055) asparagine synthetase [Triphysaria versicolor] >gi_2429282 (AF014056) asparagine synthetase [Triphysaria

versicolor] >gi_2429284 (AF014057) asparagine synthetase

[Triphysaria versicolor]

Seq. No. 215201

Seq. ID LIB3147-004-Q1-K1-G7

Method BLASTX
NCBI GI g3540219
BLAST score 208
E value 1.0e-16
Match length 59
% identity 59

NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 215202

Seq. ID LIB3147-004-Q1-K1-G8

Method BLASTX
NCBI GI g3252807
BLAST score 488
E value 3.0e-49
Match length 147
% identity 63

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 215203

Seq. ID LIB3147-004-Q1-K1-G9

Method BLASTX
NCBI GI g626029
BLAST score 164
E value 2.0e-11
Match length 89
% identity 40

NCBI Description pollen allergen Lol p XI - perennial ryegrass

 $>gi_1582249_prf_2118270A$ allergen Lol p XI [Lolium

perenne]

Seq. No. 215204

Seq. ID LIB3147-004-Q1-K1-H1

Method BLASTX
NCBI GI g129248
BLAST score 173
E value 2.0e-12



```
Match length
                    100
% identity
                    24
                    ORGAN SPECIFIC PROTEIN S2 >qi 72318 pir KNPMS2 protein S2
NCBI Description
                    - garden pea >gi_295831_{emb}C\overline{A}A3594\overline{4} (\overline{X5}1595) S2 protein
                    [Pisum sativum]
Seq. No.
                    215205
Seq. ID
                    LIB3147-004-Q1-K1-H10
Method
                    BLASTN
NCBI GI
                    g3046851
BLAST score
                    43
E value
                    6.0e-15
Match length
                    139
% identity
                    39
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. ID LIB3147-004-Q1-K1-H11 Method BLASTX NCBI GI g2982434 BLAST score 269 E value 1.0e-23 Match length 119 % identity 45

215206

Seq. No.

% identity

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

 Seq. No.
 215207

 Seq. ID
 LIB3147-004-Q1-K1-H3

 Method
 BLASTX

 NCBI GI
 g872116

 BLAST score
 639

 E value
 6.0e-67

 Match length
 148

NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 215208

Seq. ID LIB3147-004-Q1-K1-H4

36

Method BLASTX
NCBI GI g1351014
BLAST score 367
E value 3.0e-35
Match length 91
% identity 80

NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)

ribosomal protein S8 [Oryza sativa]

Seq. No. 215209

Seq. ID LIB3147-004-Q1-K1-H5

Method BLASTX
NCBI GI g3176668
BLAST score 480
E value 1.0e-61
Match length 141
% identity 85

NCBI Description (AC004393) Similar to ribosomal protein L17 gb_X62724 from



Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

```
Seq. No.
                  215210
                  LIB3147-004-Q1-K1-H6
Seq. ID
Method
                  BLASTX
                  q2827634
NCBI GI
BLAST score
                  193
E value
                  1.0e-14
                  93
Match length
% identity
                  48
                 (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  215211
Seq. No.
Seq. ID
                  LIB3147-004-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3559814
                  536
BLAST score
                  5.0e-55
E value
Match length
                  114
                  92
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
                  215212
Seq. No.
                  LIB3147-005-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1864017
BLAST score
                   497
                   1.0e-50
E value
Match length
                  95
% identity
                   99
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   215213
Seq. ID
                  LIB3147-005-Q1-K1-A10
Method
                  BLASTX
                   q1653702
NCBI GI
BLAST score
                   501
E value
                   8.0e-51
Match length
                   142
% identity
                   69
                  (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                  of pyruvate dehydrogenase complex [Synechocystis sp.]
                   215214
Seq. No.
Seq. ID
                   LIB3147-005-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g1619300
BLAST score
                   412
E value
                   2.0e-40
Match length
                   100
                   73
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
```

Seq. No. 215215
Seq. ID LIB3147-005-Q1-K1-A4

Mathad DIACTY

Method BLASTX



```
q3080390
NCBI GI
BLAST score
                  402
                  3.0e-39
E value
Match length
                  117
% identity
                   64
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  215216
Seq. No.
                  LIB3147-005-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                  g868156
NCBI GI
BLAST score
                  159
E value
                  1.0e-17
                  78
Match length
                   67
% identity
                  (U26538) similar to mipB gene product in Mesembryanthemum
NCBI Description
                  crystallinum, encoded by Genbank Accession Number L36097;
                  MIP homolog; Method: conceptual translation supplied by
                  author. [Mesembryanthemum crystallinum]
                  215217
Seq. No.
                  LIB3147-005-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2114046
BLAST score
                   468
E value
                   3.0e-47
Match length
                  102
                   91
% identity
                  (AB002147) water channel protein [Nicotiana excelsior]
NCBI Description
Seq. No.
                   215218
                  LIB3147-005-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2695931
BLAST score
                   376
E value
                   3.0e - 36
Match length
                   82
% identity
NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.
                   215219
                   LIB3147-005-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464980
BLAST score
                   403
E value
                   2.0e-39
                   76
Match length
                   99
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
```

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 (L06967)

ubiquitin carrier protein [Medicago sativa]

215220 Seq. No.

Seq. ID LIB3147-005-Q1-K1-B8

BLASTX Method NCBI GI g3094012 BLAST score 356

```
E value
                   6.0e-34
Match length
                  76
% identity
                  84
                 (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
NCBI Description
Seq. No.
                  215221
                  LIB3147-005-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567251
BLAST score
                  226
E value
                  1.0e-18
Match length
                  55
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  215222
Seq. ID
                  LIB3147-005-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g829169
BLAST score
                  472
E value
                  6.0e-51
Match length
                  113
% identity
NCBI Description (L33263) beta-tubulin [Oryza sativa]
Seq. No.
                  215223
Seq. ID
                  LIB3147-005-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1173027
BLAST score
                  197
E value
                  3.0e-15
Match length
                  63
                  67
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                  215224
Seq. ID
                  LIB3147-005-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  176
E value
                  4.0e-13
Match length
                  39
                  95
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
```

Seq. No. 215225

Seq. ID LIB3147-005-Q1-K1-C6

Method BLASTX NCBI GI g1742953 BLAST score 347 E value 8.0e-33 Match length 85 % identity

NCBI Description (Z71445) CLC-a chloride channel protein [Arabidopsis

thaliana]

Seq. No.

Seq. ID

215231

LIB3147-005-Q1-K1-D6



```
Seq. No.
                   215226
Seq. ID
                   LIB3147-005-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2960216
BLAST score
                   496
E value
                   3.0e-50
Match length
                   120
% identity
                   80
NCBI Description (AJ223384) 26S proteasome regulatory ATPase subunit 10b
                   (S10b) [Manduca sexta]
Seq. No.
                   215227
Seq. ID
                   LIB3147-005-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g730450
BLAST score
                   575
                   2.0e-59
E value
Match length
                   131
% identity
                   81
NCBI Description
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
>gi_398922_emb_CAA80343_ (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   215228
Seq. No.
Seq. ID
                   LIB3147-005-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4455328
BLAST score
                   276
E value
                   1.0e-24
Match length
                   59
% identity
                   81
NCBI Description (AL035525) hypothetical protein [Arabidopsis thaliana]
                   215229
Seq. No.
Seq. ID
                   LIB3147-005-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   q4514716
BLAST score
                   205
E value
                   2.0e-16
                   91
Match length
                   41
% identity
NCBI Description (AB017533) EPc [Nicotiana tabacum]
                   215230
Seq. No.
Seq. ID
                   LIB3147-005-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   q2970051
BLAST score
                   262
E value
                   6.0e-23
Match length
                   60
% identity
                   82
NCBI Description (AB012110) ARG10 [Vigna radiata]
```



Method BLASTX NCBI GI q4191791 BLAST score 187 E value 5.0e-14Match length 49 % identity 76 (AC005917) putative sf21 {Helianthus annuus} protein NCBI Description [Arabidopsis thaliana] Seq. No. 215232 LIB3147-005-Q1-K1-D7 Seq. ID Method BLASTX NCBI GI g2129783 BLAST score 158 E value 1.0e-10 Match length 59 % identity 54 NCBI Description cystatin - field mustard >gi 762785 (L41355) cysteine proteinase inhibitor [Brassica campestris] Seq. No. 215233 Seq. ID LIB3147-005-Q1-K1-D9 Method BLASTN NCBI GI g2062705 BLAST score 36 E value 7.0e-11 Match length 48 % identity 33 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds Seq. No. 215234 Seq. ID LIB3147-005-Q1-K1-E11 Method BLASTX NCBI GI g136644 BLAST score 190 E value 2.0e-14 71 Match length 52 % identity NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100765 pir A34506 23K ubiquitin carrier protein E2 - wheat $>gi_170782$ (M28059) ubiquitin carrier protein [Triticum vulgare] Seq. No. 215235 Seq. ID LIB3147-005-Q1-K1-E2 Method BLASTX NCBI GI q3063396 BLAST score 357 E value 3.0e - 34Match length 72

% identity 90

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 215236

Seq. ID LIB3147-005-Q1-K1-E7

Method BLASTN NCBI GI g2267582

NCBI GI

E value

BLAST score

Match length

g549056

5.0e-11

161

46



```
BLAST score
                   201
E value
                   1.0e-109
Match length
                  251
% identity
                  96
                  Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA,
NCBI Description
                  complete cds
Seq. No.
                  215237
Seq. ID
                  LIB3147-005-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4539545
BLAST score
                  349
                  3.0e - 33
E value
Match length
                  91
                  79
% identity
NCBI Description
                 (Y16644) PRCI [Nicotiana tabacum]
                  215238
Seq. No.
                  LIB3147-005-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4176531
BLAST score
                  243
E value
                  1.0e-20
Match length
                  130
% identity
                  45
NCBI Description
                  (AL035263) weak similarity to chick phosphatidylcholine-ste
                  rol acetyltransferase [Schizosaccharomyces pombe]
                  215239
Seq. No.
                  LIB3147-005-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191128
BLAST score
                   374
                   6.0e - 36
E value
Match length
                  131
% identity
NCBI Description
                  (AF007269) belongs to the L5P family of ribosomal proteins
                   [Arabidopsis thaliana]
Seq. No.
                   215240
Seq. ID
                  LIB3147-005-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                   g2191128
BLAST score
                  346
E value
                   1.0e-32
Match length
                  112
% identity
                   69
                  (AF007269) belongs to the L5P family of ribosomal proteins
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   215241
Seq. ID
                  LIB3147-005-Q1-K1-F2
Method
                  BLASTX
```



```
% identity
                   T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA)
NCBI Description
                   >gi 631651 pir S43059 CCT (chaperonin containing TCP-1)
                   beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
Seq. No.
                   215242
Seq. ID
                   LIB3147-005-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g2275196
BLAST score
                   271
E value
                   3.0e-24
Match length
                   74
% identity
                   70
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   215243
Seq. ID
                   LIB3147-005-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g3241943
BLAST score
                   461
E value
                   2.0e-46
Match length
                   98
                   85
% identity
NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]
                   215244
Seq. No.
                   LIB3147-005-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2661840
BLAST score
                   328
                   7.0e-31
E value
Match length
                   93
% identity
                   63
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                   215245
Seq. No.
Seq. ID
                   LIB3147-005-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g3924596
BLAST score
                   616
E value
                   3.0e-64
Match length
                   140
% identity
                   81
NCBI Description
                  (AF069442) putative phospho-ser/thr phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                   215246
Seq. ID
                   LIB3147-005-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g951427
BLAST score
                   496
E value
                   3.0e-50
Match length
                   112
% identity
```

30052

NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus



communis]

```
Seq. No.
                  215247
                  LIB3147-005-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827630
BLAST score
                  297
E value
                   4.0e-27
Match length
                  78
                  81
% identity
                 (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  215248
Seq. No.
Seq. ID
                  LIB3147-005-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1706329
BLAST score
                  476
                   6.0e-48
E value
Match length
                  119
% identity
                   76
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                   >gi_2146788_pir__S65471 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC2) - Garden pea (fragment)
                   >gi_1177605_emb_CAA91445_ (Z66544) pyruvate decarboxylase
                   [Pisum sativum]
                   215249
Seq. No.
                   LIB3147-005-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g81857
BLAST score
                   340
                   5.0e-32
E value
                   71
Match length
% identity
                   90
NCBI Description
                  IgE-dependent histamine-releasing factor homolog - alfalfa
                   (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally
                   controlled tumor protein [Medicago sativa]
Seq. No.
                   215250
Seq. ID
                   LIB3147-005-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                   g4455207
                   398
BLAST score
E value
                   9.0e-39
Match length
                   95
% identity
NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                   215251
Seq. ID
                   LIB3147-005-Q1-K1-G8
                  BLASTX
Method
NCBI GI
                   g1407705
BLAST score
                   249
E value
                   2.0e-21
Match length
                  83
% identity
```

NCBI Description (U60202) lipoxygenase [Solanum tuberosum]



```
Seq. No.
                   215252
                   LIB3147-005-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911070
                   326
BLAST score
                   3.0e-30
E value
Match length
                   124
% identity
                   49
                  (AL021960) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215253
                   LIB3147-005-Q1-K1-H11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2865522
                   38
BLAST score
                   6.0e-12
E value
Match length
                   103
                   92
% identity
NCBI Description Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
                   complete cds
                   215254
Seq. No.
                   LIB3147-005-Q1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3122673
                   503
BLAST score
                   5.0e-51
E value
                   130
Match length
                   76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   215255
Seq. No.
Seq. ID
                   LIB3147-005-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   q464849
BLAST score
                   611
E value
                   1.0e-63
Match length
                   142
% identity
                   86
                   TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20\overline{4}\overline{13} emb \overline{CAA4763}5 (X67162)
                   alpha-tubulin [Prunus dulcis]
Seq. No.
                   215256
Seq. ID
                   LIB3147-005-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   q625509
BLAST score
                   556
E value
                   2.0e-57
Match length
                   124
                   25
% identity
```

Seq. No. 215257

Seq. ID LIB3147-005-Q1-K1-H6

30054

NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)



Method BLASTX
NCBI GI g2909781
BLAST score 246
E value 2.0e-21
Match length 101
% identity 60

NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump

[Arabidopsis thaliana]

Seq. No. 215258

Seq. ID LIB3147-005-Q1-K1-H9

Method BLASTN
NCBI GI g563624
BLAST score 53
E value 6.0e-21
Match length 170
% identity 92

NCBI Description S.tuberosum (PU141) mRNA for U14 small nucleolar RNA

Seq. No. 215259

Seq. ID LIB3147-006-Q1-K1-A1

Method BLASTX
NCBI GI g2353173
BLAST score 380
E value 1.0e-36
Match length 94
% identity 79

NCBI Description (AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No. 215260

Seq. ID LIB3147-006-Q1-K1-A11

Method BLASTX
NCBI GI g2623310
BLAST score 176
E value 6.0e-13
Match length 105
% identity 43

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

>qi 3402721 (AC004261) unknown protein [Arabidopsis

thaliana]

Seq. No. 215261

Seq. ID LIB3147-006-Q1-K1-A12

Method BLASTX
NCBI GI g2129842
BLAST score 169
E value 7.0e-12
Match length 53
% identity 57

NCBI Description SE60 protein - soybean >gi_509769_emb_CAA79164_ (Z18359)

seed-specific low molecular weight sulfur-rich protein

[Glycine max]

Seq. No. 215262

Seq. ID LIB3147-006-Q1-K1-A5

Method BLASTX NCBI GI g1052956



```
BLAST score
                  6.0e-11
E value
Match length
                  44
                  76
% identity
NCBI Description (U39747) high mobility group protein 2 HMG2 [Ipomoea nil]
                  215263
Seq. No.
                  LIB3147-006-Q1-K1-A6
Seq. ID
Method
                  BLASTX
                  g3600047
NCBI GI
BLAST score
                  344
                  3.0e - 39
E value
Match length
                  146
                  63
% identity
                  (AF080120) similar to elongation factor EF-Ts [Arabidopsis
NCBI Description
                  thaliana]
                  215264
Seq. No.
                  LIB3147-006-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974782
BLAST score
                   425
                  7.0e-42
E value
                  85
Match length
                   98
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   215265
Seq. No.
                  LIB3147-006-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                   g3242704
NCBI GI
BLAST score
                   308
                   2.0e-28
E value
Match length
                   109
% identity
                   54
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]
                   215266
Seq. No.
                   LIB3147-006-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1477428
BLAST score
                   520
                   6.0e-53
E value
                   106
Match length
% identity
                   92
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
                   215267
Seq. No.
Seq. ID
                   LIB3147-006-Q1-K1-B3
                   BLASTX
Method
NCBI GI
                   g1346882
                   390
BLAST score
                   7.0e-38
E value
                   93
Match length
                   80
% identity
NCBI Description PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi_2129505_pir_S56668
```

Seq. No.

geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) precursor - muskmelon >gi_870985_emb_CAA85775_ (Z37543) phytoene synthase [Cucumis melo]

215268 Seq. No. LIB3147-006-Q1-K1-B7 Seq. ID Method BLASTX q1172977 NCBI GI BLAST score 387 2.0e-37 E value Match length 97 76 % identity 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic NCBI Description ribosomal protein L18 [Arabidopsis thaliana] 215269 Seq. No. LIB3147-006-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI q2244792 BLAST score 684 3.0e-72E value 152 Match length 49 % identity (Z97336) ankyrin homolog [Arabidopsis thaliana] NCBI Description Seq. No. 215270 LIB3147-006-Q1-K1-C10 Seq. ID Method BLASTX NCBI GI g2677830 BLAST score 474 E value 1.0e-47Match length 108 87 % identity NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca] Seq. No. 215271 LIB3147-006-Q1-K1-C12 Seq. ID Method BLASTX NCBI GI q2511570 BLAST score 167 6.0e-12 E value Match length 42 81 % identity (Y13174) multicatalytic endopeptidase [Arabidopsis NCBI Description thaliana] 215272 Seq. No. Seq. ID LIB3147-006-Q1-K1-C2 ${\tt BLASTX}$ Method NCBI GI q1361987 BLAST score 486 4.0e-49 E value 121 Match length 80 % identity

30057

NCBI Description GF14 protein chi chain - Arabidopsis thaliana



```
LIB3147-006-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3617741
BLAST score
                  527
E value
                  6.0e-54
Match length
                  125
                  80
% identity
                  (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  215274
                  LIB3147-006-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263795
BLAST score
                  338
                  1.0e-31
E value
Match length
                  144
% identity
                  49
                  (AC006068) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  215275
Seq. No.
Seq. ID
                  LIB3147-006-Q1-K1-D4
Method
                  BLASTX
                  q132944
NCBI GI
BLAST score
                  180
                   9.0e-14
E value
Match length
                  34
                   94
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  215276
Seq. ID
                  LIB3147-006-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q116923
                   522
BLAST score
                   3.0e-53
E value
                  147
Match length
% identity
                   68
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir__S13520 beta-COP protein - rat
                   >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
                   norvegicus]
                   215277
Seq. No.
Seq. ID
                  LIB3147-006-Q1-K1-D9
                   BLASTX
Method
NCBI GI
                   q1169014
BLAST score
                   167
                   1.0e-11
E value
Match length
                   133
                   32
% identity
```

>gi 472343 (L31852) bcop [Drosophila melanogaster]

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

NCBI Description



```
215278
Seq. No.
                    LIB3147-006-Q1-K1-E10
Seq. ID
Method
                    BLASTX
                    q3334138
NCBI GI
                    275
BLAST score
                    2.0e-24
E value
                    97
Match length
                    57
% identity
                   CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin
NCBI Description
                    [Glycine max]
                    215279
Seq. No.
                    LIB3147-006-Q1-K1-E11
Seq. ID
                    BLASTX
Method
                    g4185513
NCBI GI
BLAST score
                    228
                    6.0e-19
E value
                    49
Match length
                    86
% identity
                    (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                    thaliana] >gi_4185517 (AF102825) actin depolymerizing
                    factor 5 [Arabidopsis thaliana]
                    215280
Seq. No.
                    LIB3147-006-Q1-K1-E12
Seq. ID
Method
                    BLASTX
                    q464707
NCBI GI
BLAST score
                    607
                    3.0e-63
E value
                    134
Match length
                    87
% identity
                   40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                    protein S18.A - Arabidopsis thaliana
                    >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                    [Arabidopsis thaliana] >gi 434343 emb_CAA82273 (Z28701)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                    [Arabidopsis thaliana] >gi 434906 emb CAA82275_ (Z28962)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                    ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                    gb_R30430 come from this gene. [Arabidopsis thaliana]
                    >g\bar{1} 4538910 emb CAB39647.1 (AL049482) $18.A ribosomal
                    protein [Arabidopsis thaliana]
Seq. No.
                    215281
                    LIB3147-006-Q1-K1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g136057
BLAST score
                    340
E value
                    4.0e-32
Match length
                    103
% identity
                    50
```

>gi 99499 pir A32187 (S)-tetrahydroberberine oxidase -

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)



Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No. 215282

Seq. ID LIB3147-006-Q1-K1-E7

Method BLASTX
NCBI GI 9730526
BLAST score 385
E value 3.0e-37
Match length 99
% identity 76

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 215283

Seq. ID LIB3147-006-Q1-K1-E9

Method BLASTX
NCBI GI g122070
BLAST score 403
E value 2.0e-39
Match length 83
% identity 98

NCBI Description HISTONE H3 >gi_82483_pir_A25564 histone H3 - rice

>gi 169793 (M15664) histone 3 [Oryza sativa] >gi_940018

(U25664) histone H3 [Oryza sativa]

Seq. No. 215284

Seq. ID LIB3147-006-Q1-K1-F1

Method BLASTX
NCBI GI g4539350
BLAST score 240
E value 3.0e-20
Match length 100
% identity 45

NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 215285

Seq. ID LIB3147-006-Q1-K1-F11

Method BLASTX
NCBI GI g3024020
BLAST score 657
E value 4.0e-69
Match length 131
% identity 93

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 215286

Seq. ID LIB3147-006-Q1-K1-F12

Method BLASTX
NCBI GI g586145
BLAST score 538
E value 4.0e-55
Match length 103



% identity UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT NCBI Description PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 488848 emb CAA55894 (X79332) Rieske iron sulphur protein [Solanum tuberosum] 215287 Seq. No. LIB3147-006-Q1-K1-F6 Seq. ID BLASTX Method g2494076 NCBI GI BLAST score 481 1.0e-48 E value 108 Match length 83 % identity NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE NCBI Description (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi 1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia] 215288 Seq. No. LIB3147-006-Q1-K1-F7 Seq. ID BLASTX Method g2827143 NCBI GI BLAST score 631 E value 5.0e-66 Match length 139 85 % identity NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana] 215289 Seq. No. LIB3147-006-Q1-K1-F8 Seq. ID Method BLASTX NCBI GI q2827143 BLAST score 418 E value 4.0e-41 101 Match length % identity (AF027174) cellulose synthase catalytic subunit NCBI Description [Arabidopsis thaliana] 215290 Seq. No. LIB3147-006-Q1-K1-F9 Seq. ID BLASTX Method NCBI GI q1710838 BLAST score 610 E value 1.0e-63 Match length 139 % identity 82

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi 535584 (L36119) adenosylhomocysteinase [Medicago sativa]

215291 Seq. No.

LIB3147-006-Q1-K1-G11 Seq. ID

NCBI GI

BLAST score

g1710807 502



```
BLASTX
Method
                  g1931644
NCBI GI
                  263
BLAST score
E value
                  6.0e-23
                  122
Match length
                  39
% identity
                  (U95973) membrane protein PTM1 precursor isolog
NCBI Description
                  [Arabidopsis thaliana]
                  215292
Seq. No.
                  LIB3147-006-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263779
BLAST score
                  289
E value
                  5.0e-26
                  93
Match length
% identity
                  61
NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]
                  215293
Seq. No.
                  LIB3147-006-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482975
BLAST score
                  198
                   3.0e-15
E value
Match length
                  125
                   37
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                  215294
Seq. No.
                  LIB3147-006-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4218014
BLAST score
                  271
E value
                   8.0e-24
Match length
                  76
                   71
% identity
                  (AC006135) putative spliceosomal protein (RNA binding
NCBI Description
                  protein) [Arabidopsis thaliana]
Seq. No.
                   215295
                  LIB3147-006-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                   g1346675
NCBI GI
BLAST score
                   560
E value
                   9.0e-58
                  120
Match length
                   88
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
NCBI Description
                   >gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                  bidentis]
                   215296
Seq. No.
Seq. ID
                   LIB3147-006-Q1-K1-H10
Method
                   BLASTX
```



3.0e-60 E value 141 Match length 87 % identity RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 NCBI Description KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi 1185390 (U21105) alphacpn60 [Pisum sativum] 215297 Seq. No. LIB3147-006-Q1-K1-H11 Seq. ID Method BLASTX g2347189 NCBI GI BLAST score 331 6.0e-31 E value 93 Match length 71 % identity (AC002338) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 3150399 (AC004165) hypothetical protein [Arabidopsis thaliana] 215298 Seq. No. LIB3147-006-Q1-K1-H4 Seq. ID Method BLASTN g2244733 NCBI GI 119 BLAST score 2.0e-60 E value 313 Match length % identity 87 NCBI Description Cotton mRNA for actin, clone CF456, partial cds Seq. No. 215299 LIB3147-006-Q1-K1-H5 Seq. ID Method BLASTX q2065531 NCBI GI 609 BLAST score E value 2.0e-63 Match length 128 % identity 83 (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] NCBI Description 215300 Seq. No. Seq. ID LIB3147-006-Q1-K1-H8 Method BLASTX NCBI GI g2245026 BLAST score 202 1.0e-15 E value Match length 57 % identity 72 (Z97341) hypothetical protein [Arabidopsis thaliana] NCBI Description 215301 Seq. No. LIB3147-007-Q1-K1-A1 Seq. ID Method BLASTX g3885328 NCBI GI BLAST score 208 2.0e-23 E value

30063

89

63

Match length

% identity



```
(AC005623) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  215302
Seq. No.
                  LIB3147-007-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2832300
                  349
BLAST score
                  4.0e-33
E value
                  119
Match length
% identity
                  61
                  (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
NCBI Description
                  roseus]
                  215303
Seq. No.
                  LIB3147-007-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1587206
BLAST score
                  631
                  4.0e-66
E value
                  128
Match length
                  95
% identity
NCBI Description T complex protein [Cucumis sativus]
                  215304
Seq. No.
                  LIB3147-007-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1843527
BLAST score
                  521
                   4.0e-53
E value
                  135
Match length
                   43
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
                   215305
Seq. No.
                  LIB3147-007-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1008904
                   452
BLAST score
                   5.0e-45
E value
                   133
Match length
                   60
% identity
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
                   215306
Seq. No.
                   LIB3147-007-Q1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q575942
                   451
BLAST score
                   5.0e-45
E value
                   110
Match length
                   75
% identity
                  (D42086) stearoyl-acyl carrier protein desaturase [Sesamum
NCBI Description
                   indicum]
Seq. No.
                   215307
Seq. ID
                   LIB3147-007-Q1-K1-A9
```

Seq. ID

Method

```
BLASTX
Method
                  q1498053
NCBI GI
                  152
BLAST score
                  4.0e-10
E value
Match length
                  29
                  97
% identity
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
                  215308
Seq. No.
                  LIB3147-007-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g1619300
NCBI GI
BLAST score
                  331
                  6.0e-31
E value
                  66
Match length
                  94
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                  215309
Seq. No.
                  LIB3147-007-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4240116
BLAST score
                  405
                  5.0e-40
E value
Match length
                  81
% identity
                   90
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                  thaliana] >gi 4240118_dbj_BAA74838_ (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                   215310
                  LIB3147-007-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                   q4371290
NCBI GI
BLAST score
                   551
E value
                   9.0e-57
Match length
                   123
                   76
% identity
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215311
                   LIB3147-007-Q1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1173253
BLAST score
                   557
E value
                   2.0e-57
Match length
                   132
                   83
% identity
                  40S RIBOSOMAL PROTEIN S3 >gi_543317 pir S41170 ribosomal
NCBI Description
                   protein S3 - mouse >gi 57728 emb CAA35916 (X51536)
                   ribosomal protein S3 (AA 1-243) [Rattus rattus]
                   >gi 439522 emb CAA54167_ (X76772) ribosomal protein S3 [Mus
                   musculus]
                   215312
Seq. No.
```

30065

LIB3147-007-Q1-K1-B8

BLASTX

% identity

89



```
g2914706
NCBI GI
                  661
BLAST score
                  1.0e-69
E value
                  143
Match length
                  82
% identity
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                  215313
Seq. No.
                  LIB3147-007-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g441457
NCBI GI
BLAST score
                  671
                  9.0e-71
E value
Match length
                  126
                  98
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  215314
Seq. No.
                  LIB3147-007-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3355468
NCBI GI
BLAST score
                  515
                   2.0e-52
E value
Match length
                  122
% identity
                   87
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   215315
Seq. No.
                  LIB3147-007-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g1563719
NCBI GI
                   435
BLAST score
                   4.0e-43
E value
                   89
Match length
                   90
% identity
NCBI Description (Y08320) cyclophylin [Digitalis lanata]
                   215316
Seq. No.
                   LIB3147-007-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3915826
                   569
BLAST score
                   8.0e-59
E value
                   136
Match length
% identity
                   75
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   215317
Seq. No.
                   LIB3147-007-Q1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2160322
BLAST score
                   187
E value
                   5.0e-14
                   38
Match length
```



(D16139) cytokinin binding protein CBP57 [Nicotiana NCBI Description sylvestris] 215318 Seq. No. LIB3147-007-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI g4559346 BLAST score 408 E value 6.0e-40Match length 122 % identity 59 (AC006585) early nodulin 16 [Arabidopsis thaliana] NCBI Description 215319 Seq. No. LIB3147-007-Q1-K1-D11 Seq. ID Method BLASTX NCBI GI g2583108 BLAST score 151 E value 9.0e-10 Match length 37 73 % identity (AC002387) putative surface protein [Arabidopsis thaliana] NCBI Description Seq. No. 215320 LIB3147-007-Q1-K1-D12 Seq. ID Method BLASTX g3935187 NCBI GI BLAST score 311 E value 8.0e-29 Match length 98 % identity 64 (AC004557) F17L21.30 [Arabidopsis thaliana] NCBI Description Seq. No. 215321 LIB3147-007-Q1-K1-D4 Seq. ID BLASTX Method q1762309 NCBI GI 378 BLAST score 2.0e-36 E value 79 Match length % identity (U53345) AP-1 Golgi-related complex component; clathrin NCBI Description coated vesicles; clathrin assembly protein [Camptotheca acuminata] 215322 Seq. No. Seq. ID LIB3147-007-Q1-K1-D5 BLASTN Method

Method BLASTN
NCBI GI g3046852
BLAST score 37
E value 3.0e-11
Match length 148

Match length 148 % identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No. 215323

% identity

NCBI Description



```
LIB3147-007-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g1730172
NCBI GI
                  357
BLAST score
                  6.0e - 34
E value
                  82
Match length
                  83
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi_1364077_pir__S57830 glucose-6-phosphate isomerase
                   (EC 5.3.1.9) isoenzyme 1, cytosolic - Clarkia xantiana
                   >gi 784974 emb CAA56693_ (X80666) glucose-6-phosphate
                   isomerase [Clarkia xantiana] >gi_1370068_emb_CAA61566_
                   (X89386) glucose-6-phosphate isomerase [Clarkia xantiana]
                   215324
Seq. No.
                  LIB3147-007-Q1-K1-D7
Seq. ID
Method
                  BLASTN
                   g2687442
NCBI GI
                   189
BLAST score
                   1.0e-102
E value
Match length
                   220
                   97
% identity
NCBI Description Mitella pentandra large subunit 26S ribosomal RNA gene,
                   partial sequence
                   215325
Seq. No.
                   LIB3147-007-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3075392
NCBI GI
                   530
BLAST score
                   3.0e-54
E value
                   128
Match length
                   76
% identity
                   (AC004484) putative steroid dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   215326
                   LIB3147-007-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   g4539292
NCBI GI
BLAST score
                   443
                   5.0e-44
E value
                   93
Match length
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   215327
                   LIB3147-007-Q1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2621249
BLAST score
                   140
                   1.0e-08
E value
Match length
                   113
```

(AE000807) conserved protein [Methanobacterium



thermoautotrophicum]

```
215328
Seq. No.
                  LIB3147-007-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                  g3885328
NCBI GI
                  272
BLAST score
                   6.0e-24
E value
                  136
Match length
                   43
% identity
                   (ACO05623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   215329
Seq. No.
                  LIB3147-007-Q1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3413697
                   165
BLAST score
                   2.0e-11
E value
                   134
Match length
                   39
% identity
                  (AC004747) SF16-like protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   215330
Seq. No.
                   LIB3147-007-Q1-K1-E5
Seq. ID
Method
                   BLASTX
                   g3201627
NCBI GI
                   341
BLAST score
E value
                   5.0e-32
                   84
Match length
                   67
% identity
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
                   215331
Seq. No.
                   LIB3147-007-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   g2832664
NCBI GI
                   200
BLAST score
                   2.0e-15
E value
                   103
Match length
                   44
% identity
                   (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                   thaliana]
                   215332
Seq. No.
Seq. ID
                   LIB3147-007-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q19611
BLAST score
                   320
E value
                   1.0e-29
Match length
                   83
% identity
                   78
                   (X13675) histone H3 (AA 1-123) [Medicago sativa]
NCBI Description
```

sativum]

>gi 2916748_emb_CAA05554_ (AJ002555) histone H3 [Pisum



```
215333
Seq. No.
                  LIB3147-007-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  g3747089
NCBI GI
                  176
BLAST score
                  4.0e-13
E value
                  45
Match length
% identity
                  78
                  (AF095445) NADP-dependent isocitrate dehydrogenase [Glycine
NCBI Description
                  max]
                  215334
Seq. No.
                  LIB3147-007-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g3395441
NCBI GI
BLAST score
                  454
                  3.0e-45
E value
Match length
                  114
% identity
                  82
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  215335
Seq. No.
                  LIB3147-007-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710807
                  599
BLAST score
                  2.0e-62
E value
                  141
Match length
                  86
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390
                  (U21105) alphacpn60 [Pisum sativum]
                  215336
Seq. No.
                  LIB3147-007-Q1-K1-F12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3510342
BLAST score
                  36
E value
                  7.0e-11
                  72
Match length
                  88
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MGN6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  215337
                  LIB3147-007-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                   g1710590
NCBI GI
BLAST score
                  175
                   1.0e-12
E value
                  89
Match length
                   45
% identity
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P1 (L12) >gi 1209701 (U40147)
                   ribosomal protein L12 [Zea mays]
```

30070

215338

LIB3147-007-Q1-K1-F3

Seq. No.

Seq. ID

NCBI GI



```
BLASTX
Method
                   q3135693
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
Match length
                   64
                   48
% identity
NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum]
                   215339
Seq. No.
                   LIB3147-007-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351272
BLAST score
                   447
                   2.0e-44
E value
                   103
Match length
                   83
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
NCBI Description
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
                   215340
Seq. No.
                   LIB3147-007-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   g1710780
NCBI GI
                   315
BLAST score
                   5.0e-29
E value
                   74
Match length
                   80
% identity
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                    (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserinal
                   215341
Seq. No.
                   LIB3147-007-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3603473
BLAST score
                    334
                    3.0e - 31
E value
Match length
                   83
% identity
                    71
                   (AF090698) elicitor-responsive gene-3 [Oryza sativa]
NCBI Description
                    215342
Seq. No.
                    LIB3147-007-Q1-K1-F9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1350680
BLAST score
                    410
E value
                    2.0e-40
Match length
                    98
                    79
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
Seq. No.
                    215343
                    LIB3147-007-Q1-K1-G11
Seq. ID
Method
                    BLASTX
```

30071

g3335361

NCBI GI

E value

BLAST score

g1008904

4.0e-28

307



```
BLAST score
                  592
                  2.0e-61
E value
                  123
Match length
                  89
% identity
                  (AC003028) putative acyltransferase [Arabidopsis thaliana]
NCBI Description
                  215344
Seq. No.
                  LIB3147-007-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421876
BLAST score
                  485
                  6.0e-49
E value
Match length
                  140
                  70
% identity
                  probable ATP synthase chain - soybean
NCBI Description
                  >gi_396230_emb_CAA52349_ (X74296) putative ATP synthase
                  subunit [Glycine max]
                  215345
Seq. No.
                  LIB3147-007-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213595
BLAST score
                  361
                  2.0e-34
E value
Match length
                  125
% identity
                  59
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
                  215346
Seq. No.
                  LIB3147-007-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1313909
BLAST score
                   308
E value
                   3.0e-28
Match length
                  82
% identity
                   68
NCBI Description (D84508) CDPK-related protein kinase [Zea mays]
Seq. No.
                   215347
                  LIB3147-007-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                  g1173043
                   259
BLAST score
                   2.0e-22
E value
                   69
Match length
% identity
                   77
                  60S RIBOSOMAL PROTEIN L38 >gi_479441_pir__S33899 ribosomal
NCBI Description
                   protein L38 - tomato (cv. Moneymaker)
                   >gi 313027 emb CAA49599 (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
Seq. No.
                   215348
Seq. ID
                  LIB3147-007-Q1-K1-G8
                   BLASTX
Method
```



```
59
Match length
                  86
% identity
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
                  215349
Seq. No.
                  LIB3147-007-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g4218121
NCBI GI
                  152
BLAST score
                  7.0e-10
E value
                  144
Match length
                   29
% identity
                  (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                   215350
Seq. No.
                  LIB3147-007-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                   g3150239
NCBI GI
                   151
BLAST score
                   9.0e-10
E value
                   84
Match length
                   40
% identity
                   (AL023635) hypothetical protein MLCB1243.38 [Mycobacterium
NCBI Description
                   leprae]
                   215351
Seq. No.
                   LIB3147-007-Q1-K1-H10
Seq. ID
Method
                   BLASTX
                   g2651316
NCBI GI
                   410
BLAST score
                   3.0e-40
E value
Match length
                   97
                   76
% identity
                  (AC002336) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215352
Seq. No.
Seq. ID
                   LIB3147-007-Q1-K1-H11
Method
                   BLASTX
                   q3319882
NCBI GI
                   451
BLAST score
                   3.0e-45
E value
Match length
                   89
% identity
                   97
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
Seq. No.
                   215353
                   LIB3147-007-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   q3877595
NCBI GI
BLAST score
                   298
                   4.0e-27
E value
Match length
                   112
 % identity
                   54
                   (Z79696) predicted using Genefinder; Similarity to Human
NCBI Description
```

this gene; cDNA EST yk281b1.3 comes from this gene

HEP27 protein (TR:G1079566); cDNA EST yk281b1.5 comes from



[Caenorhabditis elegans] >gi_3879853_emb_CAB04734_ (Z81592) predicted using Genefinder; Similarity to Human HEP27 protein (TR:G1079566); cDNA EST yk281b1.5 comes from this gene; cDNA EST yk281b1.3 comes from this gene [Caenorhabditis elegans]

Seq. No. 215354

Seq. ID LIB3147-007-Q1-K1-H7

Method BLASTX
NCBI GI g122007
BLAST score 293
E value 1.0e-26
Match length 81
% identity 73

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley

>gi_20448_emb_CAA37828 (X $\overline{53}$ 831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 215355

Seq. ID LIB3147-007-Q1-K1-H8

Method BLASTX
NCBI GI g1542941
BLAST score 594
E value 1.0e-61
Match length 143
% identity 83

NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No. 215356

Seq. ID LIB3147-008-Q1-K1-A1

Method BLASTX
NCBI GI g4467137
BLAST score 366
E value 4.0e-35
Match length 114
% identity 60

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 215357

Seq. ID LIB3147-008-Q1-K1-A10

Method BLASTX
NCBI GI g2497733
BLAST score 157
E value 2.0e-10
Match length 64
% identity 50

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)

>gi_1177796 (M80567) non-specific lipid transfer protein
[Arabidopsis thaliana] >gi 3786018 (AC005499) unknown

protein [Arabidopsis thaliana]

Seq. No. 215358

Seq. ID LIB3147-008-Q1-K1-A11

Method BLASTX
NCBI GI g2498490
BLAST score 201
E value 9.0e-16



Match length 76 53 % identity VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) NCBI Description Int-6 [Mus musculus] $>gi_2114363$ (U62962) similar to mouse Int-6 [Homo sapiens] $>gi_2351382$ (U54562) eIF3-p48 [Homo sapiens] $>gi_2688818$ (U8 $\overline{5}947$) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6_ murine mammary tumor integration site 6 (oncogene homolog) 215359 Seq. No. Seq. ID LIB3147-008-Q1-K1-A2 Method BLASTX NCBI GI q439278 BLAST score 262 E value 5.0e-23 83 Match length 64 % identity (X69205) ribosomal protein [Triticum aestivum] NCBI Description 215360 Seq. No. LIB3147-008-Q1-K1-A3 Seq. ID Method BLASTX NCBI GI g2851508 BLAST score 414 8.0e-41 E value Match length 80 89 % identity 60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to NCBI Description ribosomal protein L21 (gb L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana] Seq. No. 215361 Seq. ID LIB3147-008-Q1-K1-A4 Method BLASTX NCBI GI q3980403 BLAST score 260 E value 7.0e-23 Match length 86 % identity NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana] 215362 Seq. No. Seq. ID LIB3147-008-Q1-K1-A5 Method BLASTX NCBI GI q3776003 BLAST score 288 E value 5.0e-26 Match length 114

% identity

NCBI Description (AJ010465) RNA helicase [Arabidopsis thaliana]

Seq. No. 215363

Seq. ID LIB3147-008-Q1-K1-A9

Method

NCBI GI

BLASTX

g1065505



```
Method
                  BLASTX
                  g1086249
NCBI GI
BLAST score
                  188
                  3.0e-14
E value
Match length
                  86
                  49
% identity
                  subtilisin-like protease - Alnus glutinosa
NCBI Description
                  >gi 757522 emb CAA59964 (X85975) subtilisin-like protease
                  [Alnus glutinosa]
                  215364
Seq. No.
                  LIB3147-008-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g445613
BLAST score
                  467
E value
                  6.0e-47
Match length
                  119
% identity
                  74
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                  215365
                  LIB3147-008-Q1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1553128
BLAST score
                  74
                  1.0e-33
E value
Match length
                  78
                  99
% identity
                  Gossypium hirsutum ribosomal protein L44 isoform a (RL44),
NCBI Description
                  complete cds
                  215366
Seq. No.
                  LIB3147-008-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g3851636
NCBI GI
                  460
BLAST score
                   4.0e-46
E value
Match length
                  109
% identity
                  80
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   215367
Seq. No.
                  LIB3147-008-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334261
                  187
BLAST score
                   4.0e-14
E value
                   39
Match length
                   77
% identity
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
                  metallothionein-like protein [Malus domestica]
                   215368
Seq. No.
                  LIB3147-008-Q1-K1-B6
Seq. ID
```



BLAST score 154 3.0e-10E value 55 Match length 55 % identity

NCBI Description (U40419) similar to S. cerevisiae gene YCR47C, putative

30.7 kd methyltransferase (SP:YCT7 YEAST, P25627)

[Caenorhabditis elegans]

215369 Seq. No.

LIB3147-008-Q1-K1-B7 Seq. ID

Method BLASTX NCBI GI g122085 BLAST score 484 7.0e-49E value Match length 115 84 % identity

NCBI Description

HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi 82482 pir S04099 histone H3 (variant H3R-21)

- rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]

>gi 168497 (M13379) histone H3 [Zea mays] >gi_168506

(M35388) histone H3 [Zea mays] >gi 169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377)

histone 3 [Zea mays] $>gi_1\overline{040764}$ (M35 $\overline{387}$) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and

gb T42306 come from this gene. [Arabidopsis thaliana] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 215370

Seq. ID LIB3147-008-Q1-K1-B8

Method BLASTX NCBI GI q3269284 BLAST score 188 E value 3.0e-14Match length 95 % identity 47

NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No. 215371

LIB3147-008-Q1-K1-B9 Seq. ID

Method BLASTX NCBI GI g224293 BLAST score 393 E value 3.0e-38



```
Match length 92
% identity 88
NCBI Description histone H4 [Triticum aestivum]
Seq. No. 215372
```

Seq. ID LIB3147-008-Q1-K1-C1
Method BLASTX
NCBI GI g1766046
BLAST score 315
E value 3.0e-29
Match length 66
% identity 86

NCBI Description (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1

[Arabidopsis thaliana]

Seq. No. 215373

Seq. ID LIB3147-008-Q1-K1-C2

Method BLASTX
NCBI GI g136057
BLAST score 203
E value 4.0e-16
Match length 66
% identity 62

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 215374

Seq. ID LIB3147-008-Q1-K1-C5

Method BLASTX
NCBI GI g3182981
BLAST score 382
E value 6.0e-37
Match length 88
% identity 80

NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_

(D86494) diminuto [Pisum sativum]

Seq. No. 215375

Seq. ID LIB3147-008-Q1-K1-C6

Method BLASTX
NCBI GI g548770
BLAST score 576
E value 9.0e-60
Match length 118
% identity 88

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi 303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 215376

Seq. ID LIB3147-008-Q1-K1-C7

Method BLASTX
NCBI GI g3128168
BLAST score 415
E value 8.0e-41



Match length 116 % identity 62

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 215377

Seq. ID LIB3147-008-Q1-K1-C8

Method BLASTX
NCBI GI g134101
BLAST score 535
E value 7.0e-55
Match length 123
% identity 90

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD

CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_72958_pir__HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

Seq. No. 215378

Seq. ID LIB3147-008-Q1-K1-D4

Method BLASTX
NCBI GI g1771162
BLAST score 395
E value 1.0e-38
Match length 107
% identity 68

NCBI Description (X98930) SBT2 [Lycopersicon esculentum]

>gi 3687307 emb CAA07000 (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 215379

Seq. ID LIB3147-008-Q1-K1-D6

Method BLASTX
NCBI GI g1710530
BLAST score 537
E value 3.0e-55
Match length 104
% identity 90

NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256

ribosomal protein L27a - Arabidopsis thaliana

>gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No. 215380

Seq. ID LIB3147-008-Q1-K1-D8

Method BLASTX
NCBI GI 9457517
BLAST score 167
E value 7.0e-12
Match length 68
% identity 47

NCBI Description (L12579) alternatively spliced [Homo sapiens]

>gi_4503169_ref_NP_001904.1_pCUTL1_ cut (Drosophila)-like 1

(CCAAT displacement protein)

Seq. No. 215381

Seq. No.

Seq. ID

215386

LIB3147-008-Q1-K1-E8



```
Seq. ID
                   LIB3147-008-Q1-K1-D9
Method
                   BLASTN
NCBI GI
                   g530836
BLAST score
                   59
E value
                   2.0e-25
Match length
                   59
% identity
                   100
NCBI Description
                  Gossypium tomentosum 5.8S rRNA gene and internal
                   transcribed spacer 1 and 2 >gi_530838_gb U12719 GHU12719
                   Gossypium hirsutum 5.8S rRNA gene and internal transcribed
                   spacer 1 and
                   215382
Seq. No.
Seq. ID
                   LIB3147-008-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   g3983665
BLAST score
                   534
E value
                   8.0e-55
Match length
                  120
% identity
                   82
NCBI Description
                  (AB011271) importin-beta2 [Oryza sativa]
Seq. No.
                   215383
Seq. ID
                  LIB3147-008-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  38
E value
                   6.0e-12
Match length
                  74
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  215384
Seq. ID
                  LIB3147-008-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1350945
BLAST score
                  283
E value
                  2.0e-25
Match length
                  69
% identity
                  86
                  40S RIBOSOMAL PROTEIN S17 >gi_1076596_pir__S51665 ribosomal
NCBI Description
                  protein S17 - tomato (fragment) >gi_603570_emb_CAA58444
                  (X83421) ribosomal protein S17 [Lycopersicon esculentum]
Seq. No.
                  215385
Seq. ID
                  LIB3147-008-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2431767
BLAST score
                  238
E value
                  4.0e-20
Match length
                  113
% identity
                  43
NCBI Description
                  (U62751) acidic ribosomal protein P3a [Zea mays]
```

Seq. ID

Method

NCBI GI



```
Method
                   BLASTX
NCBI GI
                   g3947719
BLAST score
                   249
                   2.0e-21
E value
Match length
                   53
                   92
% identity
NCBI Description
                   (AJ012653) ribosomal protein S28 [Prunus persica]
                   >gi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi 3947723 emb CAA10103 (AJ012655)
                   ribosomal protein S28 [Prunus persica]
                   215387
Seq. No.
                  LIB3147-008-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3608485
                  566
BLAST score
E value
                   2.0e-58
Match length
                  113
                   93
% identity
NCBI Description
                 (AF088915) proteasome beta subunit [Petunia x hybrida]
Seq. No.
                  215388
                  LIB3147-008-Q1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2865522
BLAST score
                  43
E value
                   6.0e-15
Match length
                  71
                  90
% identity
NCBI Description
                 Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
                  complete cds
Seq. No.
                  215389
                  LIB3147-008-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982268
BLAST score
                  469
                  4.0e-47
E value
Match length
                  106
% identity
                  89
NCBI Description
                  (AF051217) probable 40S ribosomal protein S15 [Picea
                  mariana]
Seq. No.
                  215390
Seq. ID
                  LIB3147-008-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q1228074
BLAST score
                  271
E value
                  4.0e-24
Match length
                  75
% identity
                  72
NCBI Description (X95763) histone h2a homologue [Allium cepa]
Seq. No.
                  215391
```

30081

LIB3147-008-Q1-K1-F6

BLASTX

g4530585



BLAST score 348
E value 6.0e-33
Match length 85
% identity 73

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 215392

Seq. ID LIB3147-008-Q1-K1-G1

Method BLASTX
NCBI GI g515377
BLAST score 420
E value 2.0e-41
Match length 86
% identity 98

NCBI Description (X79715) histone H4 [Lolium temulentum]

Seq. No. 215393

Seq. ID LIB3147-008-Q1-K1-G12

Method BLASTX
NCBI GI g1169013
BLAST score 389
E value 1.0e-37
Match length 106
% identity 69

NCBI Description COP9 PROTEIN (FUSCA PROTEIN FUS7) >gi_625971_pir__A54842

COP9 protein - Arabidopsis thaliana >\overline{\text{gi}} 530870 (\overline{\text{L}}32874) COP9 [Arabidopsis thaliana] >\overline{\text{gi}} 2244767 emb CAB10190

(Z97335) COP9 protein [Arabidopsis thaliana]

Seq. No. 215394

Seq. ID LIB3147-008-Q1-K1-G4

Method BLASTX
NCBI GI g3860321
BLAST score 365
E value 5.0e-35
Match length 106
% identity 65

NCBI Description (AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No. 215395

Seq. ID LIB3147-008-Q1-K1-G6

Method BLASTN
NCBI GI g2687434
BLAST score 273
E value 1.0e-152
Match length 357
% identity 94

NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 215396

Seq. ID LIB3147-008-Q1-K1-G7

Method BLASTX
NCBI GI g3236242
BLAST score 414
E value 1.0e-40
Match length 96



```
% identity
                  85
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  215397
                  LIB3147-008-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3912920
NCBI GI
BLAST score
                  144
                  5.0e-09
E value
Match length
                  120
                  33
% identity
                  (AF001308) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  215398
Seq. No.
Seq. ID
                  LIB3147-008-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1136741
                  334
BLAST score
                  3.0e - 31
E value
                  96
Match length
                  66
% identity
                  (D42052) predicted protein of 548 amino acids [Homo
NCBI Description
                  sapiens]
Seq. No.
                  215399
                  LIB3147-008-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3136336
BLAST score
                  313
                  5.0e-48
E value
Match length
                  153
                  55
% identity
NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]
                  215400
Seq. No.
                  LIB3147-008-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2828291
BLAST score
                  246
                   4.0e-21
E value
Match length
                  92
                   34
% identity
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
                  215401
Seq. No.
Seq. ID
                  LIB3147-008-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2492952
BLAST score
                  293
E value
                   1.0e-26
Match length
                  69
% identity
                  81
                  CHORISMATE SYNTHASE 1 PRECURSOR
NCBI Description
```

30083

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)

>gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
precursor - tomato >gi_410482_emb_CAA79859_ (Z21796)



chorismate synthase 1 [Lycopersicon esculentum]

 Seq. No.
 215402

 Seq. ID
 LIB3147-009-Q1-K1-A4

 Method
 BLASTX

 NCBI GI
 q3212862

NCBI GI g3212862 BLAST score 483 E value 1.0e-48 Match length 126 % identity 70

NCBI Description (AC004005) putative riboflavin synthase [Arabidopsis

thaliana]

Seq. No. 215403

Seq. ID LIB3147-009-Q1-K1-A9

Method BLASTX
NCBI GI g2498490
BLAST score 169
E value 3.0e-12
Match length 90
% identity 44

NCBI Description VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556)

Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo

sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens]

>gi_2695701 (U94175) mammary tumor-associated protein INT6
[Homo sapiens] >gi 4503521 ref_NP_001559.1_pEIF3S6_ murine

mammary tumor integration site 6 (oncogene homolog)

Seq. No. 215404

Seq. ID LIB3147-009-Q1-K1-B1

Method BLASTX
NCBI GI g2191187
BLAST score 230
E value 4.0e-19
Match length 114
% identity 23

NCBI Description (AF007271) contains similarity to a DNAJ-like domain

[Arabidopsis thaliana]

Seq. No. 215405

Seq. ID LIB3147-009-Q1-K1-B10

Method BLASTX
NCBI GI g3738322
BLAST score 244
E value 6.0e-21
Match length 78
% identity 72

NCBI Description (AC005170) putative small nuclear ribonucleoprotein

[Arabidopsis thaliana]

Seq. No. 215406

Seq. ID LIB3147-009-Q1-K1-B2

Method BLASTX
NCBI GI g3393062
BLAST score 382
E value 5.0e-37



```
103
Match length
                  64
% identity
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                  215407
Seq. No.
                  LIB3147-009-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3393062
                  175
BLAST score
                  8.0e-13
E value
Match length
                  43
% identity
                  67
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
Seq. No.
                  215408
                  LIB3147-009-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860247
                  469
BLAST score
                  3.0e-47
E value
                  100
Match length
% identity
                  86
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
                  215409
Seq. No.
                  LIB3147-009-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334113
BLAST score
                  466
                  8.0e-47
E value
                  89
Match length
                  100
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
NCBI Description
                  acyl-CoA-binding protein [Gossypium hirsutum]
                  215410
Seq. No.
                  LIB3147-009-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q461736
BLAST score
                  302
E value
                  1.0e-27
Match length
                  103
% identity
                   62
                  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
NCBI Description
                  >gi_478786_pir__S29316 chaperonin 60 - cucurbit
                  >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                  215411
                  LIB3147-009-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1905785
BLAST score
                  137
E value
                   1.0e-08
Match length
                  55
```

30085

(Y10685) G/HBF-1 [Glycine max]

49

% identity

NCBI Description

Seq. No.

Seq. ID

215417

LIB3147-009-Q1-K1-C7



```
Seq. No.
                  215412
Seq. ID
                  LIB3147-009-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  506
E value
                  1.0e-51
                  99
Match length
                  99
% identity
NCBI Description
                  ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  215413
Seq. ID
                  LIB3147-009-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2462762
BLAST score
                  360
                  2.0e-34
E value
Match length
                  116
                  65
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  215414
Seq. ID
                  LIB3147-009-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3024017
                  558
BLAST score
E value
                  2.0e-57
                  124
Match length
                  89
% identity
NCBI Description
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                   (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.
                  215415
                  LIB3147-009-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860257
BLAST score
                  293
E value
                  1.0e-26
Match length
                  112
% identity
                  53
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  215416
Seq. ID
                  LIB3147-009-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q2244780
BLAST score
                  247
E value
                  3.0e-21
Match length
                  101
% identity
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
```



Method BLASTX
NCBI GI g1666173
BLAST score 353
E value 1.0e-33
Match length 110
% identity 67

NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No. 215418

Seq. ID LIB3147-009-Q1-K1-D1

Method BLASTX
NCBI GI g114682
BLAST score 306
E value 6.0e-28
Match length 105
% identity 64

NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR

(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi_100471_pir__A35227 H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, mitochondrial - sweet
potato >gi_168270 (J05397) F-1-ATPase delta subunit

precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No. 215419

Seq. ID LIB3147-009-Q1-K1-D3

Method BLASTX
NCBI GI g3915826
BLAST score 471
E value 2.0e-47
Match length 103
% identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 215420

Seq. ID LIB3147-009-Q1-K1-D6

Method BLASTX
NCBI GI 9445613
BLAST score 270
E value 6.0e-24
Match length 81
% identity 69

NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 215421

Seq. ID LIB3147-009-Q1-K1-D8

Method BLASTX
NCBI GI g1710008
BLAST score 302
E value 1.0e-27
Match length 79
% identity 72

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN1B >gi_1370205_emb_CAA98188_

(Z73960) RAN1B [Lotus japonicus]

Seq. No. 215422

Seq. ID LIB3147-009-Q1-K1-E12

Method BLASTX

% identity

77



```
NCBI GI
                  q3660467
                  513
BLAST score
E value
                  3.0e-52
Match length
                  136
                  76
% identity
                  (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                  thaliana]
                  215423
Seq. No.
                  LIB3147-009-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104712
BLAST score
                  192
                  9.0e-15
E value
Match length
                  109
% identity
                  42
                  (U95180) endosperm specific protein [Zea mays]
NCBI Description
Seq. No.
                  215424
                  LIB3147-009-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2351380
BLAST score
                  246
                  5.0e-21
E value
Match length
                  111
% identity
                  50
                  (U54559) translation initiation factor eIF3 p40 subunit
NCBI Description
                   [Homo sapiens] >gi 4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN
                  215425
Seq. No.
                  LIB3147-009-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982243
                  173
BLAST score
                  1.0e-12
E value
                  77
Match length
                  51
% identity
NCBI Description
                  (AF051204) hypothetical protein [Picea mariana]
                  215426
Seq. No.
                  LIB3147-009-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g3193296
NCBI GI
                  286
BLAST score
                  8.0e-26
E value
                  108
Match length
                   57
% identity
                  (AF069298) similar to pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215427
                  LIB3147-009-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4309698
                   502
BLAST score
                   6.0e-51
E value
Match length
                  134
```



```
(AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  215428
Seq. No.
                  LIB3147-009-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2494111
BLAST score
                  184
                  1.0e-13
E value
Match length
                  55
                  62
% identity
                  (AC002376) Contains similarity to Glycine protein kinase 6
NCBI Description
                   (gb_M67449). [Arabidopsis thaliana]
                  215429
Seq. No.
                  LIB3147-009-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  g3785976
NCBI GI
BLAST score
                  186
                  5.0e-14
E value
                  70
Match length
% identity
                   61
                  (AC005560) Sec12p-like protein [Arabidopsis thaliana]
NCBI Description
                   215430
Seq. No.
                  LIB3147-009-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3386613
BLAST score
                   502
                   4.0e-51
E value
                   114
Match length
                   83
% identity
                   (AC004665) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   215431
Seq. No.
                   LIB3147-009-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g2497538
NCBI GI
                   491
BLAST score
                   9.0e-50
E value
                   101
Match length
                   98
% identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
NCBI Description
                   pyruvate kinase [Glycine max]
                   215432
Seq. No.
Seq. ID
                   LIB3147-009-Q1-K1-G6
                   BLASTX
Method
NCBI GI
                   g2129473
BLAST score
                   217
                   1.0e-17
E value
Match length
                   69
% identity
                   arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
```

(U09556) arabinogalactan-like protein [Pinus taeda]



79

2.0e-36

BLAST score

E value

```
Seq. No.
                  215433
                  LIB3147-009-Q1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4204575
BLAST score
                  315
                  3.0e-29
E value
Match length
                  108
% identity
                  59
                  (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
NCBI Description
                  215434
Seq. No.
                  LIB3147-009-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2244955
BLAST score
                  162
                   3.0e-11
E value
Match length
                   47
                   53
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   215435
Seq. No.
                  LIB3147-009-Q1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2088822
                   146
BLAST score
                   2.0e-09
E value
Match length
                   94
                   38
% identity
                  (AF003384) K07B1.4 gene product [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   215436
                   LIB3147-009-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2570827
                   572
BLAST score
                   3.0e-59
E value
                   132
Match length
                   76
% identity
NCBI Description (AF026058) anthocyanidin synthase [Matthiola incana]
                   215437
Seq. No.
                   LIB3147-009-Q1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325324
BLAST score
                   110
                   5.0e-13
E value
                   66
Match length
                   59
% identity
                  (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                   thaliana]
                   215438
Seq. No.
                   LIB3147-010-Q1-K1-A1
Seq. ID
Method
                   BLASTN
                   q3046853
NCBI GI
```

E value

Match length

% identity

2.0e-56

106 99



223 Match length 84 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRA19, complete sequence [Arabidopsis thaliana] 215439 Seq. No. LIB3147-010-Q1-K1-A3 Seq. ID BLASTX Method g2444174 NCBI GI 388 BLAST score 1.0e-37 E value Match length 128 % identity 62 (U94781) unconventional myosin [Helianthus annuus] NCBI Description 215440 Seq. No. LIB3147-010-Q1-K1-A5 Seq. ID Method BLASTX q4262149 NCBI GI 548 BLAST score 2.0e-56 E value Match length 118 % identity 80 (AC005275) putative xyloglucan endotransglycosylase NCBI Description [Arabidopsis thaliana] 215441 Seq. No. Seq. ID LIB3147-010-Q1-K1-A6 Method BLASTX q549063 NCBI GI 207 BLAST score 2.0e-16 E value Match length 90 49 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626) 21kd polypeptide [Oryza sativa] 215442 Seq. No. LIB3147-010-Q1-K1-B1 Seq. ID BLASTX Method NCBI GI q1666096 493 BLAST score E value 7.0e-50 103 Match length 90 % identity NCBI Description (Y09113) dioxygenase [Marah macrocarpus] 215443 Seq. No. LIB3147-010-Q1-K1-B2 Seq. ID BLASTX Method NCBI GI g1173256 BLAST score 547



40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal NCBI Description protein S4 - upland cotton >gi 488739 emb CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum] 215444 Seq. No. LIB3147-010-Q1-K1-B7 Seq. ID Method BLASTX g3098571 NCBI GI 227 BLAST score 1.0e-18 E value Match length 93 % identity 45 (AF049028) BURP domain containing protein [Brassica napus] NCBI Description Seq. No. 215445 LIB3147-010-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI q120675 577 BLAST score 9.0e-60 E value 134 Match length % identity 83 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi 66011 pir DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis alba] 215446 Seq. No. LIB3147-010-Q1-K1-C4 Seq. ID Method BLASTX NCBI GI g3123264 275 BLAST score 3.0e-25 E value 89 Match length 72 % identity 60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana] 215447 Seq. No. Seq. ID LIB3147-010-Q1-K1-C7 Method BLASTX NCBI GI q2058273 493 BLAST score 7.0e-50 E value Match length 108 % identity 88 NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 215448

Seq. ID LIB3147-010-Q1-K1-C8

Method BLASTX
NCBI GI g729051
BLAST score 384
E value 3.0e-37
Match length 89



Seq. No. 215449

Seq. ID LIB3147-010-Q1-K1-D1

Method BLASTX
NCBI GI 94432866
BLAST score 188
E value 3.0e-14
Match length 114
% identity 36

NCBI Description (AC006300) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 215450

Seq. ID LIB3147-010-Q1-K1-D2

Method BLASTX
NCBI GI 9730645
BLAST score 312
E value 6.0e-29
Match length 72
% identity 88

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 215451

Seq. ID LIB3147-010-Q1-K1-D3

Method BLASTX
NCBI GI g1040877
BLAST score 530
E value 4.0e-54
Match length 102
% identity 87

NCBI Description (U30460) expansin S2 precursor [Cucumis sativus]

Seq. No. 215452

Seq. ID LIB3147-010-Q1-K1-D6

Method BLASTX
NCBI GI g2146734
BLAST score 229
E value 4.0e-19
Match length 57
% identity 67

NCBI Description GAST1 protein homolog (clone GASA4) - Arabidopsis thaliana

Seq. No. 215453

Seq. ID LIB3147-010-Q1-K1-D7

Method BLASTX NCBI GI g4538913 BLAST score 266



E value 3.0e-2394 Match length % identity 67 (ALO49482) putative protein [Arabidopsis thaliana] NCBI Description 215454 Seq. No. LIB3147-010-Q1-K1-D8 Seq. ID Method BLASTX NCBI GI q225267 BLAST score 264 5.0e-23E value Match length 134 % identity 46 ORF 1244 [Nicotiana tabacum] NCBI Description 215455 Seq. No. Seq. ID LIB3147-010-Q1-K1-D9 BLASTX Method NCBI GI q1168940 BLAST score 222 5.0e-18 E value Match length 72 65 % identity CHORISMATE MUTASE PRECURSOR (CM-1) >gi_629509_pir__S38958 NCBI Description chorismate mutase precursor - Arabidopsis thaliana >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase precursor [Arabidopsis thaliana] Seq. No. 215456 LIB3147-010-Q1-K1-E11 Seq. ID Method BLASTX q2789434 NCBI GI 500 BLAST score 8.0e-51 E value 114 Match length % identity 82 (AB001389) CLB1 [Lycopersicon esculentum] NCBI Description Seq. No. 215457 LIB3147-010-Q1-K1-E3 Seq. ID Method BLASTX g1469930 NCBI GI BLAST score 375 5.0e-36 E value 100 Match length 76 % identity (U48777) fiber-specific acyl carrier protein [Gossypium NCBI Description hirsutum] 215458 Seq. No. LIB3147-010-Q1-K1-F10 Seq. ID Method BLASTX g1652704 NCBI GI BLAST score 173 E value 2.0e-12

30094

131

34

Match length

% identity

NCBI Description



```
(D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                  215459
Seq. No.
                  LIB3147-010-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   q4185133
NCBI GI
BLAST score
                   142
                   6.0e-09
E value
                   37
Match length
                   59
% identity
                   (ACO05724) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   215460
Seq. No.
                   LIB3147-010-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g3522952
NCBI GI
BLAST score
                   359
                   3.0e - 34
E value
Match length
                   111
% identity
                   63
                   (AC004411) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   215461
Seq. No.
                   LIB3147-010-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1168322
BLAST score
                   317
                   2.0e-29
E value
                   63
Match length
                   97
% identity
                   ACTIN 71 >gi_21538_emb_CAA39279_ (X55750) actin [Solanum
NCBI Description
                   tuberosum]
                   215462
Seq. No.
                   LIB3147-010-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   q1350720
NCBI GI
                   439
BLAST score
                   1.0e-43
E value
                   109
Match length
% identity
                   76
NCBI Description 60S RIBOSOMAL PROTEIN L32
                   215463
Seq. No.
                   LIB3147-010-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g2851508
NCBI GI
                   245
BLAST score
                   1.0e-21
E value
Match length
                   75
                   63
% identity
```

30095

ribosomal protein L21 (gb_L38826). ESTs

60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to

gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 (AC003970) Putative ribosomal protein



L21 [Arabidopsis thaliana]

```
215464
Seq. No.
Seq. ID
                  LIB3147-010-Q1-K1-H3
Method
                  BLASTN
                  q3869075
NCBI GI
                  35
BLAST score
                  4.0e-10
E value
                  155
Match length
                  82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                  215465
Seq. No.
                  LIB3147-010-Q1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2497538
                  236
BLAST score
E value
                  1.0e-21
                  79
Match length
                  72
% identity
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
                  pyruvate kinase [Glycine max]
                  215466
Seq. No.
                  LIB3147-010-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  q3811009
NCBI GI
BLAST score
                  628
E value
                  1.0e-65
                  144
Match length
                  82
% identity
                  (AB019328) NADP specific isocitrate dehydrogenase [Daucus
NCBI Description
                  carota]
Seq. No.
                  215467
                  LIB3147-010-Q1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2497538
BLAST score
                  156
                  7.0e-11
E value
Match length
                   53
                   58
% identity
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
                  pyruvate kinase [Glycine max]
                   215468
Seq. No.
                   LIB3147-011-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3927830
                   217
BLAST score
                   2.0e-17
E value
Match length
                   57
                   38
% identity
                  (AC005727) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

30096

215469

Seq. No.

Seq. ID Method



LIB3147-011-Q1-K1-A11 Seq. ID Method BLASTX g2213867 NCBI GI BLAST score 162 3.0e-11 E value Match length 82 45 % identity (AF003124) fructose-biphosphate aldolase [Mesembryanthemum NCBI Description crystallinum] Seq. No. 215470 LIB3147-011-Q1-K1-A12 Seq. ID Method BLASTX NCBI GI g4512685 BLAST score 266 3.0e-23 E value 135 Match length % identity 43 (AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana] Seq. No. 215471 LIB3147-011-Q1-K1-A3 Seq. ID Method BLASTX NCBI GI q3184280 BLAST score 592 E value 2.0e-61 Match length 151 73 % identity (AC004136) putative small multi-drug export protein NCBI Description [Arabidopsis thaliana] 215472 Seq. No. LIB3147-011-Q1-K1-A8 Seq. ID Method BLASTX NCBI GI g2262158 BLAST score 160 E value 2.0e-11 Match length 64 56 % identity (AC002329) putative mitochondrial phosphate translocator NCBI Description protein [Arabidopsis thaliana] 215473 Seq. No. LIB3147-011-Q1-K1-B10 Seq. ID Method BLASTX NCBI GI q4090257 BLAST score 381 4.0e-37 E value Match length 72 % identity (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii] NCBI Description 215474 Seq. No.

30097

LIB3147-011-Q1-K1-B11

BLASTX

BLAST score

E value

371

7.0e-36



```
NCBI GI
                   q548774
BLAST score
                   169
E value
                   3.0e-12
Match length
                   43
% identity
                   72
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__$38360 ribosomal
NCBI Description
                   protein L7a - rice >gi_303855_dbj BAA02156 (D12631)
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   215475
Seq. ID
                   LIB3147-011-Q1-K1-B12
Method
                   BLASTX
                   g4220482
NCBI GI
BLAST score
                   227
E value
                   1.0e-18
Match length
                   66
% identity
                   35
NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   215476
                   LIB3147-011-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1199772
BLAST score
                   294
E value
                   2.0e-26
Match length
                   60
% identity
                   90
NCBI Description
                   (D83226) extensin like protein [Populus nigra]
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
Seq. No.
                   215477
Seq. ID
                   LIB3147-011-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   g4415992
BLAST score
                   650
E value
                   2.0e-68
Match length
                   123
% identity
                   100
NCBI Description
                  (AF059288) beta-tubulin 2 [Eleusine indica]
Seq. No.
                   215478
Seq. ID
                  LIB3147-011-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g4454097
BLAST score
                   230
E value
                   5.0e-19
Match length
                  77
% identity
                   64
NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]
Seq. No.
                  215479
Seq. ID
                  LIB3147-011-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1168896
```



```
Match length
                  91
% identity
                  70
NCBI Description
                  G2/MITOTIC-SPECIFIC CYCLIN 2 (B-LIKE CYCLIN) (CYCMS2)
                  >gi 914863 emb CAA57560 (X82040) cycMs2 [Medicago sativa
                  subsp. X varia]
Seq. No.
                  215480
                  LIB3147-011-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4098128
BLAST score
                  465
E value
                  9.0e-47
Match length
                  110
                  82
% identity
NCBI Description
                  (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                  215481
Seq. ID
                  LIB3147-011-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3851636
BLAST score
                  642
                  3.0e-67
E value
Match length
                  153
% identity
                  82
NCBI Description
                  (AF098519) unknown [Avicennia marina] >qi 4128206
                  (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  215482
Seq. ID
                  LIB3147-011-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4510383
BLAST score
                  295
                  9.0e-27
E value
Match length
                  105
                  62
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215483
                  LIB3147-011-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  g3851636
NCBI GI
BLAST score
                  315
E value
                  4.0e-29
                  106
Match length
                  58
% identity
NCBI Description
                  (AF098519) unknown [Avicennia marina] >gi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
```

Seq. No. 215484

Seq. ID LIB3147-011-Q1-K1-D8

Method BLASTN
NCBI GI g2244733
BLAST score 245
E value 1.0e-135
Match length 384
% identity 91

NCBI Description Cotton mRNA for actin, clone CF456, partial cds



```
215485
Seq. No.
                   LIB3147-011-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   q464621
NCBI GI
                   252
BLAST score
                   1.0e-21
E value
                   93
Match length
                   57
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant
                   >gi 19539 emb CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   215486
Seq. No.
                   LIB3147-011-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   q464621
NCBI GI
                   229
BLAST score
                   3.0e-19
E value
                   90
Match length
                   53
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   215487
Seq. No.
                   LIB3147-011-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g1707012
NCBI GI
                   389
BLAST score
                   6.0e-38
E value
                   82
Match length
                   85
% identity
                   (U78721) tyrosyl-tRNA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   215488
Seq. No.
                   LIB3147-011-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4240116
                   169
BLAST score
                   4.0e-12
E value
                   38
Match length
                   76
% identity
NCBI Description
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
                   thaliana] >qi 4240118 dbj BAA74838 (AB007800)
                   NADH-cytochrome b5 reductase [Arabidopsis thaliana]
                   215489
Seq. No.
Seq. ID
                   LIB3147-011-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g3309243
```

30100

621

126

6.0e-65

BLAST score

Match length

E value



```
% identity
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                  limon]
Seq. No.
                  215490
                  LIB3147-011-Q1-K1-F10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4519259
                  64
BLAST score
E value
                  2.0e-27
                  116
Match length
                  89
% identity
NCBI Description Citrus unshiu (CitVATP c-1) mRNA for vacuolar H+-ATPase c
                  subunit, complete cds
                  215491
Seq. No.
Seq. ID
                  LIB3147-011-Q1-K1-F2
                  BLASTX
Method
NCBI GI
                  q2245131
BLAST score
                  169
E value
                  5.0e-12
Match length
                  75
% identity
                  52
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  215492
                  LIB3147-011-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g1477428
NCBI GI
                  497
BLAST score
E value
                  1.0e-50
                  92
Match length
                  99
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.
                  215493
Seq. ID
                  LIB3147-011-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2511533
BLAST score
                  218
E value
                  8.0e-18
Match length
                  43
% identity
NCBI Description (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.
                  215494
                  LIB3147-011-Q1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3064039
BLAST score
                  180
E value
                  1.0e-13
Match length
                  70
                  41
% identity
NCBI Description (AF054445) major latex protein homolog [Mesembryanthemum
```

Seq. No. 215495

crystallinum]



```
LIB3147-011-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  q3779024
NCBI GI
                  263
BLAST score
                  5.0e-23
E value
                  69
Match length
                  86
% identity
                  (AC005171) unknown protein [Arabidopsis thaliana]
NCBI Description
                  215496
Seq. No.
                  LIB3147-011-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  g3108209
NCBI GI
                  187
BLAST score
                  3.0e-14
E value
                  52
Match length
                   69
% identity
                  (AF028809) eukaryotic cap-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   215497
Seq. No.
                   LIB3147-011-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g3355468
NCBI GI
                   137
BLAST score
                   1.0e-08
E value
                   60
Match length
                   55
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   215498
Seq. No.
                   LIB3147-011-Q1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325345
BLAST score
                   216
                   5.0e-18
E value
                   58
Match length
                   26
% identity
                   (AF128393) similar to thioredoxin-like proteins (Pfam:
NCBI Description
                   PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity
                   to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,
                   N=1) [Arabidopsis thaliana]
                   215499
 Seq. No.
                   LIB3147-011-Q1-K1-H2
 Seq. ID
                   BLASTX
Method
                   g1085384
 NCBI GI
                   263
 BLAST score
                   4.0e-23
 E value
                   64
 Match length
                   72
 % identity
                   Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm
 NCBI Description
                   protein F [Homo sapiens]
```

ribonucleoprotein polypeptide F

>gi_4507131_ref_NP_003086.1_pSNRPF_ small nuclear



Seq. No.

215500

```
LIB3147-011-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g4508079
NCBI GI
                  434
BLAST score
                  5.0e-43
E value
                  98
Match length
                  79
% identity
                  (AC005882) 66284 [Arabidopsis thaliana]
NCBI Description
                  215501
Seq. No.
                  LIB3147-011-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g3551257
NCBI GI
                   308
BLAST score
                   2.0e-28
E value
                  104
Match length
                   20
% identity
                  (AB012708) 98b [Daucus carota]
NCBI Description
                   215502
Seq. No.
                   LIB3147-013-Q1-K1-A12
Seq. ID
Method
                   BLASTX
                   g70753
NCBI GI
                   508
BLAST score
                   1.0e-51
E value
                   125
Match length
% identity
                   82
NCBI Description histone H3 - garden pea >gi_82610_pir__S00373 histone H3 -
                   wheat
                   215503
Seq. No.
                   LIB3147-013-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   g2160166
NCBI GI
                   214
BLAST score
                   3.0e-17
E value
Match length
                   118
                   41
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                   215504
 Seq. No.
                   LIB3147-013-Q1-K1-A4
 Seq. ID
                   BLASTX
Method
                   q1658197
 NCBI GI
                   429
 BLAST score
                   2.0e-42
 E value
 Match length
                   94
                   84
 % identity
 NCBI Description (U74630) calreticulin [Ricinus communis] >gi_1763297
                    (U74631) calreticulin [Ricinus communis]
                    215505
 Seq. No.
                    LIB3147-013-Q1-K1-A7
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g398994
 BLAST score
                    196
```



```
5.0e-15
E value
                  47
Match length
                  79
% identity
                  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                  (ETHYLENE-FORMING ENZYME) (EFE) >gi 166313 (M97961) tomato
                  and apple ACC oxidase homologue [Actinidia deliciosa]
                  215506
Seq. No.
                  LIB3147-013-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g2829893
NCBI GI
                  331
BLAST score
                  4.0e-31
E value
                  105
Match length
                  69
% identity
                  (AC002311) phosphoglucomutase [Arabidopsis thaliana]
NCBI Description
                  215507
Seq. No.
                  LIB3147-013-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g1174621
NCBI GI
                  385
BLAST score
                   3.0e-37
E value
                  148
Match length
                   47
% identity
                  T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                   (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing
                   cytosolic chaperonin (CCT) theta chain - mouse
                   >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit
                   of the chaperonin containing TCP-1 (CCT) [Mus musculus]
                   215508
Seq. No.
                   LIB3147-013-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g508304
NCBI GI
                   352
BLAST score
                   3.0e - 33
E value
                   79
Match length
                   80
% identity
NCBI Description (L22305) corC [Medicago sativa]
                   215509
Seq. No.
                   LIB3147-013-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   q3319355
NCBI GI
                   679
BLAST score
                   1.0e-71
E value
Match length
                   142
 % identity
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                   gamma chain [Arabidopsis thaliana]
                   215510
 Seq. No.
                   LIB3147-013-Q1-K1-B6
 Seq. ID
```

30104

BLASTX

559

g1531758

Method

NCBI GI BLAST score



```
E value
                  1.0e-57
Match length
                  112
                  93
% identity
                  (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
                  215511
Seq. No.
                  LIB3147-013-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g4127456
NCBI GI
                  382
BLAST score
                  7.0e - 37
E value
Match length
                  125
                  35
% identity
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215512
                  LIB3147-013-Q1-K1-B9
Seq. ID
Method
                  BLASTX
                  q4263528
NCBI GI
BLAST score
                  145
                   5.0e-09
E value
                   91
Match length
% identity :
                   40
                  (AC004044) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   215513
Seq. No.
Seq. ID
                   LIB3147-013-Q1-K1-C1
Method
                   BLASTX
                   q3927825
NCBI GI
BLAST score
                   236
                   7.0e-20
E value
Match length
                   55
                   78
% identity
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   215514
                   LIB3147-013-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   g417488
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
                   69
Match length
                   88
% identity
                   ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                   H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                   H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
                   type H isozyme [Solanum tuberosum]
                   215515
Seq. No.
                   LIB3147-013-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g2618721
NCBI GI
```

30105

422

5.0e-46

BLAST score

E value

```
108
Match length
                  88
% identity
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
                  215516
Seq. No.
Seq. ID
                  LIB3147-013-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g115486
BLAST score
                  567
E value
                  1.0e-58
                  114
Match length
% identity
NCBI Description CALMODULIN-2/3/5 >gi 99671 pir S22503 calmodulin -
                  Arabidopsis thaliana >gi 1076437 pir S53006 calmodulin -
                  leaf mustard >gi 2146726 pir S71513 calmodulin -
                  Arabidopsis thaliana >gi 166651 (M38380) calmodulin-2
                  [Arabidopsis thaliana] >gi 166653 (M73711) calmodulin-3
                  [Arabidopsis thaliana] >qi 474183 emb CAA47690 (X67273)
                  calmodulin [Arabidopsis thaliana] >gi 497992 (U10150)
                  calmodulin [Brassica napus] >qi 899058 (M88307) calmodulin
                  [Brassica juncea] >gi 1183005 dbj BAA08283 (D45848)
                  calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261)
                  unknown protein [Arabidopsis thaliana] >gi_3885333
                  (AC005623) calmodulin [Arabidopsis thaliana]
                  >gi_228407 prf 1803520A calmodulin 2 [Arabidopsis
                  thaliana]
                  215517
Seq. No.
                  LIB3147-013-Q1-K1-C3
Seq. ID
Method
                  BLASTX
```

NCBI GI q1172995 287 BLAST score 1.0e-25 E value Match length 117 % identity 55

NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204 (X78444) ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

215518 Seq. No.

Seq. ID LIB3147-013-Q1-K1-C5

Method BLASTX NCBI GI q464849 602 BLAST score 1.0e-62 E value 114 Match length % identity

NCBI Description TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha

chain - almond >gi $2041\overline{3}$ emb $\overline{CAA47635}$ (X67162)

alpha-tubulin [Prunus dulcis]

215519 Seq. No.

LIB3147-013-Q1-K1-C6 Seq. ID

Method BLASTX NCBI GI g3355311

E value Match length

% identity

75

65



```
BLAST score
                  1.0e-52
E value
                  131
Match length
                  77
% identity
NCBI Description (AJ009737) eukaryotic translation initiation factor 6 [Beta
                  vulgaris]
                  215520
Seq. No.
Seq. ID
                  LIB3147-013-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  q3334113
                  302
BLAST score
E value
                  1.0e-27
                  74
Match length
                  77
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  215521
Seq. ID
                  LIB3147-013-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2558962
BLAST score
                  339
                  9.0e-32
E value
                  76
Match length
                  93
% identity
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
                  215522
Seq. No.
                  LIB3147-013-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4457221
                  176
BLAST score
E value
                  9.0e-13
Match length
                  53
% identity
                  64
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum
                  chinense]
Seq. No.
                  215523
Seq. ID
                  LIB3147-013-Q1-K1-D2
                 BLASTX
Method
NCBI GI
                  g2558962
BLAST score
                 280
                  5.0e-25
E value
                  57
Match length
% identity
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
                  215524
Seq. No.
                  LIB3147-013-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1848210
BLAST score
                  197
                  1.0e-15
```



```
NCBI Description (Y11208) histone H2B1 [Nicotiana tabacum]
Seq. No.
                  215525
Seq. ID
                  LIB3147-013-Q1-K1-D5
                  BLASTX
Method
NCBI GI
                  q441457
                  572
BLAST score
E value
                  3.0e-59
                  110
Match length
% identity
                  96
                 (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  215526
Seq. ID
                  LIB3147-013-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q548852
BLAST score
                  210
                  1.0e-16
E value
Match length
                  89
                  52
% identity
NCBI Description 408 RIBOSOMAL PROTEIN S21 >gi 481227_pir__S38357 ribosomal
                  protein S21 - rice >gi_303839 dbj_BAA02158_ (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  215527
Seq. ID
                  LIB3147-013-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q541954
BLAST score
                  555
E value
                  4.0e-57
Match length
                  139
                  81
% identity
NCBI Description
                  ubiquitin extension protein - white lupine
                  >gi_438111_emb_CAA80334_ (Z22613) ubiquitin extension
                  protein [Lupinus albus]
Seq. No.
                  215528
Seq. ID
                  LIB3147-013-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1743242
BLAST score
                  211
                  1.0e-16
E value
Match length
                  64
% identity
NCBI Description (Y10035) alpha-tubulin [Histriculus cavicola]
Seq. No.
                  215529
                  LIB3147-013-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  q4406814
NCBI GI
```

Method BLASTX
NCBI GI 94406814
BLAST score 301
E value 2.0e-27
Match length 78
% identity 76

NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]



```
215530
Seq. No.
                  LIB3147-013-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                  q4204297
NCBI GI
                  157
BLAST score
                  2.0e-10
E value
                  118
Match length
                  42
% identity
                  (AC003027) ADK1 [Arabidopsis thaliana]
NCBI Description
                  215531
Seq. No.
                  LIB3147-013-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                   q2795809
NCBI GI
BLAST score
                   565
                   2.0e-58
E value
Match length
                   128
% identity
                   83
                  (AC003674) putative expansin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215532
                   LIB3147-013-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   q548774
NCBI GI
                   410
BLAST score
                   3.0e-40
E value
                   109
Match length
% identity
                   73
                  60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
NCBI Description
                   protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                   ribosomal protein L7A [Oryza sativa]
                   215533
Seq. No.
                   LIB3147-013-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g19611
NCBI GI
                   318
BLAST score
E value
                   2.0e-29
Match length
                   85
                   78
% identity
                   (X13675) histone H3 (AA 1-123) [Medicago sativa]
NCBI Description
                   >gi 2916748 emb CAA05554_ (AJ002555) histone H3 [Pisum
                   sativum]
                   215534
Seq. No.
                   LIB3147-013-Q1-K1-E8
Seq. ID
                   BLASTX
Method
                   g1169534
NCBI GI
                   727
BLAST score
                   3.0e-77
E value
                   152
Match length
                   93
% identity
```

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus

Seq. No.

215540



communis]

```
215535
Seq. No.
Seq. ID
                  LIB3147-013-Q1-K1-F11
                  BLASTX
Method
NCBI GI
                  g3047125
BLAST score
                  401
E value
                  5.0e-39
Match length
                  105
% identity
                  69
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  215536
                  LIB3147-013-Q1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869075
BLAST score
                  35
E value
                  4.0e-10
Match length
                  155
% identity
                  82
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  215537
                  LIB3147-013-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334115
                  367
BLAST score
E value
                  4.0e-41
Match length
                  95
% identity
                  60
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  215538
Seq. No.
Seq. ID
                  LIB3147-013-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  195
E value
                  2.0e-32
                  133
Match length
% identity
                  53
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.
                  215539
Seq. ID
                  LIB3147-013-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  351
E value
                  3.0e-33
Match length
                  95
% identity
                  68
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
```



LIB3147-013-Q1-K1-G2 Seq. ID BLASTX Method g3334299 NCBI GI BLAST score 576 1.0e-59 E value 120 Match length 94 % identity PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE NCBI Description COMPLEX ALPHA SUBUNIT) >gi_2315211_emb_CAA74725_ (Y14339) proteasome alpha subunit [Lycopersicon esculentum] 215541 Seq. No. LIB3147-013-Q1-K1-G3 Seq. ID BLASTX Method q4220532 NCBI GI 210 BLAST score 8.0e-17 E value 84 Match length % identity 58 (AL035356) putative protein [Arabidopsis thaliana] NCBI Description 215542 Seq. No. LIB3147-013-Q1-K1-H10 Seq. ID Method BLASTX g585963 NCBI GI 263 BLAST score 6.0e-23 E value 69 Match length 78 % identity PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT NCBI Description 215543 Seq. No. LIB3147-013-Q1-K1-H4 Seq. ID Method BLASTX g4314387 NCBI GI 292 BLAST score 3. 2.0e-26 E value 69 Match length 81 % identity (AC006232) putative beta-alanine synthetase [Arabidopsis NCBI Description thaliana] 215544 Seq. No. LIB3147-013-Q1-K1-H6 Seq. ID BLASTX Method g3264769 NCBI GI 587 BLAST score 7.0e-61 E value 135 Match length 41 % identity (AF071894) late embryogenesis-like protein [Prunus

NCBI Description (AF071894) late embryogenesis-like prote armeniaca]

Seq. No. 215545

Seq. ID LIB3147-015-Q1-K1-A1

Method BLASTX NCBI GI g2982259

Method

NCBI GI

BLASTX

q1170747



```
515
BLAST score
                 1.0e-52
E value
Match length
                 118
% identity
                 80
NCBI Description
                 (AF051212) probable 60s ribosomal protein L13a [Picea
                 mariana]
                 215546
Seq. No.
Seq. ID
                 LIB3147-015-Q1-K1-A2
                 BLASTN
Method
                 g2791833
NCBI GI
BLAST score
                 61
E value
                 1.0e-25
                 93
Match length
                 91
% identity
NCBI Description Manihot esculenta elongation factor 1-alpha (MeEF1) gene,
                 complete cds
Seq. No.
                 215547
                 LIB3147-015-Q1-K1-A3
Seq. ID
                 BLASTX
Method
                 q1170748
NCBI GI
BLAST score
                 142
E value
                 1.0e-08
Match length
                 30
                 90
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-D >gi 167349
                 (M88323) late embryogenesis-abundant protein [Gossypium
                 hirsutum] >gi 167351 (L01102) late embryogenesis-abundant
                 protein [Gossypium hirsutum]
Seq. No.
                 215548
                 LIB3147-015-Q1-K1-A4
Seq. ID
Method
                 BLASTX
NCBI GI
                 g122007
BLAST score
                 384
E value
                 4.0e-37
                 99
Match length
                 78
% identity
- 149) [Petroselinum crispum]
                 215549
Seq. No.
Seq. ID
                 LIB3147-015-Q1-K1-A7
Method
                 BLASTX
NCBI GI
                 g3641868
BLAST score
                 228
                 1.0e-19
E value
Match length
                 88
% identity
NCBI Description (AJ011012) hypothetical protein [Cicer arietinum]
Seq. No.
                 215550
                 LIB3147-015-Q1-K1-A8
Seq. ID
```



```
380
BLAST score
E value
                  1.0e-36
Match length
                  86
                  85
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  215551
Seq. No.
Seq. ID
                  LIB3147-015-Q1-K1-B1
                  BLASTX
Method
NCBI GI
                  q1658197
BLAST score
                  605
E value
                  5.0e-63
Match length
                  141
% identity
                  78
NCBI Description (U74630) calreticulin [Ricinus communis] >gi 1763297
                  (U74631) calreticulin [Ricinus communis]
                  215552
Seq. No.
                  LIB3147-015-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2864615
BLAST score
                  231
E value
                  3.0e-19
Match length
                  129
                  49
% identity
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                  215553
Seq. ID
                  LIB3147-015-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3702121
BLAST score
                  148
E value
                  2.0e-09
                  43
Match length
                  77
% identity
NCBI Description (AJ011681) retinoblastoma-related protein [Chenopodium
                  rubrum]
                  215554
Seq. No.
Seq. ID
                  LIB3147-015-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3377797
BLAST score
                  329
E value
                  1.0e-30
Match length
                  66
% identity
                  97
NCBI Description
                  (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
```

Seq. No. 215555

Seq. ID LIB3147-015-Q1-K1-B5

R90691 [Ara



```
BLASTX
Method
NCBI GI
                   g3885515
BLAST score
                   245
                   8.0e-21
E value
                   64
Match length
                   73
% identity
NCBI Description
                  (AF084202) similar to ribosomal protein S26 [Medicago
                   sativa]
                   215556
Seq. No.
Seq. ID
                   LIB3147-015-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g71634
BLAST score
                   648
                   5.0e-68
E value
Match length
                   122
% identity
                   98
NCBI Description actin 1 - rice
Seq. No.
                   215557
Seq. ID
                   LIB3147-015-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g4432855
BLAST score
                   248
                   4.0e-21
E value
Match length
                   141
                   49
% identity
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]
                   215558
Seq. No.
                   LIB3147-015-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q120668
BLAST score
                   668
E value
                   2.0e-70
Match length
                   142
% identity
                   92
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
                   215559
Seq. No.
Seq. ID
                   LIB3147-015-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3914424
BLAST score
                   457
                   1.0e-45
E value
Match length
                   107
% identity
                   80
NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                   >gi 2511592 emb CAA74027.1 (Y13693) multicatalytic
```

endopeptidase complex, proteasome component, alpha subunit



[Arabidopsis thaliana]

```
Seq. No.
                  215560
                  LIB3147-015-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  g3850816
NCBI GI
                  463
BLAST score
                  2.0e-46
E value
                  88
Match length
                   92
% identity
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
                   215561
Seq. No.
                  LIB3147-015-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                   g1174162
NCBI GI
                   695
BLAST score
                   2.0e-73
E value
                   132
Match length
                   92
% identity
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                   thaliana] >gi 3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   215562
Seq. No.
                   LIB3147-015-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   g1754795
NCBI GI
                   671
BLAST score
                   9.0e-71
E value
                   131
Match length
                   89
% identity
                  (U59477) omega-3 fatty acid desaturase [Perilla frutescens]
NCBI Description
                   215563
Seq. No.
                   LIB3147-015-Q1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1209703
                   448
BLAST score
                   1.0e-44
E value
                   115
Match length
                   71
% identity
                  (U40489) maize gll homolog [Arabidopsis thaliana]
NCBI Description
                   215564
Seq. No.
                   LIB3147-015-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q136057
                   553
BLAST score
                   6.0e-57
E value
                   138
Match length
% identity
                   77
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi_556171 (J04121) triosephosphate
```

isomerase [Coptis japonica]

NCBI GI



```
Seq. No.
                  215565
                  LIB3147-015-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  g3123264
NCBI GI
                  538
BLAST score
                  4.0e-55
E value
                  135
Match length
                  77
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                  215566
Seq. No.
                  LIB3147-015-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g2829897
NCBI GI
                  192
BLAST score
                  1.0e-14
E value
Match length
                   80
                   54
% identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
                   215567
Seq. No.
                   LIB3147-015-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3334138
BLAST score
                   234
                   2.0e-19
E value
Match length
                   85
                   55
% identity
                  CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin
NCBI Description
                   [Glycine max]
                   215568
Seq. No.
                   LIB3147-015-Q1-K1-D6
Seq. ID
                   BLASTX
Method
                   g643469
NCBI GI
BLAST score
                   416
                   7.0e-41
E value
                   128
Match length
                   61
% identity
NCBI Description (U19886) unknown [Lycopersicon esculentum]
                   215569
Seq. No.
                   LIB3147-015-Q1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4008159
BLAST score
                   639
                   5.0e-67
E value
                   144
Match length
                   83
% identity
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                   215570
                   LIB3147-015-Q1-K1-E10
Seq. ID
                   BLASTX
Method
```

30116

g2062173



```
257
BLAST score
                   3.0e-22
E value
                   75
Match length
% identity
                   (AC001645) cell division protein FtsH isolog [Arabidopsis
NCBI Description
                   thaliana]
                   215571
Seq. No.
                   LIB3147-015-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   q4510346
NCBI GI
                   202
BLAST score
                   9.0e-16
E value
                   49
Match length
                   76
% identity
                   (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   215572
Seq. No.
                   LIB3147-015-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   q1708971
NCBI GI
                   183
BLAST score
                   2.0e-13
E value
                   137
Match length
                   35
% identity
                   (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
NCBI Description
                    (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                   >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
                   black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                    (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                    serotina] >gi_1090776_prf__2019441A mandelonitrile lyase
                    [Prunus serotina]
                    215573
Seq. No.
                    LIB3147-015-Q1-K1-E8
Seq. ID
                    BLASTX
Method
                    g3878264
NCBI GI
BLAST score
                    230
                    5.0e-19
E value
                    116
Match length
                    38
 % identity
                   (Z75712) Similarity to some prokaryotic esterases; cDNA EST
 NCBI Description
                    EMBL: D71448 comes from this gene; cDNA EST EMBL: D74156
                    comes from this gene [Caenorhabditis elegans]
                    215574
 Seq. No.
                    LIB3147-015-Q1-K1-E9
 Seq. ID
                    BLASTX
 Method
                    g1493813
 NCBI GI
                    385
 BLAST score
                    3.0e-37
 E value
                    86
 Match length
                    88
 % identity
```

NCBI Description (U37576) histone H4-VIII [Gallus gallus]

Seq. No.

215575

Seq. ID



```
LIB3147-015-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4426565
                  190
BLAST score
                  2.0e-14
E value
Match length
                  91
                   42
% identity
                  (AF031483) unknown [Rattus norvegicus]
NCBI Description
                  215576
Seq. No.
                  LIB3147-015-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   q2842490
NCBI GI
BLAST score
                   512
                   4.0e-52
E value
                   142
Match length
% identity
                   71
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   215577
Seq. No.
                   LIB3147-015-Q1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1477565
BLAST score
                   292
                   3.0e-26
E value
Match length
                   142
                   4
% identity
                   (U50078) p532 [Homo sapiens]
NCBI Description
                   >gi 4557026_ref_NP_003913.1_pHERC1_ hect (homologous to the
                   E6-AP (UBE3A) carboxyl terminus) domain and RCC1
                   (CHC1)-like domain (RLD)
                   215578
Seq. No.
                   LIB3147-015-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g123544
NCBI GI
                   395
BLAST score
                   2.0e-41
E value
                   135
Match length
                   66
% identity
                   18.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.5)
NCBI Description
                   >gi_81788_pir__S00646 heat shock protein 18.5-C - soybean
                   >gi_18654_emb_CAA30154_ (X07160) hsp18.5-C protein (AA 1 -
                   161) [Glycine max]
                   215579
Seq. No.
                   LIB3147-015-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   q2829897
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   87
Match length
 % identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
                   215580
 Seq. No.
```

30118

LIB3147-015-Q1-K1-G10



Method BLASTX
NCBI GI g1173187
BLAST score 591
E value 2.0e-61
Match length 117
% identity 96

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 215581

Seq. ID LIB3147-015-Q1-K1-G12

Method BLASTX
NCBI GI g1174451
BLAST score 142
E value 1.0e-08
Match length 110
% identity 33

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, BETA SUBUNIT PRECURSOR

(TRAP-BETA) (SIGNAL SEQUENCE RECEPTOR BETA SUBUNIT) (SSR-BETA) >gi_631473_pir__S41063 translocon-associated protein beta chain - human >gi_452757_emb_CAA52207_(X74104) translocon-associated protein [Homo sapiens] >gi_1736880_dbj_BAA07206_(D37991) beta-signal sequence receptor [Homo sapiens] >gi_4507239_ref_NP_003136.1_pSSR2_

signal sequence receptor, beta (translocon-associated

protein beta)

Seq. No. 215582

Seq. ID LIB3147-015-Q1-K1-G2

Method BLASTX
NCBI GI g3319355
BLAST score 558
E value 2.0e-57
Match length 120
% identity 91

NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex

gamma chain [Arabidopsis thaliana]

Seq. No. 215583

Seq. ID LIB3147-015-Q1-K1-G3

Method BLASTN
NCBI GI g166929
BLAST score 34
E value 2.0e-09
Match length 65
% identity 89

NCBI Description A.thaliana ubiquitin extension protein (UBQ1) gene,

complete cds

Seq. No. 215584

Seq. ID LIB3147-015-Q1-K1-G4

Method BLASTX NCBI GI g4325372 BLAST score 289 E value 5.0e-26



```
Match length
                   128
% identity
                   55
                   (AF128396) contains similarity to protein disulfide
NCBI Description
                  isomerases [Arabidopsis thaliana]
                  215585
Seq. No.
                  LIB3147-015-Q1-K1-G6
Seq. ID
                  BLASTN
Method
NCBI GI
                   q2275090
                   169
BLAST score
                   4.0e-90
E value
                   228
Match length
                   97
% identity
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
                   215586
Seq. No.
Seq. ID
                   LIB3147-015-Q1-K1-G7
                   BLASTX
Method
NCBI GI
                   q2879867
                   370
BLAST score
                   2.0e-35
E value
                   106
Match length
                   67
% identity
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                   pombe]
                   215587
Seq. No.
                   LIB3147-015-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   556
                   3.0e-57
E value
Match length
                   133
                   82
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   215588
Seq. No.
                   LIB3147-015-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   g3355465
NCBI GI
BLAST score
                   361
                   2.0e-34
E value
Match length
                   142
                   54
% identity
                   (AC004218) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   215589
Seq. No.
                   LIB3147-015-Q1-K1-H1
Seq. ID
Method
                   BLASTX
                   g2459420
NCBI GI
BLAST score
                   652
                   1.0e-68
E value
Match length
                   128
                   97
% identity
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
```

30120

thaliana]

NCBI Description



```
215590
Seq. No.
                  LIB3147-015-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g1174621
NCBI GI
                  379
BLAST score
                  2.0e-36
E value
                  137
Match length
                  48
% identity
                  T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                   (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing
                  cytosolic chaperonin (CCT) theta chain - mouse
                  >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit
                  of the chaperonin containing TCP-1 (CCT) [Mus musculus]
                   215591
Seq. No.
                  LIB3147-015-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                   q231574
NCBI GI
                   350
BLAST score
                   4.0e-33
E value
                   99
Match length
                   68
% identity
                   L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi_81837_pir__S22523 asparaginase (EC 3.5.1.1) - tree
                   lupine (fragment) >gi_19137_emb_CAA36824_ (X52588)
                   asparaginase [Lupinus arboreus]
                   215592
Seq. No.
                   LIB3147-015-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   g1518540
NCBI GI
                   659
BLAST score
                   2.0e-69
E value
                   137
Match length
                   88
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   215593
Seq. No.
                   LIB3147-015-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g4580461
NCBI GI
                   671
BLAST score
                   9.0e-71
E value
                   142
Match length
                   89
 % identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215594
Seq. No.
                   LIB3147-017-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   q3759184
NCBI GI
                   250
BLAST score
                   9.0e-26
 E value
                   99
Match length
 % identity
```

(AB018441) phi-1 [Nicotiana tabacum]



Seq. No.

215595

```
LIB3147-017-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  g3063691
NCBI GI
                  253
BLAST score
                  5.0e-27
E value
                  88
Match length
                  61
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                  215596
Seq. No.
                  LIB3147-017-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g1362086
NCBI GI
                  545
BLAST score
                  4.0e-56
E value
                  109
Match length
                  94
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919_pir__$65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                  215597
Seq. No.
                  LIB3147-017-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                   g4544443
NCBI GI
BLAST score
                   360
                   5.0e-35
E value
                  124
Match length
                   42
% identity
                  (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   215598
Seq. No.
                   LIB3147-017-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3776013
                   184
BLAST score
                   3.0e-14
E value
                   48
Match length
                   77
% identity
NCBI Description (AJ010470) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   215599
                   LIB3147-017-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3851636
BLAST score
                   371
E value
                   7.0e-36
                   87
Match length
                   80
% identity
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
```



(AF056316) 40S ribosome protein S7 [Avicennia marina]

```
Seq. No.
                  215600
                  LIB3147-017-Q1-K1-B6
Seq. ID
Method
                  BLASTX
                   g2401257
NCBI GI
BLAST score
                   282
                   3.0e-25
E value
Match length
                   126
                   48
% identity
                  (D63951) TBZ17 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   215601
                   LIB3147-017-Q1-K1-B8
Seq. ID
Method
                   BLASTX
                   g2500345
NCBI GI
BLAST score
                   269
                   8.0e-24
E value
Match length
                   78
                   72
% identity
                   NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY
NCBI Description
                   GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)
                   >gi 2618578 dbj BAA23363 (D50420) OTK27 [Homo sapiens]
                   >gi^{-}3859990^{-}(AF^{-}091076) OTK27 [Homo sapiens]
                   >gi 1589072 prf 2210268A nuclear protein-NHP2-like protein
                   [Homo sapiens]
                   215602
Seq. No.
                   LIB3147-017-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   q2454182
NCBI GI
                   433
BLAST score
                   5.0e-43
E value
                   99
Match length
                   83
% identity
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
                   215603
Seq. No.
                   LIB3147-017-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g1498053
NCBI GI
                   455
BLAST score
                   2.0e-45
E value
                   130
Match length
                   72
% identity
                   (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                   215604
Seq. No.
                   LIB3147-017-Q1-K1-C4
Seq. ID
                   BLASTN
Method
                   g2570118
NCBI GI
                   43
BLAST score
                   4.0e-15
E value
                   83
Match length
                   88
% identity
```

30123

NCBI Description S.latifolia mRNA, clone CCLS



215605

Seq. No.

```
LIB3147-017-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  q2558962
NCBI GI
BLAST score
                  312
                  8.0e-29
E value
                  64
Match length
                  100
% identity
                  (AF025667) histone H2B1 [Gossypium hirsutum]
NCBI Description
Seq. No.
                  215606
                  LIB3147-017-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g1199772
NCBI GI
                  186
BLAST score
                  5.0e-14
E value
                  40
Match length
                  82
% identity
                  (D83226) extensin like protein [Populus nigra]
NCBI Description
                  >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                  215607
Seq. No.
                  LIB3147-017-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g585451
NCBI GI
BLAST score
                  504
                  3.0e-51
E value
                  116
Match length
                   84
% identity
                  MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 62 KD ISOFORM
NCBI Description
                   PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
                   (NAD-ME) >gi_1076667_pir__B53318 malate dehydrogenase
                   (decarboxylating) (EC 1.1.1.39) 62K chain precursor,
                   mitochondrial - potato >gi_438249_emb_CAA80559_ (Z23023)
                  malate dehydrogenase [Solanum tuberosum]
                   215608
Seq. No.
                   LIB3147-017-Q1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1498053
                   167
BLAST score
                   6.0e-12
E value
                   55
Match length
                   64
% identity
NCBI Description
                  (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                   215609
                   LIB3147-017-Q1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3868758
BLAST score
                   360
                   2.0e-34
E value
Match length
                   86
                   79
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
```

Method

NCBI GI

BLAST score

BLASTN

33

g2828278



```
215610
Seq. No.
                  LIB3147-017-Q1-K1-E10
Seq. ID
                  BLASTN
Method
                  g12614
NCBI GI
                  215
BLAST score
                  1.0e-117
E value
                  345
Match length
                  94
% identity
NCBI Description L.esculentum genes for tRNA Asn and tRNA Tyr
                  215611
Seq. No.
                  LIB3147-017-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g3341696
NCBI GI
BLAST score
                   384
                   4.0e-37
E value
                  108
Match length
                   67
% identity
                  (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215612
Seq. No.
                  LIB3147-017-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                   g1084461
NCBI GI
                   268
BLAST score
                   1.0e-23
E value
Match length
                   93
                   57
% identity
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                   215613
Seq. No.
                   LIB3147-017-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g2136800
NCBI GI
                   158
BLAST score
E value
                   1.0e-10
                   93
Match length
                   43
% identity
                   polyA binding protein II - bovine >gi_1051125_emb_CAA62006_
NCBI Description
                   (X89969) polyA binding protein II [Bos taurus]
                   215614
Seq. No.
                   LIB3147-017-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g3395441
NCBI GI
BLAST score
                   442
E value
                   6.0e-44
Match length
                   116
                   76
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215615
                   LIB3147-017-Q1-K1-F2
Seq. ID
```

30125



```
E value
                  2.0e-09
Match length
                  69
                  87
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
NCBI Description
                   (ESSAII project)
                  215616
Seq. No.
                  LIB3147-017-Q1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4191783
BLAST score
                  201
                   1.0e-15
E value
Match length
                   51
                   73
% identity
                  (AC005917) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215617
                   LIB3147-017-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q322750
BLAST score
                   468
                   4.0e-47
E value
                   95
Match length
% identity
                   95
                   ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                   >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
Seq. No.
                   215618
                   LIB3147-017-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   q1498330
NCBI GI
                   311
BLAST score
                   7.0e-29
E value
                   77
Match length
                   81
% identity
                  (U60498) actin [Glycine max]
NCBI Description
Seq. No.
                   215619
                   LIB3147-017-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4512653
NCBI GI
BLAST score
                   284
                   2.0e-42
E value
                   120
Match length
                   73
% identity
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215620
Seq. No.
                   LIB3147-017-Q1-K1-G10
Seq. ID
Method
                   BLASTX
                   g1172597
NCBI GI
                   216
BLAST score
                   2.0e-17
E value
                   46
Match length
                   89
% identity
NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888 pir__JS0731
```



wound-inducible basic protein - kidney bean >gi_169365 (L00625) basic protein [Phaseolus vulgaris] >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein [Phaseolus vulgaris]

 Seq. No.
 215621

 Seq. ID
 LIB3147-017-Q1-K1-G4

 Method
 BLASTX

 NCBI GI
 g2500376

 BLAST score
 241

 E value
 2.0e-20

E value 2.0 Match length 58 % identity 88

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_

(AC005508) 23552 [Arabidopsis thaliana]

Seq. No. 215622

Seq. ID LIB3147-017-Q1-K1-G8

Method BLASTX
NCBI GI g2190550
BLAST score 294
E value 2.0e-26
Match length 80
% identity 70

NCBI Description (AC001229) ESTs gb_T45673,gb_N37512 come from this gene.

[Arabidopsis thaliana]

Seq. No. 215623

Seq. ID LIB3147-017-Q1-K1-H2

Method BLASTX
NCBI GI g1103712
BLAST score 309
E value 8.0e-29
Match length 76
% identity 86

NCBI Description (X83729) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No. 215624

Seq. ID LIB3147-017-Q1-K1-H3

Method BLASTX
NCBI GI g2960216
BLAST score 507
E value 1.0e-51
Match length 118
% identity 86

NCBI Description (AJ223384) 26S proteasome regulatory ATPase subunit 10b

(S10b) [Manduca sexta]

Seq. No. 215625

Seq. ID LIB3147-017-Q1-K1-H8

Method BLASTX
NCBI GI g1778376
BLAST score 385
E value 2.0e-37
Match length 91
% identity 80

NCBI Description (U81288) PsRT17-1 [Pisum sativum]

NCBI Description

thaliana]



```
215626
Seq. No.
                  LIB3147-018-Q1-K1-A9
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
                  37
Match length
                  61
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   215627
Seq. No.
                  LIB3147-018-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   g1708993
NCBI GI
BLAST score
                   247
                   2.0e-21
E value
Match length
                   70
                   70
% identity
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
NCBI Description
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                   >gi_2129567_pir__S61429 cystathionine beta-lyase (EC
                   4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511)
                   cystathionine beta-lyase [Arabidopsis thaliana]
                   215628
Seq. No.
                   LIB3147-018-Q1-K1-C10
Seq. ID
Method
                   BLASTN
                   g509768
NCBI GI
                   33
BLAST score
                   6.0e-09
E value
                   81
Match length
                   85
% identity
                  Glycine max seed-specific low molecular weight sulfur-rich
NCBI Description
                   protein
                   215629
Seq. No.
                   LIB3147-018-Q1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539348
                   261
BLAST score
E value
                   8.0e-23
                   93
Match length
                   52
 % identity
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
                   215630
 Seq. No.
                   LIB3147-018-Q1-K1-C9
 Seq. ID
Method
                   BLASTX
                   q4008006
 NCBI GI
                   439
 BLAST score
                    1.0e-43
 E value
 Match length
                   137
                    68
 % identity
                    (AF084034) receptor-like protein kinase [Arabidopsis
```

% identity

NCBI Description

13



```
Seq. No.
                  215631
                  LIB3147-018-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350984
                  449
BLAST score
                  1.0e-44
E value
Match length
                  118
                  76
% identity
                  40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal
NCBI Description
                  protein S3a [Helianthus annuus]
Seq. No.
                  215632
                  LIB3147-018-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g3935165
NCBI GI
BLAST score
                  158
                  1.0e-10
E value
Match length
                   60
                   67
% identity
                  (AC004557) F17L21.8 [Arabidopsis thaliana]
NCBI Description
                   215633
Seq. No.
Seq. ID
                  LIB3147-018-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                   g1708993
BLAST score
                   387
                   1.0e-37
E value
Match length
                   97
% identity
                   77
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
NCBI Description
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                   >gi 2129567 pir S61429 cystathionine beta-lyase (EC
                   4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511)
                   cystathionine beta-lyase [Arabidopsis thaliana]
                   215634
Seq. No.
                   LIB3147-018-Q1-K1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q126985
                   449
BLAST score
                   7.0e-45
E value
                   96
Match length
                   82
% identity
                  MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis
NCBI Description
                   thaliana]
                   215635
Seq. No.
                   LIB3147-018-Q1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q421929
                   626
BLAST score
                   2.0e-65
E value
Match length
                   149
```

ubiquitin [Lycopersicon esculentum]

ubiquitin - tomato >gi 312160 emb_CAA51679_ (X73156)

Seq. ID Method

NCBI GI

BLAST score



```
215636
Seq. No.
                  LIB3147-018-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  255
                  4.0e-30
E value
                  103
Match length
% identity
                  65
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  215637
Seq. No.
                  LIB3147-018-Q1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2498731
BLAST score
                  377
E value
                  2.0e-49
                  149
Match length
                   66
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi_1362013_pir__S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                   zeta-crystallin homologue [Arabidopsis thaliana]
                   215638
Seq. No.
Seq. ID
                  LIB3147-018-Q1-K1-H9
Method
                   BLASTX
                   q1708993
NCBI GI
                   451
BLAST score
                   5.0e-45
E value
                   129
Match length
% identity
                   69
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
NCBI Description
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                   >gi_2129567_pir__S61429 cystathionine beta-lyase (EC
                   4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511)
                   cystathionine beta-lyase [Arabidopsis thaliana]
                   215639
Seq. No.
                   LIB3147-019-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   g3176668
NCBI GI
                   680
BLAST score
                   1.0e-71
E value
                   141
Match length
                   92
% identity
                   (ACO04393) Similar to ribosomal protein L17 gb_X62724 from
NCBI Description
                   Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                   gb Z33937 come from this gene. [Arabidopsis thaliana]
                   215640
Seq. No.
```

30130

LIB3147-019-Q1-K1-A12

BLASTX

507

q3885515



E value 2.0e-51 Match length 113 84

NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago

sativa]

Seq. No. 215641

Seq. ID LIB3147-019-Q1-K1-A8

Method BLASTX
NCBI GI g3860008
BLAST score 223
E value 3.0e-18
Match length 139
% identity 33

NCBI Description (AF091085) unknown [Homo sapiens]

Seq. No. 215642

Seq. ID LIB3147-019-Q1-K1-B2

Method BLASTX
NCBI GI g3450889
BLAST score 611
E value 1.0e-63
Match length 159
% identity 81

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 215643

Seq. ID LIB3147-019-Q1-K1-B3

Method BLASTX
NCBI GI g417103
BLAST score 679
E value 1.0e-71
Match length 136
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum]

>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 215644

Seq. ID LIB3147-019-Q1-K1-B4

Method BLASTX



```
g4105772
NCBI GI
                  416
BLAST score
                  5.0e-41
E value
Match length
                  108
                  43
% identity
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
                  215645
Seq. No.
                  LIB3147-019-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g132944
NCBI GI
BLAST score
                   631
                  5.0e-66
E value
                  125
Match length
                   92
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658_pir__JQ0772 ribosomal
NCBI Description
                   protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                   215646
Seq. No.
                  LIB3147-019-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g4105772
NCBI GI
                   380
BLAST score
                   1.0e-36
E. value
                   124
Match length
                   33
% identity
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
                   215647
Seq. No.
                   LIB3147-019-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g2827552
NCBI GI
                   284
BLAST score
                   3.0e-25
E value
                   114
Match length
                   54
% identity
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   215648
Seq. No.
                   LIB3147-019-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g2982268
NCBI GI
                   600
BLAST score
                   2.0e-62
E value
                   131
Match length
                   89
% identity
                   (AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                   mariana]
                   215649
Seq. No.
Seq. ID
                   LIB3147-019-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g11837
BLAST score
                   486
```

30132

2.0e-63

141

E value Match length



```
% identity
                  (Z00044) NADH dehydrogenase 27kD subunit [Nicotiana
NCBI Description
                  tabacum] >gi_225205_prf__1211235AK bhpB gene [Nicotiana
                  tabacuml
                  215650
Seq. No.
                  LIB3147-019-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  g3080420
NCBI GI
                  488
BLAST score
                  3.0e-49
E value
                  150
Match length
                  61
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  215651
Seq. No.
                  LIB3147-019-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g11837
NCBI GI
                  465
BLAST score
                  1.0e-62
E value
                  137
Match length
                   92
% identity
                  (Z00044) NADH dehydrogenase 27kD subunit [Nicotiana
NCBI Description
                   tabacum] >gi 225205 prf__1211235AK bhpB gene [Nicotiana
                   tabacum]
                   215652
Seq. No.
                   LIB3147-019-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   q4432859
NCBI GI
                   196
BLAST score
                   5.0e-15
E value
                   86
Match length
                   45
% identity
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215653
Seq. No.
                   LIB3147-019-Q1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4538968
                   344
BLAST score
                   2.0e-32
E value
Match length
                   145
% identity
                  (ALO49488) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215654
                   LIB3147-019-Q1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4090257
                   460
BLAST score
                   6.0e-46
E value
                   91
Match length
                   96
 % identity
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
```

Seq. ID

Method



```
215655
Seq. No.
                  LIB3147-019-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g3402703
NCBI GI
BLAST score
                   619
                   1.0e-64
E value
                  153
Match length
                   76
% identity
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   215656
Seq. No.
                  LIB3147-019-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                   q2130017
NCBI GI
                   436
BLAST score
                   3.0e-43
E value
                   95
Match length
                   81
% identity
                  hypothetical protein - common sunflower
NCBI Description
                   >gi_1040729_emb_CAA60621_ (X87143) cytochrome b5 containing
                   fusion protein [Helianthus annuus]
                   215657
Seq. No.
                   LIB3147-019-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512676
                   209
BLAST score
E value
                   2.0e-16
Match length
                   117
                   43
% identity
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215658
Seq. No.
                   LIB3147-019-Q1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2960216
BLAST score
                   686
                   2.0e-72
E value
Match length
                   152
                   88
% identity
                   (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
                   (S10b) [Manduca sexta]
                   215659
Seq. No.
Seq. ID
                   LIB3147-019-Q1-K1-D7
Method
                   BLASTN
NCBI GI
                   g3493171
BLAST score
                   62
                   7.0e-27
E value
                   97
Match length
                   92
% identity
NCBI Description Gossypium hirsutum fiber annexin mRNA, complete cds
                   215660
Seq. No.
```

30134

LIB3147-019-Q1-K1-D8

BLASTX

NCBI Description



```
q3687251
NCBI GI
BLAST score
                  175
                  1.0e-12
E value
Match length
                  46
                   74
% identity
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
                  215661
Seq. No.
                  LIB3147-019-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                   g3128169
NCBI GI
                   292
BLAST score
                   3.0e-26
E value
                   107
Match length
% identity
                   52
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215662
                   LIB3147-019-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g4567249
NCBI GI
BLAST score
                   625
                   3.0e-65
E value
                   142
Match length
                   80
% identity
                  (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215663
                   LIB3147-019-Q1-K1-E3
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
                   48
Match length
                   64
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   215664
                   LIB3147-019-Q1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   a3236242
BLAST score
                   438
                   2.0e-43
E value
Match length
                   111
                   79
% identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   215665
                   LIB3147-019-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245001
BLAST score
                   313
E value
                   9.0e-29
Match length
                   64
% identity
```

(Z97341) similarity to NADH dehydrogenase (ubiquinone)



[Arabidopsis thaliana]

```
215666
Seq. No.
                  LIB3147-019-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  g548852
NCBI GI
                  354
BLAST score
                  1.0e-33
E value
                  82
Match length
                  79
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
                  215667
Seq. No.
                  LIB3147-019-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g4454452
NCBI GI
                  461
BLAST score
                  5.0e-46
E value
                  124
Match length
                  67
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  215668
Seq. No.
                  LIB3147-019-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  g1174870
NCBI GI
                  273
BLAST score
                  5.0e-24
E value
                  72
Match length
                  74
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN
NCBI Description
                   >gi_633685_emb_CAA55861_ (X79274) ubiquinol--cytochrome c
                   reductase [Solanum tuberosum]
                  215669
Seq. No.
                  LIB3147-019-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q1143511
NCBI GI ·
                   676
BLAST score
                   3.0e-71
E value
Match length
                   126
                   95
% identity
                  (Z47076) Ser/Thr protein phosphatase homologous to PPX
NCBI Description
                   [Malus domestica] >gi 1586034 prf 2202340A Ser/Thr protein
                   phosphatase [Malus domestica]
                   215670
Seq. No.
                   LIB3147-019-Q1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3334113
BLAST score
                   403
                   3.0e-39
E value
Match length
                   89
                   88
 % identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015)
```



acyl-CoA-binding protein [Gossypium hirsutum]

```
215671
Seq. No.
                  LIB3147-019-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  g3334230
NCBI GI
                  301
BLAST score
                  2.0e-27
E value
                  119
Match length
                  50
% identity
                  D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >gi_2828803
NCBI Description
                   (U84197) D-hydantoinase [Pseudomonas putida]
                  215672
Seq. No.
                  LIB3147-019-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  q2764941
NCBI GI
                   409
BLAST score
                   6.0e-40
E value
                   101
Match length
                   69
% identity
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
                   215673
Seq. No.
                   LIB3147-019-Q1-K1-F6
Seq. ID
Method
                   BLASTX
                   q4204300
NCBI GI
                   145
BLAST score
                   5.0e-09
E value
                   99
Match length
                   36
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   215674
Seq. No.
                   LIB3147-019-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   q1408471
NCBI GI
                   540
BLAST score
                   3.0e-55
E value
                   119
Match length
 % identity
                   82
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
 Seq. No.
                   215675
                   LIB3147-019-Q1-K1-G10
 Seq. ID
                   BLASTX
 Method
                    g1480012
 NCBI GI
                   260
 BLAST score
                    1.0e-22
 E value
                   51
 Match length
                    96
 % identity
                   (D78492) putative ubiquitin extension protein [Brassica
 NCBI Description
```

30137

rapa]



Seq. No.

215676

LIB3147-019-Q1-K1-G11

```
Seq. ID
Method
                  BLASTX
                  g2459426
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
Match length
                  50
                   54
% identity
                   (AC002332) putative splicing factor U2AF large chain
NCBI Description
                   [Arabidopsis thaliana]
                   215677
Seq. No.
                   LIB3147-019-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   g225267
NCBI GI
BLAST score
                   428
                   3.0e-42
E value
Match length
                   159
                   54
% identity
NCBI Description ORF 1244 [Nicotiana tabacum]
                   215678
Seq. No.
                   LIB3147-019-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g3044212
NCBI GI
                   532
BLAST score
                   1.0e-60
E value
Match length
                   148
% identity
                   84
                  (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   215679
                   LIB3147-019-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g3135264
NCBI GI
                   447
BLAST score
                   2.0e-44
E value
                   119
Match length
 % identity
                   71
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]
                   215680
 Seq. No.
                   LIB3147-019-Q1-K1-G5
 Seq. ID
                   BLASTX
 Method
                   g4455365
 NCBI GI
                   296
 BLAST score
                   7.0e-27
 E value
                   59
 Match length
                   85
 % identity
 NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                   215681
 Seq. No.
                   LIB3147-019-Q1-K1-G7
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    q3135264
                    463
 BLAST score
```



```
3.0e-46
E value
Match length
                  132
                  68
% identity
                  (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                  215682
Seq. No.
                  LIB3147-019-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g1351359
NCBI GI
                  287
BLAST score
                  1.0e-25
E value
Match length
                  69
                  71
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN
NCBI Description
                   (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690
                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein
                   - potato >gi_488712_emb_CAA55860_ (X79273)
                   ubiquinol--cytochrome c reductase [Solanum tuberosum]
                   215683
Seq. No.
                   LIB3147-019-Q1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2689631
                   693
BLAST score
                   2.0e-73
E value
                   141
Match length
                   97
% identity
                  (AF022389) ADP-ribosylation factor [Vigna unguiculata]
NCBI Description
                   215684
Seq. No.
                   LIB3147-019-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g508304
NCBI GI
                   240
BLAST score
                   4.0e-20
E value
                   82
Match length
                   57
% identity
NCBI Description (L22305) corC [Medicago sativa]
                   215685
Seq. No.
                   LIB3147-019-Q1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1173256
                   763
BLAST score
                   2.0e-81
E value
                   149
Match length
                   97
 % identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi_488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   215686
 Seq. No.
```

Seq. ID LIB3147-019-Q1-K1-H2

Method BLASTN NCBI GI g436031 BLAST score 52

30139

NCBI Description



```
3.0e-20
E value
                  120
Match length
% identity
                  86
                  Nicotiana tabacum (TSC40-4) 60S ribosomal protein L34 mRNA,
NCBI Description
                  complete cds
                  215687
Seq. No.
                  LIB3147-019-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  g2746232
NCBI GI
BLAST score
                   105
                   3.0e-09
E value
                   44
Match length
                   75
% identity
                  (AF037051) glutathione peroxidase [Gossypium hirsutum]
NCBI Description
                   215688
Seq. No.
                  LIB3147-019-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   q2244904
NCBI GI
                   186
BLAST score
                   3.0e-14
E value
Match length
                   65
% identity
                   66
                   (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   215689
                   LIB3147-019-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   g3122785
NCBI GI
                   457
BLAST score
                   1.0e-45
E value
                   112
Match length
                   81
% identity
                  40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal
NCBI Description
                   protein S14 [Lupinus luteus]
                   215690
Seq. No.
                   LIB3147-020-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4417280
                   537
BLAST score
                   5.0e-55
E value
                   144
Match length
                   74
% identity
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
NCBI Description
                   215691
Seq. No.
Seq. ID
                   LIB3147-020-Q1-K1-A11
Method
                   BLASTX
                   q4455174
NCBI GI
BLAST score
                   322
                   8.0e-30
E value
Match length
                   82
                   76
% identity
```

(AL035521) putative protein [Arabidopsis thaliana]



Seq. No.

215692

```
LIB3147-020-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  g2970051
NCBI GI
                  526
BLAST score
                  8.0e-54
E value
                  127
Match length
                  80
% identity
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
                  215693
Seq. No.
                  LIB3147-020-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  q131772
NCBI GI
                  383
BLAST score
                   6.0e-37
E value
                  95
Match length
                  83
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723 pir_ A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                   215694
Seq. No.
                  LIB3147-020-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                   g3915196
NCBI GI
                   308
BLAST score
                   3.0e-28
E value
                   81
Match length
                   67
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-C (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 1493838 (U52949)
                   cyclin-specific ubiquitin carrier protein E2-C [Spisula
                   solidissima]
Seq. No.
                   215695
                   LIB3147-020-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   q4417280
NCBI GI
                   162
BLAST score
E value
                   3.0e-11
                   101
Match length
                   39
% identity
NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]
                   215696
Seq. No.
                   LIB3147-020-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352442
BLAST score
                   324
E value
                   3.0e-30
Match length
                   86
                   69
 % identity
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD
```

SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_1002917 (U34598) p28



[Oryza sativa]

```
215697
Seq. No.
                   LIB3147-020-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g2494034
NCBI GI
                   223
BLAST score
                   2.0e-18
E value
                   113
Match length
                   49
% identity
                   DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                   KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                   diacylglycerol kinase [Arabidopsis thaliana]
                   215698
Seq. No.
                   LIB3147-020-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   g3915196
NCBI GI
                   304
BLAST score
                   9.0e-28
E value
                   81
Match length
                   67
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-C (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_1493838 (U52949)
                   cyclin-specific ubiquitin carrier protein E2-C [Spisula
                   solidissima]
                   215699
Seq. No.
                   LIB3147-020-Q1-K1-A9
Seq. ID
                   BLASTN
Method
                    q4102896
NCBI GI
                    38
BLAST score
                    7.0e-13
E value
                    46
Match length
                    96
% identity
                   Tilia sp 25S ribosomal RNA gene, partial sequence
NCBI Description
                    215700
Seq. No.
                    LIB3147-020-Q1-K1-B1
Seq. ID
                    BLASTX
Method
                    q2494034
NCBI GI
BLAST score
                    690
                    6.0e-73
E value
                    149
Match length
                    87
% identity
                    DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                    KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase -
                    Arabidopsis thaliana >gi 1374772 dbj_BAA09856_ (D63787)
                    diacylglycerol kinase [Arabidopsis thaliana]
                    215701
Seq. No.
                    LIB3147-020-Q1-K1-B11
Seq. ID
                    BLASTX
Method
                    q417745
NCBI GI
```

746

2.0e-79

BLAST score

E value



Match length 147 % identity 97

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 215702

Seq. ID LIB3147-020-Q1-K1-B12

Method BLASTX
NCBI GI g122007
BLAST score 233
E value 2.0e-19
Match length 69
% identity 70

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 215703

Seq. ID LIB3147-020-Q1-K1-B3

Method BLASTX
NCBI GI g294668
BLAST score 419
E value 3.0e-41
Match length 111
% identity 75

NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No. 215704

Seq. ID LIB3147-020-Q1-K1-B5

Method BLASTX
NCBI GI g2494034
BLAST score 550
E value 1.0e-56
Match length 126
% identity 83

NCBI Description DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG

KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)

diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 215705

Seq. ID LIB3147-020-Q1-K1-C11

Method BLASTX
NCBI GI g2501460
BLAST score 152
E value 7.0e-10
Match length 141
% identity 33

NCBI Description PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP

(UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP)

(HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi 1545952_emb_CAA96580_ (Z72499) herpesvirus associated

ubiquitin-specific protease (HAUSP) [Homo sapiens]

>gi 4507857 ref_NP_003461.1_pUSP7_ Herpes virus-associated

ubiquitin-specific protease

Seq. ID Method



```
215706
Seq. No.
Seq. ID
                  LIB3147-020-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1350720
                  461
BLAST score
                  4.0e-46
E value
                  111
Match length
                  78
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
                  215707
Seq. No.
                  LIB3147-020-Q1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1350720
BLAST score
                  300
                  3.0e-27
E value
                  88
Match length
                  62
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
                  215708
Seq. No.
                  LIB3147-020-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3128177
                  458
BLAST score
E value
                  8.0e-46
                  130
Match length
                  72
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
                  215709
Seq. No.
                  LIB3147-020-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                   g1871199
NCBI GI
BLAST score
                   173
E value
                   2.0e-12
                   120
Match length
                   35
% identity
NCBI Description (U91318) pM5 (3' partial) [Homo sapiens]
Seq. No.
                   215710
                   LIB3147-020-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3024127
BLAST score
                   656
E value
                   5.0e-69
Match length
                   128
% identity
                   94
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
                   215711
Seq. No.
```

30144

LIB3147-020-Q1-K1-D2

BLASTX

NCBI GI



```
g107350
NCBI GI
                  203
BLAST score
                  7.0e-16
E value
                  110
Match length
                  41
% identity
NCBI Description Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5
                  protein [Homo sapiens]
                  215712
Seq. No.
                  LIB3147-020-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  g129245
NCBI GI
                  212
BLAST score
                  7.0e-17
E value
                  124
Match length
                  42
% identity
                  ORGAN SPECIFIC PROTEIN P4 >gi 72317 pir KNPMP4 protein P4
NCBI Description
                  - garden pea >gi_295829_emb_CAA35943_ (X51594) P4 protein
                   [Pisum sativum]
                   215713
Seq. No.
                  LIB3147-020-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                   g3024122
NCBI GI
                   247
BLAST score
                   3.0e-21
E value
                   97
Match length
% identity
                   54
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                   215714
Seq. No.
                   LIB3147-020-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   q1917019
NCBI GI
BLAST score
                   495
E value
                   4.0e-50
Match length
                   120
                   82
% identity
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                   215715
Seq. No.
                   LIB3147-020-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q419803
BLAST score
                   347
E value
                   6.0e-33
Match length
                   85
                   80
% identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   215716
Seq. No.
                   LIB3147-020-Q1-K1-E7
Seq. ID
                   BLASTX
Method
```

30145

g4185133

NCBI GI



```
294
 BLAST score
                    2.0e-26
 E value
                    82
 Match length
                    62
 % identity
                    (AC005724) putative zinc finger protein [Arabidopsis
 NCBI Description
                    thaliana]
                    215717
 Seq. No.
                   LIB3147-020-Q1-K1-E8
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1172558
                    217
 BLAST score
                    2.0e-17
 E value
                    72
 Match length
                    58
 % identity
                   OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
 NCBI Description
                    ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                    >gi_480122_pir__S36454 porin por1 - garden pea
                    >gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]
                    215718
 Seq. No.
                    LIB3147-020-Q1-K1-E9
 Seq. ID
 Method
                    BLASTX
                    g1749596
 NCBI GI
                    178
 BLAST score
                    6.0e-13
 E value
...Match length
                    44
                    70
 % identity
                   (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT
 NCBI Description
                    Accession Number P16638 [Schizosaccharomyces pombe]
                    215719
 Seq. No.
                    LIB3147-020-Q1-K1-F10
 Seq. ID
 Method
                    BLASTX
                    q4337178
 NCBI GI
 BLAST score
                    518
 E value
                    8.0e-53
                    129
 Match length
 % identity
 NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]
 Seq. No.
                    215720
                    LIB3147-020-Q1-K1-F2
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g629728
 BLAST score
                    226
 E value
                    2.0e-18
                    72
 Match length
 % identity
                    60
                    porin I, 36K - potato >gi_1076680 pir__C55364 porin (clone
 NCBI Description
                    pPOM 36.1) - potato mitochondrion >gi 515358 emb CAA56601
                    (X80388) 36kDa porin I [Solanum tuberosum]
                    215721
 Seq. No.
 Seq. ID
                    LIB3147-020-Q1-K1-F3
                    BLASTX
 Method
```

30146

g1172558



```
BLAST score
                  195
                   5.0e-15
E value
                   67
Match length
% identity
                   58
                  OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
NCBI Description
                   ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   >gi_480122_pir__S36454 porin por1 - garden pea
                   >gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]
                   215722
Seq. No.
                   LIB3147-020-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1928981
                   504
BLAST score
                   3.0e-51
E value
                   108
Match length
                   92
% identity
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   215723
Seq. No.
                   LIB3147-020-Q1-K1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q124226
                   652
BLAST score
                   2.0e-68
E value
                   131
Match length
                   92
% identity
                   INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_100278_pir S21059 translation initiation factor
                   eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (\overline{2}) [Nicotiana
                   plumbaginifolia]
                   215724
Seq. No.
                   LIB3147-020-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g124226
NCBI GI
                   538
BLAST score
                   3.0e-55
E value
                   106
Match length
                   95
% identity
                   INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_100278_pir__S21059 translation initiation factor
                   eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (\overline{2}) [Nicotiana
                   plumbaginifolia]
                   215725
Seq. No.
                   LIB3147-020-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   q71498
NCBI GI
BLAST score
                   361
```

2.0e-34

NCBI Description heat shock protein 17.7 - garden pea

111

E value

Match length % identity

Seq. ID



```
215726
Seq. No.
                  LIB3147-020-Q1-K1-G2
Seq. ID
                  BLASTN
Method
                  g167366
NCBI GI
                  336
BLAST score
                  0.0e + 00
E value
                  371
Match length
                  97
% identity
                  Gossypium hirsutum peroxidase mRNA, complete cds
NCBI Description
                  215727
Seq. No.
                  LIB3147-020-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                   g4262250
NCBI GI
                   396
BLAST score
                   2.0e-38
E value
                   86
Match length
                   86
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   215728
Seq. No.
                   LIB3147-020-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   g4512653
NCBI GI
                   456
BLAST score
                   1.0e-45
E value
                   119
Match length
                   74
% identity
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                   215729
Seq. No.
                   LIB3147-021-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   q1173256
NCBI GI
BLAST score
                   268
E value
                   1.0e-23
                   92
Match length
                   59
% identity
                   40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_ S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi_488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   215730
Seq. No.
                   LIB3147-021-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703380
BLAST score
                   536
                   2.0e-65
E value
                   128
Match length
 % identity
                   99
                   ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
NCBI Description
                   ADP-ribosylation factor [Oryza sativa]
                   215731
 Seq. No.
```

LIB3147-021-Q1-K1-B10

NCBI GI

BLAST score

g267081

559



```
BLASTX
Method
NCBI GI
                  g2689631
BLAST score
                  304
                  2.0e-30
E value
Match length
                  124
                  65
% identity
NCBI Description (AF022389) ADP-ribosylation factor [Vigna unguiculata]
                  215732
Seq. No.
                  LIB3147-021-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1350944
BLAST score
                  378
                  2.0e-36
E value
Match length
                  80
                  95
% identity
                  40S RIBOSOMAL PROTEIN S17
NCBI Description
                  215733
Seq. No.
                  LIB3147-021-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                   q1710780
NCBI GI
BLAST score
                   583
                   2.0e-60
E value
Match length
                   153
                   73
% identity
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   215734
Seq. No.
                   LIB3147-021-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g3242077
NCBI GI
                   468
BLAST score
                   4.0e-47
E value
                   106
Match length
                   79
% identity
                  (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
                   215735
Seq. No.
                   LIB3147-021-Q1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3914449
                   430
BLAST score
                   2.0e-62
E value
                   131
Match length
                   95
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                   persica]
Seq. No.
                   215736
                   LIB3147-021-Q1-K1-E9
Seq. ID
                   BLASTX
Method
```



```
9.0e-58
E value
Match length
                  113
                  95
% identity
                  TUBULIN BETA-7 CHAIN >gi 320188_pir__JQ1591 tubulin beta-7
NCBI Description
                  chain - Arabidopsis thaliana >gi_166906 (M84704) beta-7
                  tubulin [Arabidopsis thaliana] > gi_3980381 (AC004561)
                  tubulin beta-7 chain [Arabidopsis thaliana]
                  215737
Seq. No.
                  LIB3147-022-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  g135860
NCBI GI
                  193
BLAST score
                  5.0e-15
E value
Match length
                  86
% identity
                  55
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi 16312 emb CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                   (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >qi 445129 prf 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
                  215738
Seq. No.
                  LIB3147-022-Q1-K1-A10
Seq. ID
Method
                  BLASTX
                  g3360289
NCBI GI
                  547
BLAST score
                  3.0e-56
E value
Match length
                  141
                  73
% identity
                  (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  1 [Zea mays]
Seq. No.
                  215739
                  LIB3147-022-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1518540
                   611
BLAST score
                  1.0e-63
E value
                  131
Match length
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                   215740
Seq. No.
Seq. ID
                  LIB3147-022-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   q3912950
BLAST score
                   199
```

BLAST score 199
E value 1.0e-15
Match length 84

% identity 58

NCBI Description 14-3-3-LIKE PROTEIN E >gi_2689479 (U91726) 14-3-3 isoform e

[Nicotiana tabacum]



215741 Seq. No. LIB3147-022-Q1-K1-A4 Seq. ID BLASTX Method q4371282 NCBI GI 395 BLAST score 2.0e-38 E value 90 Match length 81 % identity (AC006260) putative 60S ribosomal protein L12 [Arabidopsis NCBI Description thaliana] 215742 Seq. No. LIB3147-022-Q1-K1-A5 Seq. ID BLASTX Method g2832630 NCBI GI 356 BLAST score 8.0e-34 E value 103 Match length 68 % identity (AL021711) putative protein [Arabidopsis thaliana] NCBI Description 215743 Seq. No. LIB3147-022-Q1-K1-B10 Seq. ID BLASTX Method g508304 NCBI GI 236 BLAST score 1.0e-19 E value Match length 82 56 % identity (L22305) corC [Medicago sativa] NCBI Description 215744 Seq. No. LIB3147-022-Q1-K1-B11 Seq. ID BLASTX Method q728882 NCBI GI 216 BLAST score 2.0e-17 E value Match length 46 89 % identity NCBI Description ADP-RIBOSYLATION FACTOR 3 >gi 541846 pir S41938 ADP-ribosylation factor 3 - Arabidopsis thaliana $>gi_453191_{emb}_{CAA54564}$ (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana] 215745 Seq. No. LIB3147-022-Q1-K1-B3 Seq. ID Method BLASTX NCBI GI q1498053

Method BLASTX
NCBI GI g1498053
BLAST score 513
E value 3.0e-52
Match length 133
% identity 78

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 215746

Seq. ID LIB3147-022-Q1-K1-B9

Method BLASTX

30151



```
g3023816
NCBI GI
                  270
BLAST score
                  8.0e-24
E value
                  59
Match length
                  88
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >qi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  215747
Seq. No.
                  LIB3147-022-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  g3023816
NCBI GI
                  299
BLAST score
                  4.0e-27
E value
                  59
Match length
                  95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >qi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  215748
Seq. No.
                  LIB3147-022-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g4220481
NCBI GI
                  255
BLAST score
                   5.0e-22
E value
Match length
                   93
                   53
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  215749
Seq. No.
                  LIB3147-022-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   q1710585
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
                   70
Match length
                   47
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN PO >qi 1143507 emb CAA63786
NCBI Description
                   (X93587) PO ribosomal protein [Lupinus luteus]
                   215750
Seq. No.
                   LIB3147-022-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4220476
BLAST score
                   550
E value
                   1.0e-56
Match length
                   146
% identity
                  (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 215751

Seq. ID LIB3147-022-Q1-K1-D10

Method BLASTX
NCBI GI g1708236
BLAST score 272



3.0e-24E value Match length 91 62 % identity

HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) NCBI Description

(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana

>gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

>gi_1586548_prf__2204245A hydroxy methylglutaryl CoA

synthase [Arabidopsis thaliana]

215752 Seq. No.

LIB3147-022-Q1-K1-D11 Seq. ID

BLASTX Method g2497752 NCBI GI 294 BLAST score 1.0e-26 E value 96 Match length 59 % identity

NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description

>gi 1321911 emb CAA65475_ (X96714) lipid transfer protein

[Prunus dulcis]

215753 Seq. No.

LIB3147-022-Q1-K1-D2 Seq. ID

BLASTX Method g2497753 NCBI GI 296 BLAST score 7.0e-27 E value 84 Match length 58 % identity

NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) NCBI Description

>gi 1321915_emb_CAA65477_ (X96716) lipid transfer protein

[Prunus dulcis]

215754 Seq. No.

LIB3147-022-Q1-K1-D3 Seq. ID

Method BLASTX NCBI GI q3355468 366 BLAST score E value 4.0e-35 88 Match length % identity

(AC004218) putative ribosomal protein L35 [Arabidopsis NCBI Description

thaliana]

Seq. No. 215755

LIB3147-022-Q1-K1-D4 Seq. ID

BLASTN Method NCBI GI q3269280 BLAST score 44 2.0e-15 E value Match length 117

% identity 85

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22

(ESSAII project)



```
215756
Seq. No.
                  LIB3147-022-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  q2388564
NCBI GI
                  170
BLAST score
                  4.0e-12
E value
                  116
Match length
                  40
% identity
                  (ACO00098) ESTs gb AA042402,gb_ATTS1380 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  215757
Seq. No.
                  LIB3147-022-Q1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4090533
                  527
BLAST score
                  5.0e-54
E value
                  114
Match length
                  89
% identity
                  (U68215) ACC oxidase [Carica papaya]
NCBI Description
                  215758
Seq. No.
                  LIB3147-022-Q1-K1-E12
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
                   35
Match length
                   59
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   215759
Seq. No.
                   LIB3147-022-Q1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3901014
                   235
BLAST score
                   5.0e-20
E value
Match length
                   55
                   76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   215760
Seq. No.
                   LIB3147-022-Q1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3334113
BLAST score
                   459
E value
                   7.0e-46
Match length
                   89
                   98
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015)
                   acyl-CoA-binding protein [Gossypium hirsutum]
```

30154

.*.

215761

BLASTX

LIB3147-022-Q1-K1-E4

Seq. No.

Seq. ID Method



```
NCBI GI
                  q3885515
BLAST score
                  458
                  7.0e-46
E value
                  90
Match length
                  94
% identity
                  (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                  sativa]
                  215762
Seq. No.
Seq. ID
                  LIB3147-022-Q1-K1-E5
Method
                  BLASTX
                  g1707857
NCBI GI
BLAST score
                  450
                  6.0e-45
E value
                  117
Match length
                  79
% identity
                  (Y09291) obtusifoliol 14-alpha-demethylase [Triticum
NCBI Description
                  aestivum]
                  215763
Seq. No.
                  LIB3147-022-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122703
BLAST score
                  420
E value
                  2.0e-41
Match length
                  106
% identity
                  79
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                  protein L23a [Fritillaria agrestis]
                  215764
Seq. No.
                  LIB3147-022-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4090533
                  409
BLAST score
E value
                   4.0e-40
Match length
                  117
% identity
NCBI Description (U68215) ACC oxidase [Carica papaya]
                   215765
Seq. No.
Seq. ID
                   LIB3147-022-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g731651
BLAST score
                   274
E value
                   3.0e-24
Match length
                   143
% identity
                   38
                  HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN
NCBI Description
                   PUT2-SRB2 INTERGENIC REGION >gi 626608 pir S46746
                   hypothetical protein YHR039c - yeast (Saccharomyces
                   cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces
                   cerevisiae]
```

Seq. No. 215766

Seq. ID LIB3147-022-Q1-K1-F1

Method BLASTX

E value

Match length

% identity

8.0e-20

66 73



```
NCBI GI
                 q2464914
BLAST score
                 241
                  1.0e-20
E value
Match length
                 73
% identity
                  64
                 (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                 215767
Seq. ID
                 LIB3147-022-Q1-K1-F11
Method
                 BLASTX
NCBI GI
                 g1168410
BLAST score
                 474
E value
                 1.0e-50
Match length
                 131
                 77
% identity
                 FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                 >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
                 4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                 215768
                 LIB3147-022-Q1-K1-F2
Seq. ID
Method
                 BLASTX
NCBI GI
                 q133867
BLAST score
                 412
E value
                 2.0e-40
                  97
Match length
                 82
% identity
                 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                 ribosomal protein S11 [Zea mays]
                  215769
Seq. No.
Seq. ID
                 LIB3147-022-Q1-K1-F6
Method
                 BLASTX
NCBI GI
                  g122087
BLAST score
                 526
E value
                  8.0e-54
Match length
                 123
% identity
                  86
                 NCBI Description
                  (X00937) H3 histone [Triticum aestivum] >gi 488565 (U09459)
                  histone H3.1 [Medicago sativa] >gi_2565419 (AF026803)
                 histone H3 [Onobrychis viciifolia]
Seq. No.
                  215770
Seq. ID
                  LIB3147-022-Q1-K1-F8
Method
                 BLASTX
NCBI GI
                  g4193388
BLAST score
                 234
```



(AF091455) translationally controlled tumor protein [Hevea NCBI Description brasiliensis]

215771 Seq. No. LIB3147-022-Q1-K1-G10 Seq. ID Method BLASTX NCBI GI g417103 BLAST score 676

3.0e-71E value Match length 136 99 % identity

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] $>g\overline{i}_38\overline{8}5890$ (AF $\overline{0}93633$) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

215772 Seq. No.

LIB3147-022-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI q3953471 BLAST score 507 E value 2.0e-51 Match length 107 % identity 85

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 215773

LIB3147-022-Q1-K1-G6 Seq. ID

Method BLASTX NCBI GI g1346156 BLAST score 582 E value 2.0e-60 128 Match length 86 % identity

SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR NCBI Description

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 481943 pir S40213 glycine

hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei

>gi 437997 emb CAA81079 (Z25860) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No. 215774



Seq. ID LIB3147-022-Q1-K1-G8 Method BLASTX NCBI GI q3193298 BLAST score 181 2.0e-13 E value 93 Match length % identity 38 (AF069298) T14P8.17 gene product [Arabidopsis thaliana] NCBI Description 215775 Seq. No. LIB3147-022-Q1-K1-H11 Seq. ID Method BLASTX g2160166 NCBI GI BLAST score 197 E value 4.0e-15 Match length 100 44 % identity (AC000132) No definition line found [Arabidopsis thaliana] NCBI Description 215776 Seq. No. LIB3147-022-Q1-K1-H2 Seq. ID Method BLASTX NCBI GI g3075391 BLAST score 369 5.0e-40E value Match length 140 % identity . 62 (AC004484) unknown protein [Arabidopsis thaliana] NCBI Description 215777 Seq. No. LIB3147-022-Q1-K1-H3 Seq. ID BLASTX Method g1351987 NCBI GI 234 BLAST score 1.0e-19 E value 64 Match length 67 % identity ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) NCBI Description (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_507946 (L29083) glutamine-dependent asparagine synthetase [Arabidopsis thaliana] Seq. No. 215778 LIB3147-022-Q1-K1-H5 Seq. ID Method BLASTX g1469930 NCBI GI BLAST score 352 E value 2.0e-33 Match length 74 % identity (U48777) fiber-specific acyl carrier protein [Gossypium NCBI Description hirsutum]

Seq. No. 215779

Seq. ID LIB3147-022-Q1-K1-H7

Method BLASTX NCBI GI g2,492952



```
BLAST score
                  558
                  2.0e-57
E value
Match length
                  134
% identity
                  75
                  CHORISMATE SYNTHASE 1 PRECURSOR
NCBI Description
                  (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
                  >gi 542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
                  precursor - tomato >gi_410482_emb_CAA79859 (Z21796)
                  chorismate synthase 1 [Lycopersicon esculentum]
                  215780
Seq. No.
                  LIB3147-022-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3098571
BLAST score
                  268
                  1.0e-23
E value
Match length
                  124
                  42
% identity
                  (AF049028) BURP domain containing protein [Brassica napus]
NCBI Description
Seq. No.
                   215781
                  LIB3147-022-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1666096
BLAST score
                   460
                   5.0e-46
E value
Match length
                  135
                   65
% identity
                  (Y09113) dioxygenase [Marah macrocarpus]
NCBI Description
                   215782
Seq. No.
                  LIB3147-023-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g1184123
NCBI GI
BLAST score
                   168
                   8.0e-12
E value
                   61
Match length
                   54
% identity
NCBI Description (U20809) auxin-induced protein [Vigna radiata]
                   215783
Seq. No.
Seq. ID
                   LIB3147-023-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   g133867
BLAST score
                   424
                   7.0e-42
E value
Match length
                   101
% identity
                   79
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                   ribosomal protein S11 [Zea mays]
```

215784

LIB3147-023-Q1-K1-A6 Seq. ID

BLASTX Method NCBI GI g133867 BLAST score 589

Seq. No.



```
4.0e-61
E value
Match length
                  127
                  85
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
                  215785
Seq. No.
                  LIB3147-023-Q1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g441457
                  517
BLAST score
                  6.0e-53
E value
                  99
Match length
                  96
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  215786
Seq. No.
                  LIB3147-023-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2662343
                  401
BLAST score
                 2.0e-39
E value
                  84
Match length
                   93
% identity
                 (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  215787
Seq. No.
                  LIB3147-023-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  157
                   4.0e-11
E value
Match length
                  50
                   62
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative
                   40S ribosomal protein S2 [Arabidopsis thaliana]
                   215788
Seq. No.
Seq. ID
                   LIB3147-023-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g2494320
BLAST score
                   207
```

Method BLASTX
NCBI GI g2494320
BLAST score 207
E value 2.0e-16
Match length 128
% identity 41

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation

factor-5 [Zea mays]

Seq. No. 215789

Seq. ID LIB3147-023-Q1-K1-B5

Method BLASTX NCBI GI g1945611 BLAST score 270 E value 9.0e-24



```
Match length
                  102
                  49
% identity
                  (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                  >gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
Seq. No.
                  215790
                  LIB3147-023-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  618
E value
                  1.0e-64
Match length
                  124
                  56
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
                  215791
Seq. No.
                  LIB3147-023-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174498
BLAST score
                  142
                  1.0e-08
E value
Match length
                  51
                  53
% identity
                  SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly
NCBI Description
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  215792
Seq. No.
                  LIB3147-023-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169534
BLAST score
                   624
E value
                   3.0e-65
Match length
                   148
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                   phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                   >gi 433609 emb CAA82232 (Z28386) enolase [Ricinus
                   communis]
                   215793
Seq. No.
                  LIB3147-023-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334113
BLAST score
                   383
E value
                   6.0e - 37
                  89
Match length
                  82
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
```

Seq. ID LIB3147-023-Q1-K1-C3

215794

Method BLASTX NCBI GI g3142296



```
BLAST score
                  241
                  2.0e-20
E value
Match length
                  86
                  57
% identity
                  (AC002411) Contains similarity to hypothetical
NCBI Description
                  mitochondrial import receptor subunit gb_Z98597 from S.
                  pombe. ESTs gb_T45575 and gb_Z26435 and gb_AA394576 come
                  from this gene. [Arabidopsis thaliana]
                  215795
Seq. No.
Seq. ID
                  LIB3147-023-Q1-K1-C5
                  BLASTX
Method
NCBI GI
                  g4191782
BLAST score
                  207
                  2.0e-16
E value
                  101
Match length
% identity
                  48
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
                  215796
Seq. No.
                  LIB3147-023-Q1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3287826
BLAST score
                   301
                   2.0e-27
E value
Match length
                   69
                   90
% identity
                  (+) -DELTA-CADINENE SYNTHASE ISOZYME C2 (D-CADINENE
NCBI Description
                   SYNTHASE) >gi 2879841 emb CAA76223.1 (Y16432)
                   (+)-delta-cadinene synthase [Gossypium arboreum]
                   215797
Seq. No.
                   LIB3147-023-Q1-K1-D1
Seq. ID
Method
                   BLASTX
                   g2879811
NCBI GI
                   537
BLAST score
                   5.0e-55
E value
Match length
                   111
% identity
                   92
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
                   215798
Seq. No.
                   LIB3147-023-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q1171978
NCBI GI
```

Method BLASTX
NCBI GI g1171978
BLAST score 152
E value 5.0e-10
Match length 73
% identity 41

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 215799

Seq. ID LIB3147-023-Q1-K1-E10

Method BLASTX

Match length

% identity

139

68



```
g2286153
NCBI GI
                  627
BLAST score
                  1.0e-65
E value
Match length
                  145
% identity
                  83
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  215800
Seq. No.
                  LIB3147-023-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  g2879811
NCBI GI
BLAST score
                  467
                  8.0e-47
E value
                  95
Match length
                  91
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                  215801
Seq. No.
                  LIB3147-023-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                  g2642215
NCBI GI
                  159
BLAST score
                  9.0e-11
E value
                  45
Match length
                  71
% identity
NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]
                   215802
Seq. No.
                  LIB3147-023-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3688170
                   309
BLAST score
E value
                   3.0e-28
                   70
Match length
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                   215803
Seq. No.
                   LIB3147-023-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1408471
BLAST score
                   394
                   2.0e-38
E value
Match length
                   124
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   215804
Seq. No.
                   LIB3147-023-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351279
                   400
BLAST score
                   2.0e-39
E value
```



NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi 602590 emb CAA58230 (X83227) triosephosphate isomerase

[Petunia x hybrida]

Seq. No. 215805

Seq. ID LIB3147-023-Q1-K1-F2

Method BLASTX
NCBI GI g4103635
BLAST score 187
E value 6.0e-14
Match length 75
% identity 48

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No. 215806

Seq. ID LIB3147-023-Q1-K1-F5

Method BLASTX
NCBI GI g4427003
BLAST score 289
E value 6.0e-26
Match length 89
% identity 60

NCBI Description (AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No. 215807

Seq. ID LIB3147-023-Q1-K1-F6

Method BLASTN
NCBI GI g2244991
BLAST score 34
E value 1.0e-09
Match length 70
% identity 87

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 215808

Seq. ID LIB3147-023-Q1-K1-F8

Method BLASTX
NCBI GI 94234768
BLAST score 467
E value 7.0e-47
Match length 87
% identity 87

NCBI Description (AF069468) sterol-C5-desaturase [Arabidopsis thaliana]

Seq. No. 215809

Seq. ID LIB3147-023-Q1-K1-F9

Method BLASTN
NCBI GI g4234767
BLAST score 35
E value 4.0e-10
Match length 83

Match length 83 % identity 86

NCBI Description Arabidopsis thaliana sterol-C5-desaturase gene, complete

cds

Seq. No. 215810

Seq. ID

215815

LIB3147-024-Q1-K1-A1



```
LIB3147-023-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  q1762947
NCBI GI
BLAST score
                  231
                  3.0e-19
E value
                  70
Match length
                  63
% identity
                  (U66270) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                  tabacum]
                  215811
Seq. No.
                  LIB3147-023-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485514
BLAST score
                  247
                  4.0e-21
E value
                  110
Match length
                  49
% identity
                  ADR11-2 protein - soybean (fragment)
NCBI Description
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
Seq. No.
                  215812
Seq. ID
                  LIB3147-023-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  417
                  6.0e-41
E value
Match length
                  137
% identity
                  61
                 (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  215813
Seq. No.
Seq. ID
                  LIB3147-023-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  543
E value
                   7.0e-56
Match length
                  114
% identity
                   96
                 HEAT SHOCK PROTEIN 82 >gi_100685_pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                  215814
Seq. ID
                  LIB3147-023-Q1-K1-H8
                  BLASTX
Method
NCBI GI
                  g3776005
BLAST score
                  579
E value
                   4.0e-60
Match length
                  114
                  96
% identity
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
```



Method BLASTX
NCBI GI g1350680
BLAST score 501
E value 7.0e-51
Match length 115
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 215816

Seq. ID LIB3147-024-Q1-K1-A12

Method BLASTX
NCBI GI g643469
BLAST score 190
E value 3.0e-14
Match length 49
% identity 71

NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 215817

Seq. ID LIB3147-024-Q1-K1-A2

Method BLASTX
NCBI GI g584711
BLAST score 583
E value 2.0e-60
Match length 131
% identity 85

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)

(ETHYLENE-FORMING ENZYME) (EFE) >gi_629707_pir__S42561 1-aminocyclopropane-1-carboxylate oxidase - garden petunia

>gi_347417 (L21978) 1-aminocyclopropane-1-carboxylate

oxidase [Petunia hybrida]

Seq. No. 215818

Seq. ID LIB3147-024-Q1-K1-A3

Method BLASTX
NCBI GI g3193303
BLAST score 353
E value 2.0e-33
Match length 98
% identity 69

NCBI Description (AF069298) similar to several proteins containing a tandem

repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 215819

Seq. ID LIB3147-024-Q1-K1-B1

Method BLASTX
NCBI GI g1350984
BLAST score 266
E value 2.0e-23
Match length 63
% identity 86

NCBI Description 40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal

protein S3a [Helianthus annuus]

Seq. No. 215820



Seq. ID LIB3147-024-Q1-K1-B11 BLASTX Method NCBI GI q1856971 BLAST score 495 E value 5.0e-50 Match length 107 87 % identity NCBI Description (D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus] Seq. No. 215821 Seq. ID LIB3147-024-Q1-K1-B2 Method BLASTX NCBI GI q4006893 BLAST score 676 3.0e-71E value Match length 148 80 % identity NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana] Seq. No. 215822 LIB3147-024-Q1-K1-B5 Seq. ID Method BLASTX NCBI GI g1709794 BLAST score 370 E value 9.0e-36 Match length 100 71 % identity 26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN NCBI Description BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis thaliana] >gi_4467150_emb_CAB37519_ (AL035540) multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana] Seq. No. 215823 Seq. ID LIB3147-024-Q1-K1-B8 Method BLASTN NCBI GI q2645198 BLAST score 42 E value 3.0e-14 Match length 81 % identity 94 NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 215824 Seq. ID LIB3147-024-Q1-K1-C10 Method BLASTX NCBI GI g3121848 BLAST score 431

E value 2.0e-45 Match length 100 55 % identity

NCBI Description CALMODULIN >gi_1835521 (U83402) calmodulin [Capsicum

annuum]



```
215825
Seq. No.
                  LIB3147-024-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1008904
BLAST score
                  668
                  2.0e-70
E value
                  129
Match length
                  88
% identity
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
                  215826
Seq. No.
                  LIB3147-024-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3641837
BLAST score
                  318
                  2.0e-29
E value
                  90
Match length
                  72
% identity
                  (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  215827
                  LIB3147-024-Q1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3005931
                   389
BLAST score
                  1.0e-37
E value
Match length
                  136
% identity
                  54
                  (AJ005016) ABC transporter [Homo sapiens]
NCBI Description
                  215828
Seq. No.
                  LIB3147-024-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                   g3860250
NCBI GI
                   675
BLAST score
E value
                   4.0e-71
Match length
                  153
% identity
                   83
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   215829
Seq. No.
                  LIB3147-024-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2829899
BLAST score
                  295
E value
                   1.0e-26
Match length
                   116
% identity
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
```

Seq. ID LIB3147-024-Q1-K1-D4

Method BLASTN

BLAST score

E value

561

8.0e-58



```
NCBI GI
                  q4545261
BLAST score
                  319
E value
                  1.0e-179
                  367
Match length
% identity
                  97
                  Gossypium hirsutum metallothionein-like protein mRNA,
NCBI Description
                  complete cds
                  215831
Seq. No.
                  LIB3147-024-Q1-K1-D8
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g122007
                  375
BLAST score
                  5.0e-36
E value
                  98
Match length
                  77
% identity
                  HISTONE H2A >gi 100161 pir S11498 histone H2A - parsley
NCBI Description
                  >gi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1
                  - 149) [Petroselinum crispum]
Seq. No.
                  215832
                  LIB3147-024-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585963
                  264
BLAST score
                  6.0e-23
E value
                  69
Match length
% identity
                  78
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
                  215833
Seq. No.
                  LIB3147-024-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g584795
NCBI GI
BLAST score
                  144
                   6.0e-09
E value
Match length
                  51
% identity
                   59
NCBI Description PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_170295 (M80490)
                  plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
                   215834
Seq. No.
                  LIB3147-024-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2924518
BLAST score
                   148
E value
                   7.0e-10
Match length
                   54
                   50
% identity
NCBI Description (AL022023) putative protein [Arabidopsis thaliana]
Seq. No.
                   215835
Seq. ID
                   LIB3147-024-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g119354
```



126 Match length 89 % identity ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi 19281 emb CAA41115 (X58108) enolase [Lycopersicon esculentum] Seq. No. 215836 LIB3147-024-Q1-K1-E7 Seq. ID Method BLASTX NCBI GI q98837 BLAST score 182 2.0e-13 E value Match length 116 % identity 38 NCBI Description enantiomer-selective amidase - Rhodococcus sp >gi 152052 (M74531) enantiomerase-selective amidase [Rhodococcus sp.] 215837 Seq. No. LIB3147-024-Q1-K1-E8 Seq. ID Method BLASTX NCBI GI g1808656 BLAST score 180 E value 3.0e-13 Match length 55~ % identity 60 NCBI Description (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum] Seq. No. 215838 Seq. ID LIB3147-024-Q1-K1-E9 Method BLASTX NCBI GI g2317905 BLAST score 364 E value 9.0e-35 Match length 110 % identity 69 NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana] Seq. No. 215839 Seq. ID LIB3147-024-Q1-K1-F10 Method BLASTX NCBI GI g283039 BLAST score 479 E value 3.0e-48Match length 130 % identity 72 NCBI Description gene iojap protein - maize >gi 22349 emb CAA78772_ (Z15063) putative iojap protein [Zea mays] Seq. No. 215840 Seq. ID LIB3147-024-Q1-K1-F4

Method BLASTX
NCBI GI g4510346
BLAST score 311
E value 2.0e-28
Match length 77

% identity (AC006921) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 215841 Seq. ID LIB3147-024-Q1-K1-F6 Method BLASTX NCBI GI q4115377 BLAST score 323 E value 7.0e - 30Match length 125 % identity NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] 215842 Seq. No. Seq. ID LIB3147-024-Q1-K1-F8 Method BLASTX NCBI GI q2130080 BLAST score 170 E value 4.0e-12Match length 50 66 % identity NCBI Description Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa] Seq. No. 215843 LIB3147-024-Q1-K1-G1 Seq. ID Method BLASTX g4262149 271 7.0e-2474 59 NCBI Description (AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

NCBI GI BLAST score E value

Match length % identity

Seq. No. 215844

Seq. ID LIB3147-024-Q1-K1-G12

Method BLASTX NCBI GI g544426 BLAST score 157 E value 2.0e-10 Match length 36 % identity

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN >gi_100155 pir S14857

glycine-rich protein - carrot >gi_18347_emb_CAA41152

(X58146) glycine-rich protein [Daucus carota]

>gi 445138 prf 1908438A Gly-rich protein [Daucus carota]

Seq. No. 215845

Seq. ID LIB3147-024-Q1-K1-G5

Method BLASTX NCBI GI g1071913 BLAST score 243 E value 3.0e-21



```
Match length
% identity
                  70
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                  - spinach >gi 1066153 dbj_BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                  215846
                  LIB3147-024-Q1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q531251
BLAST score
                  34
                  2.0e-09
E value
                  77
Match length
                  96
% identity
                  Apple mitochondrial atp9 gene for F0-ATPase subunit 9
NCBI Description
                   (complete cds) and nad5 gene for NADH dehydrogehase subunit
                  5 (exon a and b)
Seq. No.
                  215847
                  LIB3147-024-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072626
BLAST score
                  502
E value
                  7.0e-51
Match length
                  136
                  74
% identity
NCBI Description
                  (Y12904) hypothetical protein [Arabidopsis thaliana]
                  >gi 3281856 emb CAA19751 (AL031004) Transcription factor
                  II homolog [Arabidopsis thaliana]
                  215848
Seq. No.
Seq. ID
                  LIB3147-024-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  387
E value
                  2.0e-37
Match length
                  110
% identity
                  64
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  215849
Seq. ID
                  LIB3147-024-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q322750
BLAST score
                  618
E value
                  2.0e-64
Match length
                  125
% identity
                  96
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
                  >qi 170217 (M74100) ubiquitin fusion protein [Nicotiana
```

sylvestris]

Seq. No. 215850

Seq. ID LIB3147-024-Q1-K1-H12

Method BLASTX NCBI GI g4107099 BLAST score 374



```
7.0e-36
E value
Match length
                  95
                  75
% identity
NCBI Description
                  (AB015141) AHP1 [Arabidopsis thaliana]
                  >gi 4156245 dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                  thaliana]
                  215851
Seq. No.
                  LIB3147-024-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3152566
BLAST score
                  451
                  6.0e-45
E value
                  138
Match length
% identity
                  64
                  (AC002986) Similar to hypothetical protein YLR002c,
NCBI Description
                  gb Z7314 from S. cerevisiae. [Arabidopsis thaliana]
                  215852
Seq. No.
Seq. ID
                  LIB3147-024-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2459429
BLAST score
                  261
E value
                  8.0e-23
                  88
Match length
% identity
                  57
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
                  215853
Seq. No.
Seq. ID
                  LIB3147-024-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2213877
BLAST score
                  672
E value
                  9.0e-71
Match length
                  139
% identity
NCBI Description (AF003197) glutamine synthetase [Hevea brasiliensis]
Seq. No.
                  215854
                  LIB3147-024-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231683
                  276
BLAST score
                  9.0e-25
E value
                  77
Match length
% identity
                  68
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_421825 pir_JN0597
                  calnexin-like protein - Arabidopsis thaliana
                  >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                  [Arabidopsis thaliana]
```

Seq. ID LIB3147-026-Q1-K1-A2

BLASTX Method NCBI GI g1769907 305 BLAST score E value 5.0e-28



```
Match length
                   92
% identity
                   (X92975) xyloglucan endo-transglycosylase [Arabidopsis
NCBI Description
                   thaliana]
                   215856
Seq. No.
                  LIB3147-026-Q1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1778145
BLAST score
                   230
                   6.0e-19
E value
Match length
                   72
                   67
% identity
                  (U66402) phosphate/phosphoenolpyruvate translocator
NCBI Description
                  precursor [Nicotiana tabacum]
                   215857
Seq. No.
                   LIB3147-026-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   g3318611
NCBI GI
BLAST score
                   294
                   2.0e-26
E value
                   59
Match length
                   97
% identity
                   (AB016063) mitochondrial phosphate transporter [Glycine
NCBI Description
                   max]
                   215858
Seq. No.
                   LIB3147-026-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g2529662
NCBI GI
BLAST score
                   265
E value
                   1.0e-23
                   77
Match length
                   70
% identity
                   (AC002535) putative small nuclear ribonucleoprotein, Sm D2
NCBI Description
                   [Arabidopsis thaliana] >gi_3738278 (AC005309) putative
                   small nuclear ribonucleoprotein, Sm D2 [Arabidopsis]
                   thaliana]
                   215859
Seq. No.
Seq. ID
                   LIB3147-026-Q1-K1-B1
Method
                   BLASTX
                   q2529662
NCBI GI
                   518
BLAST score
                   7.0e-53
E value
```

Match length 107 % identity

NCBI Description (ACO02535) putative small nuclear ribonucleoprotein, Sm D2

> [Arabidopsis thaliana] >gi 3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis

thaliana]

215860 Seq. No.

LIB3147-026-Q1-K1-B10 Seq. ID

Method BLASTX NCBI GI g266398



```
BLAST score
                    2.0e-15
E value
Match length
                    84
% identity
                    50
                    TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                    INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
                    (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.
                    215861
Seq. ID
                    LIB3147-026-Q1-K1-B2
Method
                    BLASTX
NCBI GI
                    a1174592
BLAST score
                    636
                    1.0e-66
E value
Match length
                    128
% identity
                    99
                    TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                    - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                    sativum]
                    215862
Seq. No.
                    LIB3147-026-Q1-K1-B3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2306917
BLAST score
                    352
E value
                    9.0e-43
Match length
                    103
% identity
                    90
                   (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                    thaliana]
                    215863
Seq. No.
Seq. ID
                    LIB3147-026-Q1-K1-B6
Method
                    BLASTX
NCBI GI
                    g2511594
BLAST score
                    535
E value
                    7.0e-55
Match length
                    121
% identity
NCBI Description
                   (Y13694) multicatalytic endopeptidase complex, proteasome
                    precursor, beta subunit [Arabidopsis thaliana]
                    >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic
                    endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                    proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                    215864
Seq. ID
                    LIB3147-026-Q1-K1-B7
Method
                    BLASTX
NCBI GI
                    g2662377
BLAST score
                    358
```

E value 6.0e-34 151 Match length 47 % identity

NCBI Description (D89063) oligosaccharyltransferase [Mus musculus]



```
215865
Seq. No.
                   LIB3147-026-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g266398
BLAST score
                   193
E value
                   6.0e - 15
                   78
Match length
                   50
% identity
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                   INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
                   inhibitor precursor - maize >gi_22327_emb_CAA37998
                   (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.
                   215866
                   LIB3147-026-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g336392
BLAST score
                   375
E value
                   6.0e - 36
                   143
Match length
                   58
% identity
NCBI Description
                  (J05215) ribosomal protein S17 [Arabidopsis thaliana]
Seq. No.
                   215867
                   LIB3147-026-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   g133815
NCBI GI
BLAST score
                   211
E value
                   6.0e-17
Match length
                   111
% identity
                   43
                   30S RIBOSOMAL PROTEIN S17, CHLOROPLAST PRECURSOR (CS17)
NCBI Description
                   >gi_71011_pir__R3MU17 ribosomal protein S17 precursor,
chloroplast - Arabidopsis thaliana >gi_16503_emb_CAA77502_
                    (Z11151) Plastid ribosomal protein CS17 [Arabidopsis
                   thaliana]
Seq. No.
                   215868
Seq. ID
                   LIB3147-026-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2865623
BLAST score
                   539
E value
                   2.0e-55
Match length
                   121
% identity
                   83
NCBI Description
                   (AF045286)
                   GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                   215869
Seq. No.
Seq. ID
                   LIB3147-026-Q1-K1-C3
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3582333
BLAST score 228
E value 8.0e-19
Match length 144
% identity 38

Method

NCBI GI

BLAST score

BLASTX

333

g2119045



```
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
                  215870
Seq. No.
Seq. ID
                  LIB3147-026-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g3135611
                  173
BLAST score
                  2.0e-12
E value
Match length
                  55
% identity
                  56
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]
Seq. No.
                  215871
                  LIB3147-026-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1222552
                  327
BLAST score
                  2.0e-30
E value
Match length
                  125
% identity
                  56
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
Seq. No.
                  215872
Seq. ID
                  LIB3147-026-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1222552
BLAST score
                  326
                  2.0e-30
E value
Match length
                  108
% identity
                  62
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
Seq. No.
                  215873
Seq. ID
                  LIB3147-026-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4090533
BLAST score
                  537
E value
                  5.0e-55
                  142
Match length
                  75
% identity
NCBI Description (U68215) ACC oxidase [Carica papaya]
                  215874
Seq. No.
Seq. ID
                  LIB3147-026-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3201617
BLAST score
                  398
                  7.0e-39
E value
                  112
Match length
                  60
% identity
NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  215875
Seq. ID
                  LIB3147-026-Q1-K1-D6
```



```
3.0e-31
E value
Match length
                   114
                   60
% identity
                   small nuclear ribonucleoprotein U1A - potato
NCBI Description
                   >gi 1050840 emb_CAA90282_ (Z49990) UlsnRNP-specific
                   protein, U1A [Solanum tuberosum]
                   215876
Seq. No.
                   LIB3147-026-Q1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2065531
                   142
BLAST score
                   8.0e-09
E value
                   40
Match length
                   72
% identity
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   215877
                   LIB3147-026-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   g2493495
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
                   81
Match length
                   70
% identity
                   SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir__S72370
NCBI Description
                   carboxypeptidase - garden pea (fragment)
                   >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum
sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase
                    [Pisum sativum]
Seq. No.
                   215878
                   LIB3147-026-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2160180
BLAST score
                    205
E value
                    4.0e-16
Match length
                    46
                    76
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                    215879
Seq. No.
                   LIB3147-026-Q1-K1-E11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1052973
                    432
BLAST score
E value
                    1.0e-42
Match length
                    109
% identity
                    75
NCBI Description (U37838) fructokinase [Beta vulgaris]
```

Seq. ID LIB3147-026-Q1-K1-E4

Method BLASTX
NCBI GI g3513727
BLAST score 334
E value 4.0e-44



Match length 120 % identity 82

NCBI Description (AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >qi 4539358 emb CAB40052.1 (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 215881

Seq. ID LIB3147-026-Q1-K1-E7

Method BLASTX
NCBI GI g1172817
BLAST score 294
E value 2.0e-40
Match length 139
% identity 71

NCBI Description 60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_

(X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein

L11, cytosolic [Arabidopsis thaliana]

Seq. No. 215882

Seq. ID LIB3147-026-Q1-K1-E8

Method BLASTX
NCBI GI g602586
BLAST score 213
E value 3.0e-17
Match length 84
% identity 48

NCBI Description (X83229) 1-amniocyclopropane-1-carboxylate oxidase

[Nicotiana tabacum]

Seq. No. 215883

Seq. ID LIB3147-026-Q1-K1-F11

Method BLASTX
NCBI GI g2507055
BLAST score 179
E value 4.0e-13
Match length 124
% identity 32

NCBI Description LIN-10 PROTEIN >gi_3879271_emb_CAB00051_ (Z75713) similar

to LIN-10 protein; cDNA EST yk273f3.3 comes from this gene; cDNA EST yk273f3.5 comes from this gene; cDNA EST yk480b1.3 comes from this gene; cDNA EST yk480b1.5 comes from this

gene [Caenorhabditis elegans]

Seq. No. 215884

Seq. ID LIB3147-026-Q1-K1-F2

Method BLASTX
NCBI GI g1439609
BLAST score 380
E value 2.0e-50
Match length 111
% identity 97

NCBI Description (U62778) delta-tonoplast intrinsic protein [Gossypium

hirsutum]

Seq. ID Method

NCBI GI

BLAST score



```
215885
Seq. No.
                  LIB3147-026-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  g1439609
NCBI GI
                  601
BLAST score
                  1.0e-62
E value
                  123
Match length
                  55
% identity
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
                  215886
Seq. No.
                  LIB3147-026-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  g2760837
NCBI GI
                  282
BLAST score
                  2.0e-28
E value
Match length
                  136
                   49
% identity
                  (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  215887
Seq. No.
                  LIB3147-026-Q1-K1-F9
Seq. ID
Method
                  BLASTN
                  g428999
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
Match length
                   60
                   88
% identity
NCBI Description Rice mRNA for ribosomal protein L18a (gene name SS128),
                  partial cds
                   215888
Seq. No.
                  LIB3147-026-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2213610
BLAST score
                   221
                   5.0e-18
E value
                   108
Match length
                   43
% identity
NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]
                   215889
Seq. No.
                   LIB3147-026-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g100939
BLAST score
                   124
E value
                   9.0e-11
Match length
                   128
% identity
                   34
NCBI Description zein precursor - maize
Seq. No.
                   215890
```

30180

LIB3147-026-Q1-K1-G11

BLASTX

152

g4539292

Match length

% identity

48 79



```
2.0e-10
E value
Match length
                  75
                  45
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  215891
Seq. No.
                  LIB3147-026-Q1-K1-G4
Seq. ID
Method
                  BLASTX
                  g4406780
NCBI GI
BLAST score
                  586
                  9.0e-61
E value
Match length
                  143
                  75
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  215892
Seq. No.
                  LIB3147-026-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g72307
NCBI GI
BLAST score
                  282
                  5.0e-25
E value
                  141
Match length
                  49
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                  (J01246) 26.99 kd zein protein [Zea mays]
                  215893
Seq. No.
                  LIB3147-026-Q1-K1-H1
Seq. ID
Method
                  BLASTN
                  q18731
NCBI GI
                  44
BLAST score
                  2.0e-15
E value
Match length
                   164
% identity
                   85
NCBI Description
                  Soybean RPB1-B1 gene for the largest subunit of RNA
                  polymerase II (EC 2.7.7.6)
                  215894
Seq. No.
Seq. ID
                  LIB3147-026-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                   g1076820
BLAST score
                   371
E value
                   6.0e-36
Match length
                  87
% identity
                   86
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
Seq. No.
                   215895
                  LIB3147-026-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135611
BLAST score
                  214
                   3.0e-17
E value
```

BLAST score

Match length

% identity

E value

316

105

68

3.0e-29



```
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]
Seq. No.
                  215896
Seq. ID
                  LIB3147-026-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q549060
BLAST score
                  421
                  2.0e-41
E value
Match length
                  128
% identity
                  62
NCBI Description
                  T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                  >gi_631656_pir__S43058 CCTeta protein eta chain - mouse
                  >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of
                  the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.
                  215897
                  LIB3147-026-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541967
BLAST score
                  194
E value
                  8.0e-18
Match length
                  83
                  64
% identity
NCBI Description
                  glycine cleavage system protein T precursor - garden pea
                  >gi_407475_emb_CAA52800_ (X74793) T-protein of the glycine
                  decarboxylase complex [Pisum sativum]
Seq. No.
                  215898
                  LIB3147-026-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3128228
BLAST score
                  421
E value
                  1.0e-41
Match length
                  96
% identity
                  81
NCBI Description
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  215899
Seq. ID
                  LIB3147-026-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g100424
BLAST score
                  588
E value
                  5.0e-61
Match length
                  132
% identity
                  53
NCBI Description ADP, ATP carrier protein precursor - potato
Seq. No.
                  215900
Seq. ID
                  LIB3147-026-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g141603
```



NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 215901

Seq. ID LIB3147-027-Q1-K1-A1

Method BLASTX
NCBI GI g2262100
BLAST score 263
E value 2.0e-23
Match length 61
% identity 84

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 215902

Seq. ID LIB3147-027-Q1-K1-A3

Method BLASTX
NCBI GI g3334113
BLAST score 466
E value 1.0e-46
Match length 89
% identity 100

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)

acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 215903

Seq. ID LIB3147-027-Q1-K1-A5

Method BLASTN
NCBI GI g3399678
BLAST score 63
E value 7.0e-27

E value 7.0e-2
Match length 283
% identity 81

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 215904

Seq. ID LIB3147-027-Q1-K1-A8

Method BLASTX
NCBI GI g4185509
BLAST score 347
E value 7.0e-33
Match length 87
% identity 76

NCBI Description (AF102821) actin depolymerizing factor 3 [Arabidopsis

thaliana]

Seq. No. 215905

Seq. ID LIB3147-027-Q1-K1-B1

Method BLASTX
NCBI GI g2244904
BLAST score 450
E value 9.0e-45
Match length 134
% identity 22

NCBI Description (Z97339) similar to hypothetical protein C02F5.7 - Caenorha

[Arabidopsis thaliana]



```
215906
Seq. No.
                  LIB3147-027-Q1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2262173
                   429
BLAST score
                  7.0e-57
E value
                  134
Match length
                   89
% identity
                  (AC002329) NADPH thioredoxin reductase [Arabidopsis
NCBI Description
                  thaliana]
                   215907
Seq. No.
                  LIB3147-027-Q1-K1-B6
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                   g4539327
                   390
BLAST score
                   9.0e-38
E value
                   130
Match length
                   63
% identity
                  (AL035679) putative proton pump [Arabidopsis thaliana]
NCBI Description
                   215908
Seq. No.
                   LIB3147-027-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982259
                   484
BLAST score
                   9.0e-49
E value
                   142
Match length
                   59
% identity
                  (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                   mariana]
                   215909
Seq. No.
                   LIB3147-027-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4160280
BLAST score
                   251
E value
                   1.0e-21
                   70
Match length
                   63
% identity
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
                   215910
Seq. No.
                   LIB3147-027-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335337
BLAST score
                   340
E value
                   6.0e-32
Match length
                   107
% identity
                   64
NCBI Description
                  (AC004512) Similar to acyl carrier protein, mitochondrial
                   precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD
                   subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs
```

come from this gene

gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330

Seq. No. Seq. ID

Method



```
215911
Seq. No.
Seq. ID
                  LIB3147-027-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3717946
BLAST score
                  282
                  4.0e-25
E value
Match length
                  94
                  63
% identity
NCBI Description
                  (AJ005901) vag1 [Arabidopsis thaliana]
                  215912
Seq. No.
                  LIB3147-027-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4531444
BLAST score
                  218
                  1.0e-33
E value
                  114
Match length
                  64
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215913
                  LIB3147-027-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3873408
BLAST score
                  176
                  1.0e-12
E value
                  53
Match length
% identity
                   64
                  (L76926) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                   215914
Seq. No.
                  LIB3147-027-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2160322
BLAST score
                   539
E value
                   3.0e-55
Match length
                   107
                   93
% identity
                   (D16139) cytokinin binding protein CBP57 [Nicotiana
NCBI Description
                   sylvestris]
                   215915
Seq. No.
                   LIB3147-027-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3510259
                   339
BLAST score
E value
                   4.0e-51
                   124
Match length
                   74
% identity
                   (AC005310) putative inorganic pyrophosphatase [Arabidopsis
NCBI Description
                   thaliana] >gi 3522960 (AC004411) putative inorganic
                   pyrophosphatase [Arabidopsis thaliana]
                   215916
```

30185

LIB3147-027-Q1-K1-E12

BLASTX



```
NCBI GI
                  g4204313
                  462
BLAST score
                  1.0e-50
E value
Match length
                  139
                  77
% identity
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
                  215917
Seq. No.
                  LIB3147-027-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1771158
BLAST score
                  268
E value
                  2.0e-23
                  103
Match length
                  52
% identity
NCBI Description
                 (Y07861) MFP1 protein [Lycopersicon esculentum]
                  215918
Seq. No.
                  LIB3147-027-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1731146
BLAST score
                  238
E value
                  5.0e-20
Match length
                  102
% identity
                  46
NCBI Description
                  HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
                  >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein
                  [Caenorhabditis elegans]
Seq. No.
                  215919
Seq. ID
                  LIB3147-027-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1170898
BLAST score
                  465
E value
                  1.0e-46
Match length
                  129
                  78
% identity
NCBI Description
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                  >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial
                  - cider tree >gi_473206_emb_CAA55383 (X78800)
                  mitochondrial malate dehydrogenase [Eucalyptus qunnii]
Seq. No.
                  215920
Seq. ID
                  LIB3147-027-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q124224
BLAST score
                  266
E value
                  3.0e-23
Match length
                  52
% identity
```

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 215921



```
Seq. ID
                   LIB3147-027-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   q1731146
BLAST score
                   273
E value
                   2.0e-24
Match length
                   97
% identity
                   56
NCBI Description
                   HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
                   >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein
                   [Caenorhabditis elegans]
Seq. No.
                   215922
                   LIB3147-027-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464621
BLAST score
                   427
E value
                   4.0e-42
Match length
                   132
% identity
                   64
NCBI Description
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__$28586
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   215923
Seq. ID
                   LIB3147-027-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   q3176668
BLAST score
                   389
E value
                   2.0e-51
Match length
                   123
% identity
                   85
NCBI Description
                   (AC004393) Similar to ribosomal protein L17 gb X62724 from
                   Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                   gb Z33937 come from this gene. [Arabidopsis thaliana]
                   215924
Seq. No.
Seq. ID
                   LIB3147-027-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   q1871577
BLAST score
                   188
E value
                   4.0e-14
                   89
Match length
% identity
                   48
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.
                   215925
Seq. ID
                   LIB3147-027-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q3779024
BLAST score
                   509
E value
                   1.0e-51
Match length
                   120
```

% identity

NCBI Description

(AC005171) unknown protein [Arabidopsis thaliana]

Seq. ID

215931

LIB3147-027-Q1-K1-H9



```
Seq. ID
                  LIB3147-027-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q1346735
BLAST score
                  305
E value
                  6.0e-28
Match length
                  100
                  61
% identity
NCBI Description
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_1076562_pir__S49647 phosphoglycerate mutase (EC
                  5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652)
                  phosphoglycerate mutase [Ricinus communis]
                  215927
Seq. No.
Seq. ID
                  LIB3147-027-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1928983
BLAST score
                  405
E value
                  1.0e-49
Match length
                  112
% identity
NCBI Description (U92652) tonoplast intrinsic protein bobTIP26-2 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  215928
Seq. ID
                  LIB3147-027-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  a4335719
BLAST score
                  128
E value
                  5.0e-09
Match length
                  82
% identity
                  41
NCBI Description
                  (AC006248) putative RING-H2 finger protein RHG1a
                   [Arabidopsis thaliana]
Seq. No.
                  215929
Seq. ID
                  LIB3147-027-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q3287690
BLAST score
                  147
E value
                  1.0e-10
Match length
                  113
% identity
                  42
NCBI Description (AC003979) T22J18.15 [Arabidopsis thaliana]
Seq. No.
                  215930
Seq. ID
                  LIB3147-027-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q1432056
BLAST score
                  132
E value
                  1.0e-13
                  98
Match length
% identity
                  52
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
```



```
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  298
E value
                  4.0e-27
Match length
                  114
% identity
                  66
                 (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  215932
                  LIB3147-028-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173187
                  581
BLAST score
                  4.0e-60
E value
Match length
                  115
% identity
                  98
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  215933
Seq. No.
Seq. ID
                  LIB3147-028-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  349
                  6.0e-33
E value
Match length
                  103
% identity
                  69
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
                  215934
Seq. No.
Seq. ID
                  LIB3147-028-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  35
E value
                  3.0e-10
                  35
Match length
% identity
                  59
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  215935
Seq. ID
                  LIB3147-028-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4572679
BLAST score
                  367
E value
                  4.0e - 35
Match length
                  110
% identity
                  65
NCBI Description
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
                  motif [Arabidopsis thaliana]
```

Seq. ID LIB3147-028-Q1-K1-C11

Method BLASTX NCBI GI g2213558

Seq. ID Method



```
252
BLAST score
                   1.0e-21
E value
                   121
Match length
                   44
% identity
                  (Z97052) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   215937
Seq. No.
                   LIB3147-028-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2104681
                   253
BLAST score
                   1.0e-21
E value
Match length
                   127
                   50
% identity
                  (X97907) transcription factor [Vicia faba]
NCBI Description
Seq. No.
                   215938
                   LIB3147-028-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   q115515
NCBI GI
                   587
BLAST score
E value
                   6.0e-61
                   119
Match length
                   48
% identity
                   CALMODULIN >gi_71683_pir__MCAA calmodulin - alfalfa
NCBI Description
                   >gi_19579_emb_CAA366\overline{4}4 (X52398) calmodulin (AA 1-149)
                   [Medicago satīva] >gi_170070 (L01430) calmodulin [Glycine
                   max] >gi_170074 (L014\overline{3}2) calmodulin [Glycine max]
                   >gi_506852 (L20507) calmodulin [Vigna radiata] >gi_4103957
                   (AF\overline{0}30032) calmodulin [Phaseolus vulgaris]
                   >gi_1583767_prf__2121384A calmodulin [Glycine max]
                   >gi 1583769 prf 2121384C calmodulin [Glycine max]
                   215939
Seq. No.
                   LIB3147-028-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244749
BLAST score
                   201
E value
                   1.0e-15
                   49
Match length
                   73
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                   215940
Seq. No.
                   LIB3147-028-Q1-K1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2760167
                   36
BLAST score
E value
                   1.0e-10
                   72
Match length
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
                   215941
Seq. No.
```

30190

LIB3147-028-Q1-K1-E11

BLASTN



g4512590 NCBI GI BLAST score 33 E value 5.0e-09 37 Match length % identity 97 Ipomoea batatas f3h II mRNA for flavanone 3-hydroxyrase, NCBI Description complete cds 215942 Seq. No. LIB3147-028-Q1-K1-E12 Seq. ID Method BLASTX NCBI GI g1172635 BLAST score 603 E value 8.0e-63 122 Match length 98 % identity 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 2) >gi 556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa] 215943 Seq. No. LIB3147-028-Q1-K1-E5 Seq. ID Method BLASTX NCBI GI g974782 336 BLAST score 2.0e-31 E value Match length 91 77 % identity (Z49150) cobalamine-independent methionine synthase NCBI Description [Solenostemon scutellarioides] Seq. No. 215944 LIB3147-028-Q1-K1-E6 Seq. ID Method BLASTX NCBI GI g2465923 BLAST score 316 E value 4.0e-29 95 Match length % identity 67 (AF024648) receptor-like serine/threonine kinase NCBI Description [Arabidopsis thaliana] 215945 Seq. No. LIB3147-028-Q1-K1-E7 Seq. ID Method BLASTX NCBI GI g1931650 BLAST score 241 E value 3.0e-20Match length 145 % identity (U95973) disease resistance protein RPM1 isolog NCBI Description

[Arabidopsis thaliana]

215946 Seq. No.

Seq. ID LIB3147-028-Q1-K1-E8

Method BLASTX NCBI GI g4138209



BLAST score 378 3.0e-36 E value Match length 158 % identity 44 (AJ223071) serine/threonine kinase protein MSTK2L,long-form NCBI Description [Mus musculus] 215947 Seq. No. Seq. ID Method BLASTN NCBI GI BLAST score

LIB3147-028-Q1-K1-E9 q2736287 33

E value 5.0e-09 Match length 41 % identity 95

NCBI Description Camptotheca acuminata isopentenyl diphosphate isomerase II

(IPI2) mRNA, complete cds

Seq. No. 215948

Seq. ID LIB3147-028-Q1-K1-F10

Method BLASTX NCBI GI q3860277 BLAST score 489 E value 4.0e-60 Match length 162 % identity 77

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 215949

Seq. ID LIB3147-028-Q1-K1-F12

Method BLASTX NCBI GI g464734 BLAST score 430 E value 1.0e-42 95 Match length 91 % identity

ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description

HYDROLASE) (ADOHCYASE) >gi_481237_pir__ S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine

hydrolase [Catharanthus roseus]

Seq. No. 215950

Seq. ID LIB3147-028-Q1-K1-F5

Method BLASTX NCBI GI g3860277 BLAST score 281 E value 3.0e-42Match length 107 % identity 86

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 215951



```
LIB3147-028-Q1-K1-F8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g974782
                   282
 BLAST score
 E value
                   5.0e-25
                   59
 Match length
                   95
 % identity
 NCBI Description (Z49150) cobalamine-independent methionine synthase
                   [Solenostemon scutellarioides]
 Seq. No.
                   215952
 Seq. ID
                   LIB3147-028-Q1-K1-G10
 Method
                   BLASTX
 NCBI GI
                   g3395441
 BLAST score
                   164
 E value
                   1.0e-11
 Match length
                   48
 % identity
                   67
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   215953
 Seq. ID
                   LIB3147-028-Q1-K1-G12
 Method
                   BLASTX
 NCBI GI
                   g398994
 BLAST score
                   459
                   1.0e-49
 E value
Match length
                   116
                   87
 % identity
 NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
                   (ETHYLENE-FORMING ENZYME) (EFE) >gi 166313 (M97961) tomato
                   and apple ACC oxidase homologue [Actinidia deliciosa]
 Seq. No.
                   215954
 Seq. ID
                   LIB3147-028-Q1-K1-G7
Method
                   BLASTX
 NCBI GI
                   g3880441
 BLAST score
                   163
 E value
                   4.0e-11
 Match length
                   47
 % identity
                   51
 NCBI Description (Z82062) similar to Zinc finger, C3HC4 type (RING finger);
                   cDNA EST EMBL: D76353 comes from this gene; cDNA EST
                   EMBL: D71838 comes from this gene; cDNA EST EMBL: D74561
                   comes from this gene; cDNA EST EMBL:D73319 comes from this
                   ge
 Seq. No.
                   215955
 Seq. ID
                   LIB3147-028-Q1-K1-H1
 Method
                   BLASTX
 NCBI GI
                   g3860315
 BLAST score
                   400
 E value
                   5.0e-39
 Match length
                   94
 % identity
 NCBI Description (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
```

BLAST score

E value

707

6.0e-75



```
Seq. ID
                   LIB3147-028-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g99737
BLAST score
                   309
E value
                   1.0e-28
                   91
Match length
                   67
% identity
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
                   Arabidopsis thaliana >gi_16189_emb_CAA46815 (X66017)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                   215957
Seq. ID
                  LIB3147-029-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2642158
BLAST score
                   294
E value
                   1.0e-26
Match length
                   106
% identity
                   54
NCBI Description
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   215958
Seq. ID
                  LIB3147-029-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                   q4508079
BLAST score
                   185
E value
                   2.0e-15
Match length
                   96
                   53
% identity
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]
Seq. No.
                   215959
Seq. ID
                  LIB3147-029-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                   g1841870
BLAST score
                   304
E value
                   1.0e-27
Match length
                  70
                   84
% identity
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
Seq. No.
                   215960
Seq. ID
                  LIB3147-029-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2213425
BLAST score
                   682
E value
                   5.0e-72
                  151
Match length
                   43
% identity
NCBI Description
                 (Z97064) hypothetical protein [Citrus x paradisi]
                  215961
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1518540
```



```
Match length
                  148
                  86
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  215962
Seq. No.
                  LIB3147-029-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974782
                  147
BLAST score
                  3.0e-09
E value
                  37
Match length
                  84
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                  215963
Seq. No.
                  LIB3147-029-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367593
BLAST score
                   427
                  2.0e-42
E value
Match length
                  100
                  80
% identity
                  (ALO31135) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805841 emb CAA21461_ (AL031986) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  215964
                  LIB3147-029-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g1407705
NCBI GI
BLAST score
                  266
E value
                   3.0e-23
                  83
Match length
                   63
% identity
NCBI Description (U60202) lipoxygenase [Solanum tuberosum]
Seq. No.
                  215965
                  LIB3147-029-Q1-K1-B4
Seq. ID
Method
                  BLASTN
                   q4220633
NCBI GI
BLAST score
                   38
                   5.0e-12
E value
                  169
Match length
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   215966
                  LIB3147-029-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q167367
BLAST score
                   472
```

2.0e-47 E value Match length 120 77 % identity

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

NCBI Description



```
215967
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g445612
                   221
BLAST score
E value
                   6.0e-18
Match length
                  45
                   93
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                  215968
Seq. No.
                  LIB3147-029-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2559012
BLAST score
                  502
                  1.0e-52
E value
                  163
Match length
                   65
% identity
                   (AF026293) chaperonin containing t-complex polypeptide 1,
NCBI Description
                  beta subunit; CCT-beta [Homo sapiens] >gi_4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
Seq. No.
                   215969
                 · LIB3147-029-Q1-K1-B8
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
                   33
BLAST score
E value
                   7.0e-09
Match length
                   33
% identity
                   58
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   215970
Seq. No.
Seq. ID
                   LIB3147-029-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q4335864
BLAST score
                   489
E value
                   2.0e-49
Match length
                   123
% identity
NCBI Description (AF052040) calreticulin [Berberis stolonifera]
                   215971
Seq. No.
Seq. ID
                   LIB3147-029-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   q730526
BLAST score
                   690
E value
                   7.0e-73
Match length
                   160
% identity
                   81
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
```

30196

[Arabidopsis thaliana]

>gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana $>gi_404166_emb_CAA53005_ (X75162)$ BBC1 protein



```
Seq. No.
                  215972
Seq. ID
                  LIB3147-029-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q1168191
                  580
BLAST score
                  5.0e-60
E value
Match length
                  123
                  93
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN 4 (PBLT4) >gi_1362089_pir__S57272
                  14-3-3 brain protein homolog (clone pBLT4) - tomato
                  >gi_466336 (L29150) 14-3-3 protein homologue [Solanum
                  lycopersicum] >gi_1090847_prf__2019487B 14-3-3 protein
                  [Lycopersicon esculentum]
                  215973
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  q4510408
BLAST score
                  51
E value
                  5.0e-20
Match length
                  107
% identity
                  87
NCBI Description Arabidopsis thaliana chromosome II BAC T1E2 genomic
                  sequence, complete sequence
Seq. No.
                  215974
Seq. ID
                  LIB3147-029-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3204103
BLAST score
                  325
E value
                  3.0e - 30
Match length
                  110
                  60
% identity
NCBI Description (AJ006761) hypothetical protein [Cicer arietinum]
Seq. No.
                  215975
Seq. ID
                  LIB3147-029-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2760334
                  272
BLAST score
E value
                  5.0e-24
                  59
Match length
                  78
% identity
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.
                  215976
Seq. ID
                  LIB3147-029-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4006899
BLAST score
                  426
E value
                  4.0e-42
```

Match length 116 % identity 63

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 215977

Seq. ID LIB3147-029-Q1-K1-D1

E value

Match length

1.0e-45

144



```
Method
                   BLASTX
NCBI GI
                   q4105794
BLAST score
                   157
E value
                   2.0e-13
Match length
                   114
                   39
% identity
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
Seq. No.
                   215978
Seq. ID
                   LIB3147-029-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g225267
BLAST score
                   513
E value
                   4.0e-52
Match length
                   116
% identity
                   81
NCBI Description ORF 1244 [Nicotiana tabacum]
                   215979
Seq. No.
                  LIB3147-029-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3881724
BLAST score
                   284
E value
                   2.0e-25
Match length
                   90
                   57
% identity
NCBI Description (Z69385) Similarity to Yeast JTA107 protein (PIR Acc. No.
                   S55137); cDNA EST yk290e3.3 comes from this gene; cDNA EST
                   yk290e3.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                   215980
Seq. ID
                  LIB3147-029-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   g1431629
BLAST score
                   286
E value
                   1.0e-25
Match length
                  82
% identity
                   62
NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]
Seq. No.
                   215981
Seq. ID
                   LIB3147-029-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                   g3115374
BLAST score
                   217
E value
                   5.0e-18
Match length
                   71
% identity
NCBI Description (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]
Seq. No.
                   215982
Seq. ID
                  LIB3147-029-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4006917
BLAST score
                  458
```



% identity NCBI Description (Z99708) putative protein [Arabidopsis thaliana] Seq. No. 215983 Seq. ID LIB3147-029-Q1-K1-D7 Method BLASTX NCBI GI g2497752 BLAST score 288 E value 1.0e-25 96 Match length % identity 58 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1321911 emb CAA65475 (X96714) lipid transfer protein [Prunus dulcis] Seq. No. 215984 Seq. ID LIB3147-029-Q1-K1-D8 Method BLASTX NCBI GI g1173218 BLAST score 344 E value 2.0e-32 Match length 68 % identity 96 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] Seq. No. 215985 Seq. ID LIB3147-029-Q1-K1-E1 Method BLASTX NCBI GI g974782 BLAST score 500 E value 1.0e-50 Match length 101 98 % identity NCBI Description (Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides] Seq. No. 215986 Seq. ID LIB3147-029-Q1-K1-E11 Method BLASTX NCBI GI g2109293 BLAST score 150 E value 1.0e-09 Match length 35 % identity NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis thaliana] Seq. No. 215987 Seq. ID LIB3147-029-Q1-K1-E12 Method BLASTX

Method BLASTX
NCBI GI g3341681
BLAST score 339
E value 5.0e-32
Match length 86
% identity 80



NCBI Description (AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi 741994 prf 2008312A GTP-binding protein [Arabidopsis thaliana1 215988 Seq. No. Seq. ID LIB3147-029-Q1-K1-E2 Method BLASTX NCBI GI g1170508 BLAST score 514 E value 2.0e-52 Match length 103 97 % identity NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi_2119931_pir__S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi_475219_emb_CAA55639_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi_475221_emb_CAA55640_ (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum] Seq. No. 215989 Seq. ID LIB3147-029-Q1-K1-E4 Method BLASTX NCBI GI q4056469 BLAST score 657 E value 4.0e-69 Match length 127 % identity (AC005990) Strong similarity to gb_M95166 ADP-ribosylation NCBI Description factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb Z25043 come from t Seq. No. 215990 Seq. ID LIB3147-029-Q1-K1-E7 Method BLASTX NCBI GI q2244847 BLAST score 192 E value 1.0e-14 Match length 143 % identity NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana] Seq. No. 215991

Seq. ID LIB3147-029-Q1-K1-E8

Method BLASTX NCBI GI g1432083 BLAST score 277 E value 9.0e-25 Match length 79 % identity

NCBI Description (U60981) homolog to Skplp, an evolutionarily conserved

kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]

>gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]



Seq. No. 215992 Seq. ID LIB3147-029-Q1-K1-E9 Method BLASTX NCBI GI g1841870 BLAST score 185 E value 7.0e-14Match length 45 82 % identity NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa] Seq. No. 215993 Seq. ID LIB3147-029-Q1-K1-F10 Method BLASTX NCBI GI g2829899 BLAST score 295 E value 1.0e-26 Match length 123 46 % identity (AC002311) similar to ripening-induced protein, NCBI Description gp_AJ001449_2465015 and major#latex protein, gp X91961 1107495 [Arabidopsis thaliana] 215994 Seq. No. Seq. ID LIB3147-029-Q1-K1-F12 Method BLASTX NCBI GI g4544409 BLAST score 266 3.0e-23 E value Match length 85 % identity 62 (AC006955) putative transcription factor [Arabidopsis NCBI Description thaliana] 215995 Seq. No. Seq. ID LIB3147-029-Q1-K1-F4 Method BLASTX NCBI GI g232031 BLAST score 203 E value 4.0e-16 Match length 105 % identity 44 ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224 translation elongation factor eEF-1 beta' chain - rice NCBI Description >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa] Seq. No. 215996 Seq. ID LIB3147-029-Q1-K1-F5 Method BLASTX NCBI GI g1213069 BLAST score 543 E value

30201

(X79675) dihydrodipicolinate synthase [Nicotiana tabacum]

1.0e-79

164 85

Match length

NCBI Description

% identity



```
215997
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q1498053
BLAST score
                  293
                  1.0e-48
E value
                  125
Match length
                  82
% identity
                 (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  215998
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-F9
Method
                  BLASTX
                  g322750
NCBI GI
BLAST score
                  655
                  7.0e-69
E value
Match length
                  128
                  98
% identity
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                  >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
Seq. No.
                  215999
Seq. ID
                  LIB3147-029-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g445613
BLAST score
                  222
                  3.0e-18
E value
                  45
Match length
                  91
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                  216000
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                   g2618721
BLAST score
                   487
E value
                   4.0e-49
Match length
                  103
% identity
                  88
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                   216001
                  LIB3147-029-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3880399
BLAST score
                  154
E value
                   4.0e-10
Match length
                   67
% identity
                   43
                  (Z71267) predicted using Genefinder; cDNA EST yk275h2.3
NCBI Description
                   comes from this gene; cDNA EST yk309g11.3 comes from this
                   gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST
                  yk275h2.5 comes from this gene [Caenorhabditis elegans]
```

Seq. ID LIB3147-029-Q1-K1-G12



```
BLASTX
Method
NCBI GI
                  q2661840
BLAST score
                   436
E value
                   4.0e-43
Match length
                  123
                   67
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                  216003
Seq. No.
                  LIB3147-029-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  592
                  1.0e-61
E value
                  113
Match length
% identity
                   97
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  216004
                  LIB3147-029-Q1-K1-G3
Seq. ID
Method
                  BLASTX
                  g2738248
NCBI GI
BLAST score
                  587
                   5.0e-61
E value
Match length
                  116
                   96
% identity
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
                   216005
Seq. No.
                  LIB3147-029-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4206122
BLAST score
                   552
E value
                   1.0e-56
Match length
                   132
% identity
                   78
NCBI Description
                  (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                  crystallinum]
                   216006
Seq. No.
Seq. ID
                   LIB3147-029-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4467139
BLAST score
                   225
E value
                   1.0e-18
Match length
                   86
% identity
                   (AL035540) putative protein phosphatase-2c [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   216007
                  LIB3147-029-Q1-K1-G9
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3821780
```

33

5.0e-09

BLAST score E value

E value

Match length

1.0e-09

62



```
Match length
                   33
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   216008
Seq. ID
                  LIB3147-029-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g445613
BLAST score
                  288
E value
                  3.0e - 38
Match length
                  101
% identity
                  75
NCBI Description
                 ribosomal protein L7 [Solanum tuberosum]
                  216009
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1352664
BLAST score
                   352
                   2.0e-33
E value
Match length
                  81
                  78
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
NCBI Description
                   SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase
                   (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                  >gi_473259 (U08047) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana] >gi_4204949 (U60136)
                   serine/threonine protein phosphatase 2A-4 catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   216010
                  LIB3147-029-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g602076
BLAST score
                  615
E value
                   3.0e-64
Match length
                  127
% identity
                   26
NCBI Description
                  (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                  216011
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g857397
BLAST score
                   681
E value
                   8.0e-72
Match length
                  152
% identity
NCBI Description
                  (D50870) mitotic cyclin a2-type [Glycine max]
Seq. No.
                  216012
Seq. ID
                  LIB3147-029-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g3449313
BLAST score
                  34
```



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21P3, complete sequence [Arabidopsis thaliana]
                  216013
Seq. No.
Seq. ID
                  LIB3147-029-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  q3600038
BLAST score
                  194
                  9.0e-15
E value
Match length
                  57
% identity
                  65
                  (AF080119) similar to Saccharomyces cerevisiae
NCBI Description
                  transcription regulator SPO8 (SW:P41833) [Arabidopsis
                  thaliana]
                  216014
Seq. No.
                  LIB3147-031-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  773
                  1.0e-82
E value
Match length
                  151
                  99
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                  216015
Seq. No.
Seq. ID
                  LIB3147-031-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  407
E value
                  5.0e-40
Match length
                  109
% identity
                  75
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_ S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
Seq. No.
                  216016
Seq. ID
                  LIB3147-031-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4406783
BLAST score
                  445
                  3.0e-44
E value
Match length
                  98
% identity
                  (AC006532) putative glutamate decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. ID LIB3147-031-Q1-K1-B1

Method BLASTX NCBI GI g4249390



```
BLAST score
                   356
E value
                   8.0e-34
Match length
                   121
% identity
                   56
NCBI Description
                  (AC005966) Similar to gb AF039182 probable aldo-keto
                   reductase from Fragaria \bar{x} ananassa. This gene may be cut
                   off. EST gb_U74151 comes from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   216018
Seq. ID
                  LIB3147-031-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3947614
BLAST score
                   248
E value
                   4.0e-21
Match length
                  110
% identity
                   41
                  (AL023828) cDNA EST yk491f8.5 comes from this gene
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                  216019
Seq. ID
                  LIB3147-031-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3892050
BLAST score
                  288
E value
                  8.0e-26
Match length
                  103
% identity
                   60
NCBI Description
                 (AC002330) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216020
Seq. ID
                  LIB3147-031-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q3367519
BLAST score
                  304
E value
                   6.0e-28
Match length
                  82
% identity
                  (AC004392) Contains similarity to gb_U51898
NCBI Description
                  Ca2+-independent phospholipase A2 from Rattus norvegicus.
                   [Arabidopsis thaliana]
Seq. No.
                  216021
Seq. ID
                  LIB3147-031-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2244734
BLAST score
                  630
E value
                  7.0e-66
Match length
                  121
% identity
                  99
NCBI Description
                 (D88414) actin [Gossypium hirsutum]
```

Seq. ID LIB3147-031-Q1-K1-C2

Method BLASTX NCBI GI g2827082 BLAST score 663



```
E value
                   9.0e-70
Match length
                   150
% identity
                   81
NCBI Description
                  (AF020272) malate dehydrogenase [Medicago sativa]
                  216023
Seq. No.
                  LIB3147-031-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351279
BLAST score
                  454
E value
                  7.0e-58
Match length
                  140
% identity
                  80
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi 602590 emb CAA58230 (X83227) triosephosphate isomerase
                  [Petunia x hybrida]
Seq. No.
                  216024
Seq. ID
                  LIB3147-031-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3334113
BLAST score
                  292
E value
                  2.0e-26
Match length
                  78
                  77
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi ·1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  216025
Seq. ID
                  LIB3147-031-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1173223
BLAST score
                  521
E value
                   4.0e-53
Match length
                  105
% identity
                  94
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 454848 (L28831) ribosomal
                  protein S11 [Glycine max]
Seq. No.
                  216026
Seq. ID
                  LIB3147-031-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g399046
BLAST score
                  577
E value
                  1.0e-59
Match length
                  140
% identity
                  81
NCBI Description
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
                  >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
                  2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                   (X58640) adenine phosphoribosyltransferase [Arabidopsis
                  thaliana] >gi 433050 (L19637) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                  >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
```

Seq. ID LIB3147-031-Q1-K1-D2

% identity

67



```
Method
                  BLASTX
NCBI GI
                  q2673918
BLAST score
                  413
E value
                  2.0e-40
Match length
                  146
                  62
% identity
NCBI Description
                  (AC002561) unknwon protein [Arabidopsis thaliana]
Seq. No.
                  216028
                  LIB3147-031-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g595768
BLAST score
                  164
                  3.0e-11
E value
Match length
                  47
% identity
                  66
                 (U13866) non-functional lacZ alpha peptide [Cloning vector]
NCBI Description
                  216029
Seq. No.
Seq. ID
                  LIB3147-031-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g559005
BLAST score
                  318
E value
                  2.0e-29
Match length
                  95
% identity
                  65
                  (U15933) ascorbate peroxidase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  216030
Seq. ID
                  LIB3147-031-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q81811
BLAST score
                  156
E value
                  1.0e-10
Match length
                  36
% identity
                  89
NCBI Description
                  ribosomal protein S11 - soybean (fragment) >gi 170054
                   (M31024) ribosomal protein S11 [Glycine max]
Seq. No.
                  216031
Seq. ID
                  LIB3147-031-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g559684
BLAST score
                  624
E value
                  3.0e-65
Match length
                  130
% identity
                  91
NCBI Description (L36097) aquaporin [Mesembryanthemum crystallinum]
Seq. No.
                  216032
Seq. ID
                  LIB3147-031-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3329368
BLAST score
                  517
E value
                  1.0e-52
Match length
                  149
```



NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana] Seq. No. 216033 LIB3147-031-Q1-K1-E2 Seq. ID Method BLASTX NCBI GI g3913919 BLAST score 459 E value 7.0e-46Match length 108 % identity 81 NCBI Description ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI) (VACUOLAR INVERTASE) >gi 2351827 (U92438) soluble acid invertase [Phaseolus vulgaris] 216034 Seq. No. LIB3147-031-Q1-K1-E3 Seq. ID Method BLASTX g3157924 NCBI GI BLAST score 288 E value 8.0e-26 Match length 105 % identity 59 NCBI Description (AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi 4063707 (AF104327) extensin-like protein [Arabidopsis thaliana] Seq. No. 216035 LIB3147-031-Q1-K1-E4 Seq. ID Method BLASTX NCBI GI g3128173 BLAST score 420 E value 3.0e-41Match length 97 84 % identity NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana] Seq. No. 216036 Seq. ID LIB3147-031-Q1-K1-E6 Method BLASTX NCBI GI g3297823 BLAST score 249 E value 3.0e-21Match length 84 % identity

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 216037

Seq. ID LIB3147-031-Q1-K1-E8

Method BLASTX
NCBI GI g2501102
BLAST score 509
E value 1.0e-51
Match length 147



```
% identity
                  71
                  SYNTAXIN-RELATED PROTEIN KNOLLE >gi 1184165 (U39451)
NCBI Description
                  syntaxin-related [Arabidopsis thaliana] >gi_1184167
                  (U39452) syntaxin-related [Arabidopsis thaliana]
                  >gi_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
                  >gi 1587182 prf 2206310A syntaxin-related protein
                  [Arabidopsis thaliana]
                  216038
Seq. No.
                  LIB3147-031-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g2062167
NCBI GI
BLAST score
                  343
E value
                  3.0e - 32
                  110
Match length
                  61
% identity
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  216039
Seq. No.
                  LIB3147-031-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281631
                  327
BLAST score
                  2.0e-30
E value
Match length
                  135
                  55
% identity
                  (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  216040
                  LIB3147-031-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167970
BLAST score
                  419
E value
                  4.0e-41
Match length
                  154
% identity
NCBI Description (L05915) [GST1] gene product [Dianthus caryophyllus]
                  216041
Seq. No.
                  LIB3147-031-Q1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g167346
BLAST score
                  34
E value
                  1.0e-09
Match length
                  58
% identity
                  Gossypium hirsutum Lea5-A late embryogenesis-abundant
NCBI Description
                  protein (Lea5-A) gene, complete cds
Seq. No.
                  216042
Seq. ID
                  LIB3147-031-Q1-K1-F4
                  BLASTX
Method
```

NCBI GI g4193388 BLAST score 362 E value 1.0e-34

Match length

% identity

148



```
Match length
                     88
% identity
                     82
NCBI Description
                     (AF091455) translationally controlled tumor protein [Hevea
                     brasiliensis]
                     216043
Seq. No.
Seq. ID
                     LIB3147-031-Q1-K1-F5
Method
                     BLASTX
NCBI GI
                     q2218152
BLAST score
                     373
E value
                     8.0e-36
Match length
                     102
 % identity
                     71
                    (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                     unguiculata]
Seq. No.
                     216044
                     LIB3147-031-Q1-K1-F7
Seq. ID
Method
                     BLASTN
NCBI GI
                     g18777
BLAST score
                     48
                     5.0e-18
E value
Match length
                     52
% identity
                     98
NCBI Description Soybean gene for Ula small nuclear RNA
Seq. No.
                     216045
                     LIB3147-031-Q1-K1-F8
Seq. ID
Method
                     BLASTX
NCBI GI
                     q3687243
BLAST score
                     235
E value
                     1.0e-19
Match length
                     59
 % identity
                     78
NCBI Description
                     (AC005169) putative ribosomal protein [Arabidopsis
                     thaliana]
                     216046
. Seq. No.
 Seq. ID
                     LIB3147-031-Q1-K1-F9
Method
                     BLASTX
NCBI GI
                     g122007
 BLAST score
                     369
E value
                     2.0e-35
                     97
Match length
                     76
 % identity
                     <code>HISTONE H2A >gi_100161_pir__S11498</code> histone H2A - parsley <code>>gi_20448_emb_CAA37828_</code> (X53831) H2A histone protein (AA 1
NCBI Description
                     - 149) [Petroselinum crispum]
 Seq. No.
                     216047
 Seq. ID
                     LIB3147-031-Q1-K1-G1
Method
                     BLASTX
NCBI GI
                     g421929
BLAST score
                     694
E value
                     2.0e-73
```



NCBI Description ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No. 216048

Seq. ID LIB3147-031-Q1-K1-G10

Method BLASTX
NCBI GI g132897
BLAST score 188
E value 4.0e-14
Match length 43
% identity 81

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L33 >gi_71355_pir__R5ZM33

ribosomal protein L33 - maize chloroplast

>gi_12449_emb_CAA39995_ (X56673) chloroplast ribosomal
protein L33 [Zea mays] >gi_902242_emb_CAA60306_ (X86563)

ribosomal protein L33 [Zea mays]

Seq. No. 216049

Seq. ID LIB3147-031-Q1-K1-G11

Method BLASTX
NCBI GI g4455274
BLAST score 485
E value 7.0e-49
Match length 127
% identity 75

NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis

thaliana]

Seq. No. 216050

Seq. ID LIB3147-031-Q1-K1-G12

Method BLASTX
NCBI GI g3273722
BLAST score 202
E value 9.0e-16
Match length 137
% identity 38

NCBI Description (AF055286) potential-sensitive polyspecific organic cation

transporter OCT3 [Rattus norvegicus]

Seq. No. 216051

Seq. ID LIB3147-031-Q1-K1-G2

Method BLASTX
NCBI GI g3821280
BLAST score 656
E value 5.0e-69
Match length 134
% identity 89

NCBI Description (AJ009952) asparagine synthetase type II [Phaseolus

vulgaris]

Seq. No. 216052

Seq. ID LIB3147-031-Q1-K1-G7

Method BLASTX
NCBI GI 94467145
BLAST score 217
E value 1.0e-17
Match length 56



```
% identity
                  (AL035540) farnesylated protein (ATFP6) [Arabidopsis
NCBI Description
                  thaliana]
                  216053
Seq. No.
Seq. ID
                  LIB3147-031-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q2493046
BLAST score
                  574
                  2.0e-59
E value
Match length
                  141
                  77
% identity
NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                  3.6.1.34) delta' chain precursor - sweet potato
                  >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                  delta subunit [Ipomoea batatas]
                  216054
Seq. No.
Seq. ID
                  LIB3147-031-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1806283
BLAST score
                  238
E value
                  3.0e-20
Match length
                  48 ---
% identity
                  100
NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata]
                  216055
Seq. No.
Seq. ID
                  LIB3147-031-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1350707
BLAST score
                  212
E value
                   6.0e-17
Match length
                  52
% identity
                  73
                  60S RIBOSOMAL PROTEIN L29 >qi 539923 pir JC2012 ribosomal
NCBI Description
                  protein 17K - mouse >gi 404766 (L08651) ribosomal protein
                  [Mus musculus]
Seq. No.
                  216056
Seq. ID
                  LIB3147-031-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g279567
BLAST score
                  185
E value
                  9.0e-14
                  130
Match length
                  31
% identity
NCBI Description insulinase (EC 3.4.99.45) - human
Seq. No.
                  216057
Seq. ID
                  LIB3147-031-Q1-K1-H5
                  BLASTX
Method
```

Method BLASTX
NCBI GI g4103959
BLAST score 507
E value 1.0e-51
Match length 137



% identity 73

NCBI Description (AF030033) calmodulin [Phaseolus vulgaris]

Seq. No. 216058

Seq. ID LIB3147-031-Q1-K1-H6

Method BLASTX
NCBI GI g4105697
BLAST score 399
E value 8.0e-39
Match length 100
% identity 73

NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 216059

Seq. ID LIB3147-031-Q1-K1-H7

Method BLASTX
NCBI GI g1703375
BLAST score 669
E value 2.0e-70
Match length 132
% identity 99

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483_dbj_BAA08259_ (D45420)

DcARF1 [Daucus carota]

Seq. No. 216060

Seq. ID LIB3147-031-Q1-K1-H8

Method BLASTX
NCBI GI g2781231
BLAST score 259
E value 2.0e-22
Match length 151
% identity 42

NCBI Description Chain A, Agglutinin In Complex With T-Disaccharide

>gi_2781232_pdb_1JLX_B Chain B, Agglutinin In Complex With

T-Disaccharide >gi_2781233_pdb_1JLY_A Chain A, Crystal

Structure Of Amaranthus Caudatus Agglutinin

>gi_2781234_pdb_1JLY_B Chain B, Crystal Structure Of

Amaranthus Caudatus Agglutinin

Seq. No. 216061

Seq. ID LIB3147-031-Q1-K1-H9

Method BLASTX
NCBI GI g1346156
BLAST score 607
E value 3.0e-63
Match length 131
% identity 88

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi_481943_pir__S40213 glycine

hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei

>gi_437997_emb_CAA81079_ (Z25860) glycine
hydroxymethyltransferase [Flaveria pringlei]

Seq. No. 216062

Seq. ID LIB3147-032-Q1-K1-A1

Method BLASTX



```
q3860315
NCBI GI
BLAST score
                   450
E value
                  8.0e-45
Match length
                  96
% identity
                  85
NCBI Description
                  (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
                  216063
Seq. No.
Seq. ID
                  LIB3147-032-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  q3264759
BLAST score
                  500
                   1.0e-50
E value
Match length
                  135
% identity
                   74
NCBI Description
                  (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
Seq. No.
                  216064
                  LIB3147-032-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729442
BLAST score
                  457
E value
                   1.0e-45
Match length
                  127
                   71
% identity
NCBI Description
                  PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR
                  >gi 166380 (M80235) glucose-regulated endoplasmic reticular
                  protein precursor [Medicago sativa]
                  216065
Seq. No.
Seq. ID
                  LIB3147-032-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                   q3152576
BLAST score
                  523
E value
                   2.0e-53
Match length
                   149
% identity
                   64
                   (AC002986) Similar to liver-specific transport protein
NCBI Description
                  qb L27651 from Rattus norviegicus. [Arabidopsis thaliana]
Seq. No.
                   216066
Seq. ID
                  LIB3147-032-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3309269
BLAST score
                   717
E value
                   4.0e-76
Match length
                  153
% identity
                   92
                   (AF074940) ferric leghemoglobin reductase-2 precursor
NCBI Description
                   [Glycine max]
                   216067
Seq. No.
```

Seq. ID LIB3147-032-Q1-K1-B12

Method BLASTX
NCBI GI g1008904
BLAST score 684
E value 3.0e-72



```
Match length
                   131
% identity
NCBI Description
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
Seq. No.
                   216068
Seq. ID
                  LIB3147-032-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q3738092
BLAST score
                   570
E value
                  7.0e-59
Match length
                  126
% identity
                  87
NCBI Description
                  (AC005617) similar to glyoxysomal malate dehydrogenase
                   [Arabidopsis thaliana]
                  216069
Seq. No.
                  LIB3147-032-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485514
BLAST score
                  314
E value
                  7.0e-29
Match length
                  68
% identity
                  88
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                   [Glycine max]
Seq. No.
                  216070
Seq. ID
                  LIB3147-032-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  q4566614
BLAST score
                  376
E value
                   4.0e-36
Match length
                  76
% identity
                  92
NCBI Description
                  (AF112887) actin depolymerizing factor [Populus alba x
                  Populus tremula]
Seq. No.
                  216071
Seq. ID
                  LIB3147-032-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g4531442
BLAST score
                  531
E value
                  2.0e-54
Match length
                  135
% identity
                  76
NCBI Description
                  (AC006224) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216072
Seq. ID
                  LIB3147-032-Q1-K1-C11
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1839188
BLAST score 500
E value 1.0e-50
Match length 149

% identity 63

NCBI Description (U86081) root hair defective 3.[Arabidopsis thaliana]



```
Seq. No.
                   216073
Seq. ID
                   LIB3147-032-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3421109
BLAST score
                   595
E value
                   8.0e-62
Match length
                   127
% identity
NCBI Description
                  (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
                   thaliana]
Seq. No.
                   216074
Seq. ID
                   LIB3147-032-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g4469023
BLAST score
                   374
E value
                   7.0e-36
Match length
                   121
% identity
                   64
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   216075
Seq. ID
                   LIB3147-032-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   q2895866
BLAST score
                   604
E value
                   7.0e-63
Match length
                   152
% identity
                   76
NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase
                   [Oryza sativa]
Seq. No.
                   216076
Seq. ID
                   LIB3147-032-Q1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1173253
BLAST score
                   552
E value
                   9.0e-57
Match length
                   123
                   92
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3 >gi_543317_pir__S41170 ribosomal protein S3 - mouse >gi_57728_emb_CAA35916_ (X51536)
                   ribosomal protein S3 (AA 1-243) [Rattus rattus]
                   >gi_439522_emb CAA54167 (X76772) ribosomal protein S3 [Mus
                   musculus]
                   216077
Seq. No.
Seq. ID
                   LIB3147-032-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g4049349
BLAST score
                   245
E value
                   9.0e-21
```

NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

88

Match length

% identity



```
Seq. No.
                    216078
Seq. ID
                    LIB3147-032-Q1-K1-D11
Method
                    BLASTX
NCBI GI
                    g2959767
BLAST score
                    423
E value
                    1.0e-41
Match length
                   149
% identity
                    56
                    (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
NCBI Description
                    (AC005309) glutathione-conjugate transporter AtMRP4
                    [Arabidopsis thaliana]
Seq. No.
                    216079
Seq. ID
                   LIB3147-032-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g4206122
BLAST score
                   167
E value
                   1.0e-11
Match length
                   40
% identity
                   80
NCBI Description
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                   crystallinum]
Seq. No.
                   216080
Seq. ID
                   LIB3147-032-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g548852
BLAST score
                   361
E value
                   2.0e-34
Match length
                   82
% identity
                   80
                   40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
NCBI Description
                   subunit ribosomal protein [Oryza sativa]
Seq. No.
                   216081
Seq. ID
                   LIB3147-032-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2281633
BLAST score
                   387
E value
                   2.0e-37
Match length
                   123
% identity
                   63
                   (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   216082
Seq. ID
                   LIB3147-032-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g1703375
```

BLAST score 677
E value 2.0e-71
Match length 132

Match length 132 % identity 100 NCPL Pagarintian ADD

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)

DcARF1 [Daucus carota]

% identity

55



```
Seq. No.
                   216083
Seq. ID
                   LIB3147-032-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g3334405
BLAST score
                   566
E value
                   2.0e-58
Match length
                   149
% identity
                   78
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
                   >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
Seq. No.
                   216084
Seq. ID
                  LIB3147-032-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1653702
BLAST score
                   458
E value
                   9.0e - 46
Match length
                  148
% identity
                   59
NCBI Description
                  (D90915) dihydrolipoamide acetyltransferase component (E2)
                  of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.
                  216085
Seq. ID
                  LIB3147-032-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q3858935
BLAST score
                  327
E value
                  2.0e-30
Match length
                  88
% identity
                  (AL021636) synaptobrevin-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
Seq. No.
                  216086
Seq. ID
                  LIB3147-032-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1710551
BLAST score
                  179
E value
                  4.0e-13
Match length
                  34
% identity
                  91
NCBI Description
                  60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728
                   (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                  216087
Seq. ID
                  LIB3147-032-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g322641
BLAST score
                  467
E value
                  8.0e-47
Match length
                  141
```

30219

NCBI Description beta-1,3-glucanase homolog (clone A6) - rape (fragment)



>gi_17738_emb_CAA49513_ (X69887) beta-1,3-glucanase homologue [Brassica napus]

Seq. No. 216088 Seq. ID LIB3147-032-Q1-K1-E2 Method BLASTX NCBI GI q4140691 BLAST score 401 E value 4.0e-39 Match length 143 % identity 52 NCBI Description (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus] 216089 Seq. No. Seq. ID LIB3147-032-Q1-K1-E3 Method BLASTX NCBI GI g2347054 BLAST score 634 2.0e-66 E value Match length 152 % identity 80 (X96791) arginine decarboxylase [Vitis vinifera] NCBI Description Seq. No. 216090 LIB3147-032-Q1-K1-E5 Seq. ID Method BLASTX g1524121 NCBI GI BLAST score 686 E value 2.0e-72 Match length 153 % identity 84 NCBI Description (X96539) malate dehydrogenase [Mesembryanthemum crystallinum] Seq. No. 216091 Seq. ID LIB3147-032-Q1-K1-E6 Method BLASTX NCBI GI q3482921 BLAST score 223 E value 3.0e-18 85 Match length 48 % identity NCBI Description (AC003970) Unknown protein [Arabidopsis thaliana] Seq. No. 216092 Seq. ID LIB3147-032-Q1-K1-E9 Method BLASTX NCBI GI g3152660 BLAST score 216 E value 2.0e-17

NCBI Description (AF064603) GA17 protein [Homo sapiens]

123

216093

34

Seq. ID LIB3147-032-Q1-K1-F1

Match length

% identity

Seq. No.

Method BLASTX



NCBI GI g1350680 BLAST score 166 E value 1.0e-11 Match length 35 % identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 216094

Seq. ID LIB3147-032-Q1-K1-F11

Method BLASTX
NCBI GI g2662343
BLAST score 324
E value 5.0e-30
Match length 64
% identity 97

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 216095

Seq. ID LIB3147-032-Q1-K1-F12

Method BLASTX
NCBI GI g3068809
BLAST score 483
E value 1.0e-48
Match length 118
% identity 81

NCBI Description (AF059295) Skp1 homolog [Arabidopsis thaliana]

Seq. No. 216096

Seq. ID LIB3147-032-Q1-K1-F3

Method BLASTX
NCBI GI g2511590
BLAST score 599
E value 3.0e-62
Match length 143
% identity 81

NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome

component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis

thaliana]

Seq. No. 216097

Seq. ID LIB3147-032-Q1-K1-F4

Method BLASTX
NCBI GI g2244970
BLAST score 375
E value 5.0e-36
Match length 117
% identity 58

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

>gi 2326365 emb CAA74765 (Y14423) putative cell wall

protein [Arabidopsis thaliana]

Seq. No. 216098

Seq. ID LIB3147-032-Q1-K1-F6

Method BLASTX NCBI GI g2062172 BLAST score 529



```
4.0e-54
E value
Match length
                   129
                   74
% identity
                   (AC001645) unknown protein [Arabidopsis thaliana]
NCBI Description
                   216099
Seq. No.
                   LIB3147-032-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   g1350680
NCBI GI
BLAST score
                   536
E value
                   7.0e-55
                   125
Match length
% identity
                   79
                  60S RIBOSOMAL PROTEIN L1
NCBI Description
Seq. No.
                   216100
                   LIB3147-032-Q1-K1-G11
Seq. ID
Method
                   BLASTX
                   g2129610
NCBI GI
BLAST score
                   324
                   5.0e-30
E value
Match length
                   88
                   75
% identity
                   heat shock protein 17.6K - Arabidopsis thaliana
NCBI Description
                   >gi 984044 emb CAA61675 (X89504) 17.6 kD HSP [Arabidopsis
                   thaliana]
                   216101
Seq. No.
                   LIB3147-032-Q1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1061040
BLAST score
                   638
                   7.0e-67
E value
Match length
                   138
                   85
% identity
                   (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
NCBI Description
                   >gi 1587694 prf 2207220A sterol C-methyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   216102
                   LIB3147-032-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g126770
BLAST score
                   698
                   7.0e-74
E value
Match length
                   136
% identity
                   98
NCBI Description
                   MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate
                   synthase (EC 4.1.3.2) - upland cotton >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
                   [Gossypium hirsutum]
```

LIB3147-032-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI g4567210 BLAST score 453

Match length

69



```
E value
                   4.0e-45
Match length
                   95
% identity
NCBI Description
                   (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   216104
Seq. ID
                   LIB3147-032-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   q2459433
BLAST score
                   211
E value
                   9.0e-17
Match length
                   80
% identity
                   61
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216105
                   LIB3147-032-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1172995
BLAST score
                   209
                   1.0e-16
E value
Match length
                   92
% identity
                   52
NCBI Description
                   60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]
                   >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
                   norvegicus]
                   216106
Seq. No.
Seq. ID
                   LIB3147-032-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   q4406780
BLAST score
                   420
E value
                   1.0e-41
Match length
                   94
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   216107
Seq. ID
                   LIB3147-032-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g2924772
BLAST score
                   588
E value
                   5.0e-61
Match length
                   125
                   87
% identity
                  (AC002334) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216108
Seq. ID
                   LIB3147-033-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1173043
BLAST score
                   245
E value
                   9.0e-21
```

% identity



```
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi_479441_pir__S33899 ribosomal
NCBI Description
                  protein L38 - tomato (cv. Moneymaker)
                  >gi 313027 emb CAA49599 (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
                  216109
Seq. No.
                  LIB3147-033-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4160280
BLAST score
                  438
E value
                  2.0e-43
Match length
                  118
                   64
% identity
NCBI Description
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
                  216110
Seq. No.
                  LIB3147-033-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2828280
BLAST score
                  439
E value
                  1.0e-43
Match length
                  88
                   91
% identity
NCBI Description
                  (AL021687) putative protein [Arabidopsis thaliana]
                  >gi_2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  216111
                  LIB3147-033-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3821793
BLAST score
                  723
E value
                  8.0e-77
Match length
                  145
% identity
                   92
NCBI Description (Y11526) casein kinase II alpha subunit [Zea mays]
Seq. No.
                   216112
Seq. ID
                  LIB3147-033-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   g2335099
BLAST score
                   359
E value
                   3.0e - 34
Match length
                  111
% identity
                   62
                  (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216113
Seq. ID
                  LIB3147-033-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2244773
BLAST score
                  96
E value
                   3.0e-09
Match length
                  56
```

30224

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                  216114
                  LIB3147-033-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4335864
BLAST score
                  635
E value
                  2.0e-66
Match length
                  147
                  76
% identity
NCBI Description
                  (AF052040) calreticulin [Berberis stolonifera]
Seq. No.
                  216115
                  LIB3147-033-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3695019
BLAST score
                  368
E value
                  3.0e - 35
Match length
                  122
                  58
% identity
                  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216116
                  LIB3147-033-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  412
E value
                  1.0e-40
Match length
                  81
                  99
% identity
                  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
NCBI Description
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
                  216117
Seq. No.
Seq. ID
                  LIB3147-033-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  517
E value
                  1.0e-52
Match length
                  118
% identity
                  83
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                  216118
                  LIB3147-033-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q584825
BLAST score
                  604
                  7.0e-63
E value
Match length
                  120
                  93
% identity
                  B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
NCBI Description
```

30225

carota]

>gi 297889 emb CAA51078 (X72385) B2 protein [Daucus

Seq. ID

Method

NCBI GI

E value Match length

BLAST score



```
Seq. No.
                  216119
                  LIB3147-033-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  q1856971
NCBI GI
BLAST score
                  242
                  1.0e-20
E value
                  54
Match length
                  89
% identity
                  (D26058) This gene is specifically expressed at the S phase
NCBI Description
                  during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
                  216120
Seq. No.
                  LIB3147-033-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  q3643594
NCBI GI
                  162
BLAST score
                  4.0e-11
E value
                  40
Match length
                  78
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                  216121
Seq. No.
                  LIB3147-033-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170619
                  309
BLAST score
                  9.0e-29
E value
Match length
                  96
                  66
% identity
                  KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830
NCBI Description
                  kinesin-related protein katA - Arabidopsis thaliana
                  >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor
                  protein heavy chain [Arabidopsis thaliana]
                  >gi_2911084_emb_CAA17546_ (AL021960) kinesin-related
                  protein katA [Arabidopsis thaliana]
Seq. No.
                  216122
Seq. ID
                  LIB3147-033-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1706377
BLAST score
                  619
                  1.0e-64
E value
Match length
                  141
                   79
% identity
NCBI Description
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
                   4-REDUCTASE) >gi 499018 emb CAA53578 (X75964)
                  dihydroflavonol reductase [Vitis vinifera]
Seq. No.
                  216123
```

30226

LIB3147-033-Q1-K1-D2

BLASTX

592 8.0e-68

131

g441457



% identity (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon NCBI Description esculentum] 216124 Seq. No. LIB3147-033-Q1-K1-D4 Seq. ID Method BLASTX g2961390 NCBI GI 504 BLAST score 2.0e-51 E value 106 Match length % identity 87 (AL022141) beta-galactosidase like protein [Arabidopsis NCBI Description thaliana] Seq. No. 216125 LIB3147-033-Q1-K1-D5 Seq. ID Method BLASTX q4544427 NCBI GI 366 BLAST score 3.0e - 35E value 76 Match length 86 % identity (AC006955) putative ferredoxin-thioredoxin reductase NCBI Description [Arabidopsis thaliana] 216126 Seq. No. LIB3147-033-Q1-K1-D7 Seq. ID Method BLASTX g549732 NCBI GI 215 BLAST score 2.0e-17 E value 67 Match length 55 % identity HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION NCBI Description >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_ (Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF [Saccharomyces cerevisiae] Seq. No. 216127 LIB3147-033-Q1-K1-D8 Seq. ID Method BLASTX NCBI GI q3522952 BLAST score 125 E value 1.0e-12 Match length 91 49 % identity (AC004411) putative alcohol dehydrogenase [Arabidopsis NCBI Description thaliana]

Citai

Seq. No.

Seq. ID LIB3147-033-Q1-K1-D9

216128

Method BLASTX NCBI GI g3355468



```
BLAST score
                  535
                  8.0e-55
E value
Match length
                  123
                  89
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                  216129
Seq. No.
Seq. ID
                  LIB3147-033-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4454020
BLAST score
                  147
                  1.0e-09
E value
Match length
                  93
% identity
                  46
                  (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
                  216130
Seq. No.
                  LIB3147-033-Q1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g433664
BLAST score
                  63
E value
                  8.0e-27
Match length
                  163
                  88
% identity
NCBI Description A.thaliana for Sec61 beta-subunit homolog
Seq. No.
                  216131
                  LIB3147-033-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244832
BLAST score
                  166
E value
                  2.0e-11
Match length
                  63
% identity
                  56
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216132
                  LIB3147-033-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063710
BLAST score
                  479
E value
                  2.0e-48
Match length
                  109
% identity
                  81
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                  216133
Seq. No.
Seq. ID
                  LIB3147-033-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4263721
BLAST score
                  545
E value
                  4.0e-56
                  111
Match length
% identity
                   95
NCBI Description
                  (AC006223) putative DNA repair protein RAD50 [Arabidopsis
```

thaliana]

NCBI Description



```
Seq. No.
                  216134
                  LIB3147-033-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500378
BLAST score
                  388
E value
                  1.0e-37
                  85
Match length
                  84
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                  216135
                  LIB3147-033-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3786011
BLAST score
                  625
E value
                  2.0e-65
Match length
                  138
                  85
% identity
NCBI Description
                  (AC005499) putative elongation factor [Arabidopsis
                  thaliana]
Seq. No.
                  216136
                  LIB3147-033-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543868
BLAST score
                  309
E value
                  3.0e-28
Match length
                  70
% identity
                  80
                  ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
NCBI Description
                  >gi 1076683 pir B47493 H+-transporting ATP synthase (EC
                  3.6.1.34) epsilon chain - sweet potato
                  >gi_303625_dbj_BAA03527_ (D14700) F1-ATPase epsilon-subunit
                   [Ipomoea batatas]
Seq. No.
                  216137
Seq. ID
                  LIB3147-033-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2983447
BLAST score
                  203
E value
                   7.0e-16
Match length
                  134
% identity
                  40
NCBI Description
                  (AE000714) large subunit of isopropylmalate isomerase
                   [Aquifex aeolicus]
Seq. No.
                  216138
Seq. ID
                  LIB3147-033-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g4263704
BLAST score
                  195
E value
                  6.0e-15
Match length
                  109
% identity
                  41
```

[Arabidopsis thaliana]

(AC006223) putative sugar starvation-induced protein

Method

BLASTX



```
Seq. No.
                  216139
Seq. ID
                  LIB3147-033-Q1-K1-G12
Method
                  BLASTN
NCBI GI
                  g3849811
BLAST score
                  36
E value
                  1.0e-10
Match length
                  52
% identity
                  92
                  Arabidopsis thaliana chromosome I BAC T2P11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  216140
Seq. No.
Seq. ID
                  LIB3147-033-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3355468
BLAST score
                  328
                  1.0e-30
E value
Match length
                  70
% identity
                  94
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  216141
Seq. ID
                  LIB3147-033-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3132478
BLAST score
                  192
E value
                  9.0e-15
Match length
                  101
% identity
                  43
NCBI Description (AC003096) bZIP-like protein [Arabidopsis thaliana]
Seq. No.
                  216142
Seq. ID
                  LIB3147-033-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2511535
BLAST score
                  166
E value
                  9.0e-12
Match length
                  31
% identity
                  100
NCBI Description (AF008122) alpha-tubulin 3 [Eleusine indica]
                  216143
Seq. No.
Seq. ID
                  LIB3147-033-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q1710551
BLAST score
                  248
                  2.0e-21
E value
                  47
Match length
                  96
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728
                   (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                  216144
                  LIB3147-034-Q1-K1-A1
Seq. ID
```



q3341679 NCBI GI BLAST score 387 E value 1.0e-37 Match length 97 % identity 74 (AC003672) dynamin-like protein phragmoplastin 12 NCBI Description [Arabidopsis thaliana] Seq. No. 216145 LIB3147-034-Q1-K1-A4 Seq. ID BLASTX g1173466

Method NCBI GI BLAST score 260 8.0e-23 E value 98 Match length 50 % identity

POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L NCBI Description

> >gi_1078857_pir__S44645 F37A4.8 protein - Caenorhabditis elegans >gi 458966 (U00032) similar to entire SN2L HUMAN,

possible global transcription activator SNF2L

[Caenorhabditis elegans]

Seq. No. 216146

LIB3147-034-Q1-K1-A5 Seq. ID

Method BLASTX NCBI GI g3953471 BLAST score 394 1.0e-38 E value 94 Match length 80 % identity

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 216147

LIB3147-034-Q1-K1-A6 Seq. ID

Method BLASTX NCBI GI g3953471 BLAST score 118 3.0e-09 E value Match length 87

% identity 49

(AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description

Seq. No. 216148

LIB3147-034-Q1-K1-A9 Seq. ID

Method BLASTX NCBI GI q730526 BLAST score 397 E value 1.0e-38 Match length 99 % identity 77

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

> >qi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 216149

Seq. ID LIB3147-034-Q1-K1-B10

E value

3.0e - 32



```
BLASTX
Method
                  g3851636
NCBI GI
BLAST score
                  565
                   3.0e-58
E value
                  135
Match length
                   81
% identity
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   216150
Seq. No.
                  LIB3147-034-Q1-K1-B11
Seq. ID
                  BLASTN
Method
                   g4454447
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
                   79
Match length
                   86
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   216151
Seq. No.
                   LIB3147-034-Q1-K1-B12
Seq. ID
Method
                   BLASTX
                   g3142289
NCBI GI
BLAST score
                   567
                   2.0e-58
E value
                   144
Match length
% identity
                   77
                   (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                   gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                   216152
                   LIB3147-034-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g1518540
NCBI GI
                   288
BLAST score
                   3.0e-26
E value
Match length
                   86
                   67
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   216153
Seq. No.
                   LIB3147-034-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4544407
                   194
BLAST score
                   4.0e-15
E value
Match length
                   61
                   52
% identity
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   216154
Seq. No.
                   LIB3147-034-Q1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g81857
BLAST score
                   340
```



```
Match length
                  71
% identity
                  IgE-dependent histamine-releasing factor homolog - alfalfa
NCBI Description
                   (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally
                  controlled tumor protein [Medicago sativa]
                  216155
Seq. No.
                  LIB3147-034-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1170898
NCBI GI
BLAST score
                  340
                  3.0e - 32
E value
                  97
Match length
                  72
% identity
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial
                   - cider tree >gi 473206_emb_CAA55383_ (X78800)
                  mitochondrial malate dehydrogenase [Eucalyptus gunnii]
                   216156
Seq. No.
                  LIB3147-034-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                   g421929
NCBI GI
                   509
BLAST score
                   7.0e-52
E value
Match length
                   104
                   15
% identity
                  ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
NCBI Description
                   ubiquitin [Lycopersicon esculentum]
                   216157
Seq. No.
                   LIB3147-034-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g4263702
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
Match length
                   55
                   69
% identity
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216158
                   LIB3147-034-Q1-K1-C3
Seq. ID
Method
                   BLASTX
                   q1361983
NCBI GI
                   378
BLAST score
                   1.0e-36
E value
Match length
                   97
% identity
                   74
NCBI Description ARP protein - Arabidopsis thaliana >gi_886434 emb_CAA89858_
                   (Z49776) ARP protein [Arabidopsis thalīana]
                   216159
Seq. No.
                   LIB3147-034-Q1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1173327
```

30233

346

6.0e-33

BLAST score

E value

E value

Match length

4.0e-29



```
Match length
                  77
                  88
% identity
                  U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
NCBI Description
                  >gi 322619_pir__S30580 U2 snRNP protein A' - Arabidopsis
                  thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear
                  ribonucleoprotein A' [Arabidopsis thaliana]
                  216160
Seq. No.
                  LIB3147-034-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  g3851001
NCBI GI
                  213
BLAST score
                  2.0e-17
E value
Match length
                  44
                  95
% identity
                   (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2
NCBI Description
                   [Zea mays]
                  216161
Seq. No.
                  LIB3147-034-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g1657948
NCBI GI
                  243
BLAST score
                  7.0e-21
E value
                  71
Match length
                   68
% identity
                  (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                  216162
                  LIB3147-034-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                   g3258570
NCBI GI
BLAST score
                   226
                   7.0e-19
E value
                   62
Match length
                   69
% identity
                  (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   216163
Seq. No.
                   LIB3147-034-01-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q129248
                   165
BLAST score
                   2.0e-11
E value
                   96
Match length
                   21
% identity
                   ORGAN SPECIFIC PROTEIN S2 >gi_72318_pir__KNPMS2 protein S2
NCBI Description
                   - garden pea >gi_295831_emb_CAA35944_ (X51595) S2 protein
                   [Pisum sativum]
                   216164
Seq. No.
                   LIB3147-034-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g731097
                   297
BLAST score
```



% identity VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) NCBI Description (V-ATPASE 28 KD ACCESSORY PROTEIN) >gi_1083086 pir A55910 subunit D vacuolar H(+)-ATPase - bovine >gi_517446 (U11927) vacuolar H-ATPase subunit D [Bos gaurus] 216165 Seq. No. LIB3147-034-Q1-K1-D11 Seq. ID BLASTN Method g3334857 NCBI GI 230 BLAST score 1.0e-126 E value 329 Match length 93 % identity Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2 NCBI Description genes 216166 Seq. No. LIB3147-034-Q1-K1-D12 Seq. ID BLASTX Method g1168196 NCBI GI

401 BLAST score 3.0e-39 E value 89 Match length 91 % identity

14-3-3-LIKE PROTEIN >gi 555974 (U15036) 14-3-3-like protein NCBI Description

[Pisum sativum]

216167 Seq. No. LIB3147-034-Q1-K1-D2 Seq. ID

BLASTX Method g3334113 NCBI GI 334 BLAST score 2.0e-31 E value 75 Match length 85 % identity

ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015) NCBI Description

acyl-CoA-binding protein [Gossypium hirsutum]

216168 Seq. No.

LIB3147-034-Q1-K1-D3 Seq. ID

BLASTX Method NCBI GI q3080415 BLAST score 211 3.0e-17 E value Match length 51 75 % identity

(AL022604) cysteine proteinase - like protein [Arabidopsis NCBI Description

thaliana]

216169 Seq. No.

LIB3147-034-Q1-K1-D6 Seq. ID

Method BLASTX NCBI GI g3169656 370 BLAST score 9.0e-36 E value Match length 96



```
% identity
                  (AF067141) gamma-glutamyl hydrolase [Arabidopsis thaliana]
NCBI Description
                  216170
Seq. No.
                  LIB3147-034-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  q3834325
NCBI GI
BLAST score
                   226
                   8.0e-19
E value
                   92
Match length
                   53
% identity
                   (AC005679) Strong similarity to gb_AF067141 gamma-glutamyl
NCBI Description
                   hydrolase from Arabidopsis thaliana. ESTs gb_R83955,
                   gb_T45062, gb_T22220, gb_AA586207, gb_AI0998\overline{5}1 and
                   gb AI00672 come from this gene. [Arabidopsis thaliana]
                   216171
Seq. No.
                   LIB3147-034-Q1-K1-D8
Seq. ID
Method
                   BLASTN
                   q409574
NCBI GI
BLAST score
                   41
                   7.0e-14
E value
                   49
Match length
% identity
                   96
                   Atriplex nummularia glyceraldehyde-3-phosphate
NCBI Description
                   dehydrogenase (GAPDH) mRNA, complete cds.
                   >gi_414606_emb_X75597_ANDAP3DH A.nummularia mRNA for
                   glyceraldehyde-3-phosphate dehydrogenase
                   216172
Seq. No.
                   LIB3147-034-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g3128173
NCBI GI
                   539
BLAST score
                   3.0e-55
E value
                   119
Match length
                   86
% identity
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   216173
Seq. No.
                   LIB3147-034-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   q585960
NCBI GI
BLAST score
                   142
                   1.0e-08
E value
                   39
Match length
                   74
 % identity
                   PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
NCBI Description
                   >gi_433665_emb_CAA81412_ (Z26753) Sec61 beta-subunit
                   homolog [Arabidopsis thaliana]
                   216174
 Seq. No.
                   LIB3147-034-Q1-K1-E11
 Seq. ID
                   BLASTX
 Method
                   g4006860
 NCBI GI
```

472

2.0e-47

BLAST score

E value



```
Match length
                  105
                  80
% identity
                  (Z99707) thiol-disulfide interchange like protein
NCBI Description
                   [Arabidopsis thaliana]
                  216175
Seq. No.
                  LIB3147-034-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g1172977
NCBI GI
BLAST score
                   366
                   3.0e-35
E value
Match length
                  85
                   84
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                   216176
                   LIB3147-034-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   q4191791
NCBI GI
                   291
BLAST score
                   1.0e-30
E value
                   95
Match length
% identity
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   216177
Seq. No.
                   LIB3147-034-Q1-K1-E9
Seq. ID
Method
                   BLASTX
                   q3236259
NCBI GI
                   237
BLAST score
                   7.0e-20
E value
                   74
Match length
                   57
% identity
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   216178
                   LIB3147-034-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q1729868
NCBI GI
                   543
BLAST score
                   9.0e-56
E value
                   139
Match length
                   73
 % identity
                   PROBABLE T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA)
 NCBI Description
                    (CCT-BETA) >gi_1177337_emb_CAA93213_ (Z69239) unknown
                   [Schizosaccharomyces pombe]
                   216179
 Seq. No.
                   LIB3147-034-Q1-K1-F4
 Seq. ID
```

Method BLASTX g2288986 NCBI GI 349 BLAST score 3.0e - 33E value 97 Match length



```
% identity
                  (AC002335) glyoxalase II isolog [Arabidopsis thaliana]
NCBI Description
                  216180
Seq. No.
                  LIB3147-034-Q1-K1-F5
Seq. ID
                  BLASTN
Method
                  g2865522
NCBI GI
                  43
BLAST score
                  4.0e-15
E value
                  71
Match length
                  90
% identity
                  Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  216181
                  LIB3147-034-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                   g2369714
NCBI GI
                   474
BLAST score
                   6.0e-48
E value
                   91
Match length
                   97
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   216182
Seq. No.
                   LIB3147-034-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4262250
                   482
BLAST score
                   8.0e-49
E value
                   97
Match length
                   94
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   216183
Seq. No.
                   LIB3147-034-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g2662341
NCBI GI
BLAST score
                   542
                   1.0e-55
E value
                   123
Match length
                   89
% identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
Seq. No.
                   216184
                   LIB3147-034-Q1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2392769
BLAST score
                   284
E value
                   1.0e-25
                   89
Match length
                   64
 % identity
                   (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
```

30238

thaliana]

Seq. ID Method



```
216185
Seq. No.
                  LIB3147-034-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g3608133
NCBI GI
                   254
BLAST score
                   7.0e-22
E value
                   68
Match length
                   66
% identity
                  (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   216186
Seq. No.
                   LIB3147-034-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g1928981
NCBI GI
                   444
BLAST score
                   2.0e-44
E value
                   97
Match length
                   56
% identity
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   216187
Seq. No.
                   LIB3147-034-Q1-K1-H6
Seq., ID
                   BLASTX
Method
                   g4262186
NCBI GI
                   396
BLAST score
                   9.0e-39
E value
                   94
Match length
                   82
% identity
                   (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   216188
Seq. No.
                   LIB3147-035-Q1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3869088
BLAST score
                   539
E value
                   2.0e-55
                   104
Match length
                   99
% identity
                   (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                   216189
Seq. No.
                   LIB3147-035-Q1-K1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1439609
BLAST score
                   115
E value
                   3.0e-13
Match length
                   62
                   74
 % identity
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
 NCBI Description
                   hirsutum]
                   216190
 Seq. No.
```

30239

LIB3147-035-Q1-K1-A6

BLASTX



```
g2497753
NCBI GI
                  345
BLAST score
                  2.0e-32
E value
                  114
Match length
                  53
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
                   216191
Seq. No.
                  LIB3147-035-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g3738289
NCBI GI
BLAST score
                   261
                   1.0e-22
È value
                   68
Match length
                   72
% identity
                   (AC005309) Not56-like protein [Arabidopsis thaliana]
NCBI Description
                   216192
Seq. No.
                   LIB3147-035-Q1-K1-A8
Seq. ID
                   BLASTX
Method
                   q1136586
NCBI GI
BLAST score
                   166
                   2.0e-11
E value
                   74
Match length
                   49
% identity
                   (U41744) PDGF associated protein [Rattus norvegicus]
NCBI Description
                   >gi_1589641_prf__2211382A platelet-derived growth
                   factor-associated protein [Rattus norvegicus]
                   216193
Seq. No.
                   LIB3147-035-Q1-K1-B5
Seq. ID
                   BLASTX
Method
                   g3860251
NCBI GI
                   504
BLAST score
                   4.0e-51
E value
Match length
                   118
 % identity
                   81
                   (AC005824) putative permease [Arabidopsis thaliana]
NCBI Description
                   216194
 Seq. No.
                   LIB3147-035-Q1-K1-B6
 Seq. ID
                   BLASTX
 Method
                   g3860251
 NCBI GI
                   502
 BLAST score
                   6.0e-51
 E value
 Match length
                   119
                    79
 % identity
                   (AC005824) putative permease [Arabidopsis thaliana]
 NCBI Description
                   216195
 Seq. No.
                   LIB3147-035-Q1-K1-B8
 Seq. ID
                   BLASTX
 Method
                    q1008904
 NCBI GI
```

30240

504

4.0e-51

BLAST score

E value

Match length

145



```
Match length
 % identity
NCBI Description (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
                   216196
 Seq. No.
                   LIB3147-035-Q1-K1-C3
 Seq. ID
                   BLASTX
 Method
                   q3023751
 NCBI GI
                   343
 BLAST score
                    3.0e-32
 E value
                    129
 Match length
                    36
 % identity
                   70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
 NCBI Description
                    ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                    peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                    >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase
                    [Triticum aestivum]
                    216197
 Seq. No.
                    LIB3147-035-Q1-K1-C5
 Seq. ID
                    BLASTX
 Method
                    g1351279
 NCBI GI
                    296
 BLAST score
                    9.0e-27
 E value
                    90
 Match length
                    69
 % identity
                    TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 NCBI Description
                    >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase
                    [Petunia x hybrida]
                    216198
 Seq. No.
                    LIB3147-035-Q1-K1-C6
 Seq. ID
                    BLASTX
 Method
                    q3193296
 NCBI GI
                    279
 BLAST score
 E value
                    5.0e-25
 Match length
                    92
                    57
  % identity
 NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]
                    216199
  Seq. No.
                    LIB3147-035-Q1-K1-C7
  Seq. ID
                    BLASTX
  Method
                    g2529707
  NCBI GI
  BLAST score
                    290
                    4.0e-26
  E value
  Match length
                    139
  % identity
                    42
  NCBI Description (AF001434) Hpast [Homo sapiens]
                    216200
  Seq. No.
                    LIB3147-035-Q1-K1-C8
  Seq. ID
                    BLASTX
  Method
                    g2506139
  NCBI GI
                     618
  BLAST score
                    2.0e-64
  E value
```

Method NCBI GI

BLAST score



```
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                  (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
                  216201
Seq. No.
                  LIB3147-035-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432860
BLAST score
                  398
                  1.0e-38
E value
                  144
Match length
% identity
                  19
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                  216202
Seq. No.
                  LIB3147-035-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                   q4512619
NCBI GI
BLAST score
                   144
                   6.0e-09
E value
                   51
Match length
% identity
                   57
                   (AC004793) This gene is a member of the formyl transferase
NCBI Description
                   family PF_00551 and may be a pseudogene of gb X74767
                   phosphoribosylglycinamide formyl transferase (PUR3) from
                   Arabidopsis thaliana since our sequence differs from PUR3
                   216203
Seq. No.
                   LIB3147-035-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g2462746
NCBI GI
                   654
BLAST score
                   8.0e-69
E value
                   137
Match length
                   92
% identity
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   216204
Seq. No.
                   LIB3147-035-Q1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346675
                   676
BLAST score
                   3.0e-71
E value
                   140
Match length
% identity
                   NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
NCBI Description
                   >qi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                   bidentis]
 Seq. No.
                   216205
                   LIB3147-035-Q1-K1-E1
 Seq. ID
                   BLASTX
```

g4185515



```
E value
                   2.0e-32
Match length
                  94
                   68
% identity
NCBI Description
                  (AF102824) actin depolymerizing factor 6 [Arabidopsis
                  thaliana]
Seq. No.
                  216206
                  LIB3147-035-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341028
BLAST score
                  646
E value
                  8.0e-68
                  128
Match length
                  98
% identity
                  (AC000104) Strong similarity to 60S ribosomal protein L17
NCBI Description
                   (gb_X01694). EST gb_AA042332 comes from this gene.
                   [Arabidopsis thaliana]
                  216207
Seq. No.
                  LIB3147-035-Q1-K1-E2
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                  g4263048
BLAST score
                  179
E value
                  5.0e-13
Match length
                  52
                  58
% identity
NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]
                  216208
Seq. No.
Seq. ID
                  LIB3147-035-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g4206122
BLAST score
                  629
E value
                  8.0e-66
Match length
                  146
                  82
% identity
NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                  crystallinum]
                  216209
Seq. No.
Seq. ID
                  LIB3147-035-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  726
E value
                  3.0e-77
Match length
                  145
% identity
                  99
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
```

sativum]

Seq. No. 216210

Seq. ID LIB3147-035-Q1-K1-F3

Method BLASTX NCBI GI g3687251 BLAST score 465 E value 1.0e-46

BLAST score

% identity

E value Match length 426 5.0e-42

89



```
114
Match length
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  216211
                  LIB3147-035-Q1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4559388
BLAST score
                  566
E value
                  2.0e-58
Match length
                  143
                  73
% identity
NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216212
                  LIB3147-035-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1730108
BLAST score
                  553
                  6.0e-57
E value
                  144
Match length
% identity
                  73
                 LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                  HYDROXYLASE) >gi_486848_pir__S36233 flavanone 3-hydroxylase
                  homolog - garden petunia
Seq. No.
                  216213
                  LIB3147-035-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2384760
BLAST score
                  201
E value
                  8.0e-16
Match length
                  40
% identity
                  90
NCBI Description (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza
                  sativa]
                  216214
Seq. No.
Seq. ID
                  LIB3147-035-Q1-K1-G12
Method
                  BLASTX
                  g3080401
NCBI GI
BLAST score
                  97
E value
                  6.0e-10
Match length
                  71
% identity
                  53
NCBI Description
                  (AL022603) putative protein [Arabidopsis thaliana]
                  >gi 4455265 emb CAB36801.1 (AL035527) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  216215
                  LIB3147-035-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244734
```

% identity

86



```
(D88414) actin [Gossypium hirsutum]
NCBI Description
                   216216
Seq. No.
                   LIB3147-035-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   q3668082
NCBI GI
BLAST score
                   347
                   8.0e-33
E value
                   118
Match length
                   56
% identity
                   (AC004667) putative DAL1 protein [Arabidopsis thaliana]
NCBI Description
                   216217
Seq. No.
                   LIB3147-035-Q1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3152618
                   284
BLAST score
                   2.0e-25
E value
                   63
Match length
                   79
% identity
                   (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis
                   thaliana]
                   216218
Seq. No.
                   LIB3147-035-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g1200205
NCBI GI
                   163
BLAST score
                   3.0e-23
E value
                   107
Match length
                   53
% identity
                   (X95753) DAG [Antirrhinum majus]
NCBI Description
                   216219
Seq. No.
                   LIB3147-036-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3913927
                    510
BLAST score
                    7.0e-52
E value
                    141
Match length
                    70
% identity
                   ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
NCBI Description
                    SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                    (VACUOLAR INVERTASE) >gi 1084382_pir__S55521
                    beta-fructofuranosidase (EC 3.2.\overline{1.26}) - fava bean
                    >gi_861159_emb_CAA89992_ (Z49831) vacuolar invertase;
beta-fructofuranosidase [Vicia faba]
                    216220
 Seq. No.
                    LIB3147-036-Q1-K1-A10
 Seq. ID
                    BLASTX
Method
NCBI GI
                    g1710551
                    240
 BLAST score
                    2.0e-20
 E value
Match length
                    51
```



60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728 NCBI Description (X95458) ribosomal protein L39 [Zea mays]

216221 Seq. No.

LIB3147-036-Q1-K1-A11 Seq. ID

BLASTX Method g730645 NCBI GI 512 BLAST score 5.0e-52 E value 124 Match length 82 % identity

40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal NCBI Description protein S15 - Arabidopsis thaliana >gi_313152 emb_CAA80679

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788,gb_ATTS0365 come from this gene. [Arabidopsis

thaliana]

216222 Seq. No.

LIB3147-036-Q1-K1-A12 Seq. ID

Method BLASTX g730645 NCBI GI 160 BLAST score 5.0e-11 E value 103 Match length % identity 47

40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal NCBI Description protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788,gb ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 216223

LIB3147-036-Q1-K1-A2 Seq. ID

BLASTX Method g1332579 NCBI GI 285 BLAST score 1.0e-25 E value 62 Match length

% identity (X98063) polyubiquitin [Pinus sylvestris] NCBI Description

Seq. No. 216224

LIB3147-036-Q1-K1-A4 Seq. ID

BLASTX Method g3335335 NCBI GI 287 BLAST score E value 2.0e-37 97 Match length 73 % identity

(AC004512) ESTs gb_F14113 and gb_T42122 come from this NCBI Description

region. [Arabidopsīs thaliana]



```
216225
Seq. No.
                  LIB3147-036-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g629564
NCBI GI
                  240
BLAST score
                  4.0e-39
E value
                  107
Match length
                  79
% identity
                  ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
NCBI Description
                  thaliana
                  216226
Seq. No.
                  LIB3147-036-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g82035
NCBI GI
                   301
BLAST score
                   2.0e-27
E value
                   144
Match length
                   29
% identity
                  ricin E - castor bean (fragment) >gi_169715 (M17631) ricin
NCBI Description
                   E beta chain [Ricinus communis] >gi_225896_prf__1402359A
                   ricin E [Ricinus communis]
                   216227
Seq. No.
                   LIB3147-036-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g4371282
NCBI GI
                   381
BLAST score
                   8.0e-37
E value
                   88
Match length
                   81
% identity
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   216228
Seq. No.
                   LIB31-47-036-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   q4371282
NCBI GI
                   329
BLAST score
                   1.0e-30
E value
Match length
                   80
                   76
 % identity
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   216229
 Seq. No.
                   LIB3147-036-Q1-K1-B4
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g3036802
                   285
 BLAST score
                   7.0e-26
 E value
                   81
Match length
                   63
 % identity
                   (AL022373) putative protein [Arabidopsis thaliana]
 NCBI Description
                   >gi_3805864_emb_CAA21484_ (AL031986) putative protein
```

[Arabidopsis thaliana]

*



Seq. No.

Seq. ID

216230

LIB3147-036-Q1-K1-B5

```
Method
                  BLASTX
NCBI GI
                  g2281639
BLAST score
                  274
                  3.0e-24
E value
Match length
                  133
% identity
                   37
                  (AF003100) AP2 domain containing protein RAP2.7
NCBI Description
                   [Arabidopsis thaliana]
                  216231
Seq. No.
                  LIB3147-036-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  q3036802
NCBI GI
                   262
BLAST score
                   4.0e-23
E value
                   91
Match length
                   55
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3805864_emb_CAA21484_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   216232
Seq. No.
                   LIB3147-036-Q1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1346675
                   605
BLAST score
                   4.0e-63
E value
Match length
                   123
                   93
% identity
                   NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
NCBI Description
                   >gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                   bidentis]
                   216233
Seq. No.
                   LIB3147-036-Q1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3334115
                   682
BLAST score
                   5.0e-72
E value
                   142
Match length
                   61
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
                   216234
Seq. No.
                   LIB3147-036-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g1389640
NCBI GI
BLAST score
                   433
                   8.0e-43
E value
Match length
                   136
 % identity
                   67
```

216240



```
NCBI Description (D86052) PNDKN1 [Pisum sativum]
                  216235
Seq. No.
                  LIB3147-036-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  g4539399
NCBI GI
                  166
BLAST score
                  4.0e-12
E value
                  35
Match length
                  94
% identity
                  (AL035526) ras-like GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  216236
Seq. No.
                  LIB3147-036-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g3885882
NCBI GI
                   195
BLAST score
                   1.0e-21
E value
                   68
Match length
                   75
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
                   216237
Seq. No.
                   LIB3147-036-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g730512
NCBI GI
                   389
BLAST score
                   9.0e-38
E value
                   96
Match length
                   82
% identity
                  RAS-RELATED PROTEIN RIC2 >gi_481506_pir__$38741 GTP-binding
NCBI Description
                   protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758)
                   ras-related GTP binding protein [Oryza sativa]
                   216238
Seq. No.
                   LIB3147-036-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   q1911774
NCBI GI
                   185
BLAST score
                   1.0e-13
E value
Match length
                   78
                   41
 % identity
                   (S83364) putative Rab5-interacting protein {clone L1-57}
NCBI Description
                   [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]
                   216239
 Seq. No.
                   LIB3147-036-Q1-K1-D2
 Seq. ID
 Method
                   BLASTX
                   q3885329
 NCBI GI
                   326
 BLAST score
                   3.0e - 30
 E value
                   92
 Match length
                   70
 % identity
NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]
```



```
LIB3147-036-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   q2191150
NCBI GI
                   407
BLAST score
                   8.0e-40
E value
Match length
                   115
                   31
% identity
NCBI Description (AF007269) similar to mitochondrial carrier family
                   [Arabidopsis thaliana]
                   216241
Seq. No.
                   LIB3147-036-Q1-K1-D6
Seq. ID
                   BLASTX
Method
                   g3980396
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
                   88
Match length
                   62
% identity
NCBI Description (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                   thaliana]
                   216242
Seq. No.
                   LIB3147-036-Q1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q231536
                   564
BLAST score
                   4.0e-58
E value
                   144
Match length
                   75
% identity
                   CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
NCBI Description
                    (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                   AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase
                    (EC 3.4.11.1) - Arabidopsis thaliana
                   >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative
                    leucine aminopeptidase [Arabidopsis thaliana]
                    216243
Seq. No.
                    LIB3147-036-Q1-K1-D8
Seq. ID
                    BLASTX
Method
                    g1350720
NCBI GI
BLAST score
                    380
                    1.0e-36
E value
                    80
Match length
                    89
 % identity
 NCBI Description 60S RIBOSOMAL PROTEIN L32
                    216244
 Seq. No.
                    LIB3147-036-Q1-K1-D9
 Seq. ID
                    BLASTX
 Method
                    q417745
 NCBI GI
                    731
 BLAST score
                    1.0e-77
 E value
                    155
 Match length
                    90
 % identity
 NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                    HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)
```



S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

```
216245
Seq. No.
Seq. ID
                  LIB3147-036-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g122106
                  433
BLAST score
                  8.0e-43
E value
Match length
                  86
% identity
                  100
                  HISTONE H4 >gi 70771 pir HSZM4 histone H4 - maize
NCBI Description
                  >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                  >gi 2119028 pir S60475 histone H4 - garden pea
                  >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                  aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                  thaliana] >gi 166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                  >qi 168501 (M13370) histone H4 [Zea mays] >qi 168503
                  (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914
                  (Z79638) histone H4 homologue [Sesbania rostrata]
                  >gi 3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                  >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
                  [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4
                  [Arabidopsis thaliana]
Seq. No.
                  216246
Seq. ID
                  LIB3147-036-01-K1-E2
Method
                  BLASTX
NCBI GI
                  g122106
BLAST score
                  422
                  2.0e-41
E value
Match length
                  88
% identity
NCBI Description HISTONE H4 >qi 70771 pir HSZM4 histone H4 - maize
                  >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                  >gi 2119028 pir S60475 histone H4 - garden pea
                  >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                  aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                  thaliana] >gi 166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                  >gi 168501 (M13370) histone H4 [Zea mays] >gi_168503
                  (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914
                  (Z79638) histone H4 homologue [Sesbania rostrata]
                  >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                  >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
                  [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4
                  [Arabidopsis thaliana]
Seq. No.
                  216247
Seq. ID
                  LIB3147-036-Q1-K1-E3
Method
                  BLASTX
```

NCBI GI g1708110 BLAST score 249 E value 2.0e-21 101

Match length



```
% identity
                      HISTONE H4 >gi_2119025_pir__S59586 histone H4 (clone
NCBI Description
                      CH-III) - Chlamydomonas reinhardtii >gi 2119027 pir
                      histone H4 - Chlamydomonas reinhardtii \overline{>}gi_5714\overline{7}1 (\overline{\text{U1}}6724)
                      histone H4 [Chlamydomonas reinhardtii] >gi_571476 (U16725)
histone H4 [Chlamydomonas reinhardtii] >gi_576634 (U16825)
histone H4 [Chlamydomonas reinhardtii] >gi_790701 (L41841)
                      histone H4 [Chlamydomonas reinhardtii]
                      216248
Seq. No.
                      LIB3147-036-Q1-K1-E5
Seq. ID
                      BLASTX
Method
                      g266972
NCBI GI
                      204
BLAST score
                      5.0e-16
E value
                      54
Match length
                       65
% identity
                      40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal
NCBI Description
                      protein S29 - rat >gi_1362934_pir_ S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610)
                       homologous to antisense sequence of krev-1, anti oncogene
                       [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein
                       [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29
                       [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein
                       S29 [Homo sapiens] >gi 4506717 ref_NP_001023.1_pRPS29_
                       ribosomal protein S29
                       216249
Seq. No.
                       LIB3147-036-Q1-K1-E8
Seq. ID
Method
                       BLASTX
NCBI GI
                       g3334320
                       524
BLAST score
                       2.0e-53
E value
                       116
Match length
% identity
                       91
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                       ribosome-associated protein p40 [Glycine max]
                       216250
Seq. No.
Seq. ID
                       LIB3147-036-Q1-K1-E9
                       BLASTX
Method
NCBI GI
                       g420285
                       229
BLAST score
                       6.0e-19
E value
Match length
                       98
% identity
                       48
NCBI Description nucleolus-cytoplasm shuttle phosphoprotein - rat
                       216251
Seq. No.
                       LIB3147-036-Q1-K1-F1
Seq. ID
Method
                       BLASTX
NCBI GI
                       g2580438
                       173
BLAST score
                       2.0e-12
E value
```

30252

55

Match length



% identity 64

(D87260) PCF1 [Oryza sativa] NCBI Description

Seq. No.

216252

Seq. ID

LIB3147-036-Q1-K1-F10

Method NCBI GI BLAST score E value

BLASTX g4262140 332 5.0e-31

111

Match length % identity

NCBI Description

61 (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No.

216253

Seq. ID

LIB3147-036-Q1-K1-F11

BLASTX Method q1172977 NCBI GI 251 BLAST score 8.0e-22 E value 63 Match length 83 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.

216254

LIB3147-036-Q1-K1-G1 Seq. ID

Method BLASTX NCBI GI q1731144 164 BLAST score 2.0e-11 E value 129 Match length 33

% identity

NCBI Description HYPOTHETICAL 28.6 KD PROTEIN T07A5.2 IN CHROMOSOME III

>gi_3879519_emb_CAA88132_ (Z48055) similar to the yeast
hypothetical protein YK10 (Swiss Prot accession number P36125); cDNA EST EMBL:C11826 comes from this gene

[Caenorhabditis elegans]

216255 Seq. No.

LIB3147-036-01-K1-G4 Seq. ID

Method BLASTX NCBI GI q4512619 BLAST score 267 2.0e-23 E value 77 Match length % identity

NCBI Description (AC004793) This gene is a member of the formyl transferase

family PF 00551 and may be a pseudogene of gb X74767 phosphoribosylglycinamide formyl transferase (PUR3) from Arabidopsis thaliana since our sequence differs from PUR3

216256 Seq. No.

LIB3147-036-Q1-K1-G6 Seq. ID

Method BLASTX NCBI GI g2662341 BLAST score 706 E value 7.0e-75



Match length 141 96 % identity (D63580) EF-1 alpha [Oryza sativa] NCBI Description >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa] 216257 Seq. No. LIB3147-036-Q1-K1-G7 Seq. ID BLASTX Method g1694976 NCBI GI 383 BLAST score 5.0e-37 E value 106 Match length 68 % identity (Y09482) HMG1 [Arabidopsis thaliana] NCBI Description >gi 2832361 emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana] 216258 Seq. No. LIB3147-036-Q1-K1-G8 Seq. ID BLASTX Method g2642157 NCBI GI 341 BLAST score 3.0e-55 E value 145 Match length 70 % identity (AC003000) ankyrin-like protein [Arabidopsis thaliana] NCBI Description 216259 Seq. No. LIB3147-036-Q1-K1-H4 Seq. ID BLASTX Method NCBI GI q3319355 342 BLAST score 3.0e-32 E value Match length 120 % identity 62 (AF077407) similar to chaperonin containing TCP-1 complex NCBI Description gamma chain [Arabidopsis thaliana] 216260 Seq. No. LIB3147-036-Q1-K1-H5 Seq. ID BLASTX Method q3319355 NCBI GI

470 BLAST score 2.0e-52 E value Match length 114 %-identity 92

(AF077407) similar to chaperonin containing TCP-1 complex NCBI Description

gamma chain [Arabidopsis thaliana]

Seq. No. 216261

LIB3147-036-Q1-K1-H6 Seq. ID

BLASTX Method g3892057 NCBI GI 497 BLAST score 2.0e-50 E value



```
Match length
                   122
% identity
NCBI Description
                  (AC002330) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216262
                  LIB3147-037-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2351374
BLAST score
                  381
                  1.0e-36
E value
Match length
                  82
% identity
                  89
                  (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  216263
Seq. ID
                  LIB3147-037-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g170352
BLAST score
                  121
E value
                  1.0e-12
                  43
Match length
                  16
% identity
NCBI Description
                  (M74101) hexameric polyubiquitin [Nicotiana sylvestris]
                  >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
                  >gi 4115333 (L81139) ubiquitin [Pisum sativum] >gi 4115335
                   (L81140) ubiquitin [Pisum sativum]
Seq. No.
                  216264
Seq. ID
                  LIB3147-037-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  459
E value
                  7.0e-46
                  97
Match length
                  89
% identity
NCBI Description (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
                  216265
Seq. No.
Seq. ID
                  LIB3147-037-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g100525
BLAST score
                  517
E value
                  6.0e-53
Match length
                  107
% identity
                  23
NCBI Description
                  ubiquitin precursor UbB2 - common sunflower (fragment)
                  >gi 18803 emb CAA40323 (X57003) polyubiquitin protein
```

[Helianthus annuus]

Seq. No. 216266

Seq. ID LIB3147-037-Q1-K1-A8

Method BLASTN NCBI GI g2687434 BLAST score 305 E value 1.0e-171



```
368
Match length
                  96
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                  216267
Seq. No.
                  LIB3147-037-Q1-K1-A9
Seq. ID
                  BLASTN
Method
                  g871509
NCBI GI
                  41
BLAST score
                   5.0e-14
E value
                   53
Match length
                   94
% identity
NCBI Description P.sativum mRNA for small GTP-binding protein (clone pGTP6)
                   216268
Seq. No.
                  LIB3147-037-Q1-K1-B5
Seq. ID
                  BLASTN
Method
                   g1161925
NCBI GI
                   45
BLAST score
                   4.0e-16
E value
                   89
Match length
                   88
% identity
                  Glycine max alpha-carboxyltransferase aCT-1 precursor mRNA,
NCBI Description
                   complete cds
Seq. No.
                   216269
                   LIB3147-037-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g445613
NCBI GI
                   424
BLAST score
                   8.0e-42
E value
                   120
Match length
                   70
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                   216270
                   LIB3147-037-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   q132939
NCBI GI
                   607
BLAST score
E value
                   3.0e-63
                   129
Match length
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal
NCBI Description
                   protein L3 (ARP1) - Arabidopsis thaliana >gi_166858
                   (M32654) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   216271
                   LIB3147-037-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2842489
                   155
BLAST score
                   1.0e-12
E value
                   72
Match length
% identity
                  (AL021749) putative protein [Arabidopsis thaliana]
NCBI Description
```



127

32

Match length % identity

NCBI Description

```
216272
Seq. No.
                  LIB3147-037-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g464981
NCBI GI
                  208
BLAST score
                  1.0e-16
E value
                  40
Match length
                  97
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
                  216273
Seq. No.
                  LIB3147-037-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g4056480
NCBI GI
                  160
BLAST score
                   8.0e-11
E value
                   61
Match length
                   49
% identity
                  (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
                   216274
Seq. No.
                  LIB3147-037-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g2811029
NCBI GI
BLAST score
                   340
                   3.0e - 32
E value
Match length
                   94
                   70
% identity
                  ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)
NCBI Description
                   (ACETYLORNITHINE TRANSAMINASE) (AOTA)
                   >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine
                   aminotransferase [Alnus glutinosa]
Seq. No.
                   216275
                   LIB3147-037-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   q4467157
NCBI GI
                   186
BLAST score
E value
                   7.0e-14
                   114
Match length
                   38
% identity
                   (AL035540) disease resistance response like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   216276
                   LIB3147-037-Q1-K1-C2
Seq. ID
Method
                   BLASTX
                   q2708314
NCBI GI
BLAST score
                   337
                   1.0e-31
E value
```

30257

(AF027727) protein disulfide isomerase RB60 [Chlamydomonas

reinhardtii] >gi 4104541 (AF036939) protein disulfide

NCBI Description



isomerase [Chlamydomonas reinhardtii]

```
Seq. No.
                  216277
Seq. ID
                  LIB3147-037-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1916290
BLAST score
                  232
                   3.0e-19
E value
Match length
                  135
% identity
                   41
NCBI Description
                  (U89876) ALY [Mus musculus]
Seq. No.
                  216278
                  LIB3147-037-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4158232
BLAST score
                  581
E value
                   3.0e-60
Match length
                  118
                   92
% identity
                  (Y18626) reversibly glycosylated polypeptide [Triticum
NCBI Description
                   aestivum]
                  216279
Seq. No.
                  LIB3147-037-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  g3832528
NCBI GI
BLAST score
                   180
                   3.0e-13
E value
Match length
                  114
% identity
                   39
NCBI Description (AF100167) unknown [Glycine max]
                   216280
Seq. No.
Seq. ID
                  LIB3147-037-Q1-K1-D12
Method
                  BLASTN
NCBI GI
                   g1297184
BLAST score
                   35
E value
                   4.0e-10
Match length
                  170
% identity
                   84
                  Arabidopsis thaliana chromosome I cosmid g8261 DNA
NCBI Description
                   (cytosine-5-) methyltransferase, zinc finger protein 1,
                   nucleoporin 98, poly A+ RNA export protein, plasma membrane
                  ATPase 2, and serine/threonine protein kinase genes, co
Seq. No.
                   216281
Seq. ID
                  LIB3147-037-Q1-K1-D3
Method
                  BLASTN
NCBI GI
                   g3355463
BLAST score
                   33
                   6.0e-09
E value
                  57
Match length
                   89
% identity
```

Arabidopsis thaliana chromosome II BAC F12L6 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   216282
                  LIB3147-037-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204761
                  578
BLAST score
                  8.0e-60
E value
                  146
Match length
                   73
% identity
                  (U51192) peroxidase precursor [Glycine max]
NCBI Description
                  216283
Seq. No.
                  LIB3147-037-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4206209
BLAST score
                  240
                   3.0e-20
E value
                   60
Match length
                   68
% identity
                  (AF071527) putative glucan synthase component [Arabidopsis
NCBI Description
                   thaliana] >gi 4263042 gb AAD15311_ (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
Seq. No.
                   216284
Seq. ID
                  LIB3147-037-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                   g2431771
BLAST score
                   251
                   2.0e-21
E value
Match length
                   113
% identity
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
Seq. No.
                   216285
Seq. ID
                   LIB3147-037-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1350680
BLAST score
                   424
E value
                   5.0e-42
Match length
                   102
% identity
                   75
NCBI Description 60S RIBOSOMAL PROTEIN L1
Seq. No.
                   216286
Seq. ID
                   LIB3147-037-Q1-K1-E10
Method
                   BLASTN
NCBI GI
                   g2832639
BLAST score
                   34
                   2.0e-09
E value
                   122
Match length
                   82
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12
                   (ESSAII project)
```

Seq. ID LIB3147-037-Q1-K1-E12

Method BLASTX NCBI GI g2961346



```
565
BLAST score
                  2.0e-58
E value
                  131
Match length
                  79
% identity
                  (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  216288
Seq. No.
                  LIB3147-037-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                  g1346524
NCBI GI
                  479
BLAST score
                  3.0e-48
E value
                  101
Match length
                   93
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900
                   (M73430) S-adenosyl methionine synthetase [Populus
                   deltoides]
                   216289
Seq. No.
                  LIB3147-037-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   q4539292
NCBI GI
                   456
BLAST score
                   1.0e-45
E value
Match length
                   97
                   86
% identity
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis
                   thaliana]
                   216290
Seq. No.
                   LIB3147-037-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   q3046856
NCBI GI
BLAST score
                   33
E value
                   6.0e-09
                   203
Match length
% identity
                   85
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXI22, complete sequence [Arabidopsis thaliana]
                   216291
Seq. No.
                   LIB3147-037-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g2351374
NCBI GI
 BLAST score
                   621
E value
                   6.0e-65
                   138
Match length
                   87
 % identity
                  (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID LIB3147-037-Q1-K1-E7

Method BLASTX NCBI GI g1346524



```
396
BLAST score
                   2.0e-38
E value
Match length
                   101
                   79
 % identity
                   S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
 NCBI Description
                   ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900
                   (M73430) S-adenosyl methionine synthetase [Populus
                   deltoides]
                   216293
 Seq. No.
                   LIB3147-037-Q1-K1-E9
 Seq. ID
                   BLASTX
 Method
                   g4539405
 NCBI GI
                   402
 BLAST score
                   2.0e-39
 E value
 Match length
                   93
                   82
 % identity
                   (AL049524) putative ribosomal protein L9, cytosolic
 NCBI Description
                   [Arabidopsis thaliana]
                   216294
Seq. No.
                   LIB3147-037-Q1-K1-F10
Seq. I
 Method
                   BLASTX
                   g3878119
 NCBI GI
                   310
 BLAST score
                   2.0e-28
 E value
                   126
 Match length
 % identity
                   46
                   (Z49068) similar to GTP-binding protein; cDNA EST
 NCBI Description
                   EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709
                    comes from this gene; cDNA EST EMBL:D27708 comes from this
                    gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST
                    yk353
                    216295
 Seq. No.
                   LIB3147-037-Q1-K1-F3
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g3269289
                    162
 BLAST score
                    1.0e-11
 E value
 Match length
                    45
                    71
 % identity
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                    216296
 Seq. No.
                    LIB3147-037-Q1-K1-F6
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q2497538
 BLAST score
                    306
                    6.0e-28
 E value
                    145
 Match length
                    45
 % identity
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
```

Seq. ID LIB3147-037-Q1-K1-F9

pyruvate kinase [Glycine max]

Seq. ID



```
BLASTX
Method
                  g123539
NCBI GI
                  292
BLAST score
                  1.0e-26
E value
                  82
Match length
                  67
% identity
                  17.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.5-E) >gi_169987
NCBI Description
                  (M11395) small heat shock protein [Glycine max]
                  216298
Seq. No.
                  LIB3147-037-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g2760830
NCBI GI
                  638
BLAST score
                  6.0e-67
E value
Match length
                  127
                  88
% identity
                  (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  216299
Seq. No.
                  LIB3147-037-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                   g3123745
NCBI GI
BLAST score
                   649
                   4.0e-68
E value
                  146
Match length
                   84
% identity
                  (AB013447) aluminum-induced [Brassica napus]
NCBI Description
                   216300
Seq. No.
                   LIB3147-037-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g232274
NCBI GI
                   408
BLAST score
                   2.0e-41
E value
                   135
Match length
% identity
                   67
                  17.6 KD CLASS II HEAT SHOCK PROTEIN >gi 71499 pir HHMU17
NCBI Description
                   heat shock protein 17.6-II - Arabidopsis thaliana
                   >gi_16338_emb_CAA45039_ (X63443) heat shock protein 17.6-II
                   [Arabidopsis thaliana]
                   216301
Seq. No.
                   LIB3147-037-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   q3879145
NCBI GI
BLAST score
                   139
                   1.0e-08
E value
                   59
Match length
 % identity
                   46
                   (Z93386) predicted using Genefinder; Similarity to Human
NCBI Description
                   placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5
                   comes from this gene [Caenorhabditis elegans]
                   216302
 Seq. No.
```

LIB3147-037-Q1-K1-G5



```
BLASTX
Method
                  g2497543
NCBI GI
BLAST score
                  658
                  3.0e-69
E value
                  136
Match length
                  97
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__$41379
NCBI Description
                  pyruvate kinase - common tobacco >gi_444023 emb CAA82628
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                  216303
Seq. No.
                  LIB3147-037-Q1-K1-G7
Seq. ID
                  BLASTN
Method
                  q603218
NCBI GI
                  45
BLAST score
                  3.0e-16
E value
                  85
Match length
                  88
% identity
NCBI Description Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
                  complete cds
                   216304
Seq. No.
                  LIB3147-037-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                   q533084
NCBI GI
                   281
BLAST score
E value
                   5.0e-25
                   73
Match length
                   71
% identity
NCBI Description (U07597) delta-9 stearoyl-acyl carrier protein desaturase
                  precursor [Thunbergia alata]
                   216305
Seq. No.
                   LIB3147-037-Q1-K1-G9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1006830
BLAST score
                   33
                   5.0e-09
E value
Match length
                   33
                   100
% identity
                   Gossypium hirsutum acyl-CoA-binding protein mRNA, complete
NCBI Description
                   cds
                   216306
Seq. No.
                   LIB3147-037-Q1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g584795
                   150
BLAST score
                   9.0e-10
E value
                   52
Match length
                   60
% identity
NCBI Description PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi 170295 (M80490)
                   plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
```

Seq. ID LIB3147-037-Q1-K1-H3

Method BLASTX



```
q1174448
NCBI GI
                  328
BLAST score
                  2.0e-30
E value
                  121
Match length
                  58
% identity
                  TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                  (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative
                  [Arabidopsis thaliana]
                  216308
Seq. No.
                  LIB3147-037-Q1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172558
                  320
BLAST score
                  1.0e-29
E value
Match length
                  115
                  54
% identity
                  OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
NCBI Description
                  ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >gi_480122_pir__S36454 porin por1 - garden pea
                  >gi_396819_emb_CAA80988_ (Z25540) Porin [Pisum sativum]
                  216309
Seq. No.
                  LIB3147-037-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g1922937
NCBI GI
BLAST score
                   261
                   7.0e-23
E value
                  91
Match length
                   56
% identity
                  (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs
NCBI Description
                   gb_H76869,gb_T21700,gb_ATTS5089 come from this gene.
                   [Arabidopsis thaliana]
                   216310
Seq. No.
Seq. ID
                  LIB3147-037-Q1-K1-H9
Method
                  BLASTX
                   q2431771
NCBI GI
                   252
BLAST score
                   1.0e-21
E value
Match length
                   113
                   48
% identity
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
                   216311
Seq. No.
Seq. ID
                   LIB3147-037-Q1-K2-A11
Method
                   BLASTX
NCBI GI
                   q967125
                   475
BLAST score
                   8.0e-48
E value
```

Match length 99 59 % identity

NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No. 216312

LIB3147-037-Q1-K2-A12 Seq. ID

Method

NCBI GI

BLASTN

g2687434



```
Method
                   BLASTX
NCBI GI
                   q2351374
BLAST score
                   373
                   7.0e-36
E value
Match length
                   81
                   88
% identity
                   (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                    [Arabidopsis thaliana]
                   216313
Seq. No.
Seq. ID
                   LIB3147-037-Q1-K2-A2
                   BLASTX
Method
NCBI GI
                   q3386546
BLAST score
                   149
E value
                   1.0e-09
Match length
                   55
% identity
                   56
                   (AF079503) H-protein promoter binding factor-2a
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   216314
Seq. ID
                   LIB3147-037-Q1-K2-A4
Method
                   BLASTX
NCBI GI
                   q170354
BLAST score
                   212
E value
                    3.0e-17
Match length
                   42
                   20
% identity
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                    216315
                   LIB3147-037-Q1-K2-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   296
E value
                    2.0e-27
Match length
                   66
                    85
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    216316
Seq. No.
Seq. ID
                    LIB3147-037-Q1-K2-A7
Method
                   BLASTX
NCBI GI
                    q3882081
BLAST score
                    634
E value
                    2.0e-66
Match length
                   136
% identity
                    31
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
                    216317
Seq. No.
Seq. ID
                   LIB3147-037-Q1-K2-A8
```



BLAST score 1.0e-104 E value 272 Match length 93 % identity Eucryphia lucida large subunit 26S ribosomal RNA gene, NCBI Description partial sequence 216318 Seq. No. LIB3147-037-Q1-K2-A9 Seq. ID Method BLASTX NCBI GI g1654144 BLAST score 249 E value 2.0e-21 Match length 70 74 % identity (U38471) small GTP-binding protein rab [Brassica rapa] NCBI Description 216319 Seq. No. LIB3147-037-Q1-K2-B5 Seq. ID Method BLASTN NCBI GI g1161925 BLAST score 33 E value 5.0e-09 77 Match length % identity 86 Glycine max alpha-carboxyltransferase aCT-1 precursor mRNA, NCBI Description complete cds 216320 Seq. No. Seq. ID LIB3147-037-Q1-K2-B6 Method BLASTX NCBI GI q445613 BLAST score 441 E value 8.0e-44Match length 119 % identity 73 NCBI Description ribosomal protein L7 [Solanum tuberosum] Seq. No. 216321 Seq. ID LIB3147-037-Q1-K2-B7 Method BLASTX NCBI GI g548770 BLAST score 628 E value 9.0e-66 135 Match length % identity 83 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal NCBI Description protein L3 - rice >gi_303853_dbj_BA\(\overline{A}\)021\(\overline{55}\)_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No. 216322

Seq. ID LIB3147-037-Q1-K2-B8

Method BLASTX
NCBI GI g2842489
BLAST score 243
E value 6.0e-21
Match length 79



% identity NCBI Description (AL021749) putative protein [Arabidopsis thaliana] Seq. No. 216323 LIB3147-037-Q1-K2-B9 Seq. ID Method BLASTX NCBI GI q464981 BLAST score 210 E value 6.0e-17 Match length 40 97 % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum] Seq. No. 216324 LIB3147-037-Q1-K2-C10 Seq. ID Method BLASTX g2811029 NCBI GI BLAST score 447 E value 2.0e-44Match length 135 64 % identity NCBI Description ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa] Seq. No. 216325 LIB3147-037-Q1-K2-C2 Seq. ID Method BLASTX NCBI GI q2708314 BLAST score 318 2.0e-29 E value Match length 116 % identity NCBI Description (AF027727) protein disulfide isomerase RB60 [Chlamydomonas reinhardtii] >gi 4104541 (AF036939) protein disulfide isomerase [Chlamydomonas reinhardtii] Seq. No. 216326 Seq. ID LIB3147-037-Q1-K2-C3 Method BLASTX NCBI GI g1916290 BLAST score 221 E value 4.0e-18 Match length 78 % identity NCBI Description (U89876) ALY [Mus musculus]

Seq. ID LIB3147-037-Q1-K2-C8

216327

Method BLASTX NCBI GI g4158232 BLAST score 566 2.0e-58 E value Match length 113

Seq. No.

NCBI Description



```
% identity
                  93
                  (Y18626) reversibly glycosylated polypeptide [Triticum
NCBI Description
                  aestivum]
                  216328
Seq. No.
                  LIB3147-037-Q1-K2-D11
Seq. ID
                  BLASTX
Method
                  g3832528
NCBI GI
BLAST score
                  182
                  2.0e-13
E value
Match length
                  114
                  39
% identity
NCBI Description
                  (AF100167) unknown [Glycine max]
                  216329
Seq. No.
                  LIB3147-037-Q1-K2-D3
Seq. ID
                  BLASTN
Method
                  g3355463
NCBI GI
                  33
BLAST score
                  5.0e-09
E value
                  57
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  216330
                  LIB3147-037-Q1-K2-D5
Seq. ID
Method
                  BLASTX
                  q4204761
NCBI GI
                  299
BLAST score
                  3.0e-27
E value
Match length
                  105
                   60
% identity
                  (U51192) peroxidase precursor [Glycine max]
NCBI Description
Seq. No.
                  216331
                  LIB3147-037-Q1-K2-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730583
BLAST score
                   189
                   7.0e-15
E value
Match length
                   56
                   71
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
Seq. No.
                   216332
                   LIB3147-037-Q1-K2-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3176687
BLAST score
                   511
E value
                   5.0e-52
Match length
                   132
                   73
% identity
                  (AC003671) Strong similarity to trehalose-6-phosphate
```

synthase homolog from A. thaliana chromosome 4 contig



gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 216333

Seq. ID LIB3147-037-Q1-K2-E3

Method BLASTX
NCBI GI g1346524
BLAST score 495
E value 4.0e-50
Match length 101
% identity 95

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900 (M73430) S-adenosyl methionine synthetase [Populus

deltoides]

Seq. No. 216334

Seq. ID LIB3147-037-Q1-K2-E5

Method BLASTX
NCBI GI g4539292
BLAST score 442
E value 6.0e-44
Match length 97
% identity 84

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

Seq. No. 216335

Seq. ID LIB3147-037-Q1-K2-E6

Method BLASTN
NCBI GI g3046856
BLAST score 32
E value 1.0e-08

Match length 114 % identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 216336

Seq. ID LIB3147-037-Q1-K2-E7

Method BLASTX
NCBI GI g730449
BLAST score 351
E value 3.0e-39
Match length 104
% identity 75

NCBI Description 60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)

>gi_480647_pir__S37132 ribosomal protein L13.A - rape
>gi_398918_emb_CAA80341_ (Z22618) cold induced protein

(BnC24A) [Brassica napus]

Seq. No. 216337

Seq. ID LIB3147-037-Q1-K2-E9

Method BLASTX
NCBI GI g4539405
BLAST score 539
E value 3.0e-55



123 Match length 83 % identity (ALO49524) putative ribosomal protein L9, cytosolic NCBI Description [Arabidopsis thaliana] 216338 Seq. No. LIB3147-037-Q1-K2-F10 Seq. ID BLASTX Method g2961346 NCBI GI 339 BLAST score 7.0e-32 E value 125 Match length 55 % identity (AL022140) pectinesterase like protein [Arabidopsis NCBI Description thaliana] 216339 Seq. No. LIB3147-037-Q1-K2-F11 Seq. ID BLASTX Method g3878119 NCBI GI 249 BLAST score 2.0e-21 E value 122 Match length 40 % identity (Z49068) similar to GTP-binding protein; cDNA EST NCBI Description EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL: D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353 216340 Seq. No. LIB3147-037-Q1-K2-F3 Seq. ID Method BLASTX g3269289 NCBI GI 143 BLAST score 2.0e-09 E value Match length 42 % identity 67 NCBI Description (AL030978) putative protein [Arabidopsis thaliana] 216341 Seq. No. Seq. ID LIB3147-037-Q1-K2-F4 Method BLASTX NCBI GI g2351374 535 BLAST score 7.0e-57 E value Match length 131 % identity (U54560) putative 26S proteasome subunit athMOV34 NCBI Description [Arabidopsis thaliana] 216342 Seq. No.

Seq. ID LIB3147-037-Q1-K2-F9

Method BLASTX
NCBI GI g3341464
BLAST score 165
E value 1.0e-11



```
95
Match length
                  42
% identity
                  (AJ225046) Hsp20.1 protein [Lycopersicon peruvianum]
NCBI Description
                  216343
Seq. No.
                  LIB3147-037-Q1-K2-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760830
BLAST score
                  266
E value
                  7.0e-24
                  55
Match length
                  89
% identity
                  (ACO03105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  216344
Seq. No.
                  LIB3147-037-Q1-K2-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232274
                  361
BLAST score
E value
                  3.0e-35
                  128
Match length
                  64
% identity
                  17.6 KD CLASS II HEAT SHOCK PROTEIN >gi_71499_pir__HHMU17
NCBI Description
                  heat shock protein 17.6-II - Arabidopsis thaliana
                  >gi_16338_emb_CAA45039_ (X63443) heat shock protein 17.6-II
                  [Arabidopsis thaliana]
                  216345
Seq. No.
                  LIB3147-037-Q1-K2-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4033429
                  283
BLAST score
                  3.0e-25
E value
                  136
Match length
% identity
                  42
NCBI Description PYRUVATE KINASE (PK) >gi_2854033 (AF043910) pyruvate kinase
                   [Eimeria tenella]
                  216346
Seq. No.
                  LIB3147-037-Q1-K2-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497543
BLAST score
                  416
E value
                   3.0e-41
Match length
                  89
% identity
                   96
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379
                  pyruvate kinase - common tobacco >gi 444023 emb CAA82628
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   216347
```

Seq. No.

LIB3147-037-Q1-K2-G8 Seq. ID

Method BLASTX NCBI GI g533084 BLAST score 272 5.0e-24E value



```
Match length
                  73
                  70
% identity
                  (U07597) delta-9 stearoyl-acyl carrier protein desaturase
NCBI Description
                  precursor [Thunbergia alata]
                  216348
Seq. No.
                  LIB3147-037-Q1-K2-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170293
BLAST score
                  44
E value
                  1.0e-15
Match length
                  136
                  83
% identity
                  Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3)
NCBI Description
                  mRNA, complete cds
                  216349
Seq. No.
                  LIB3147-037-Q1-K2-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2065013
BLAST score
                  369
E value
                  2.0e-35
                  119
Match length
                  66
% identity
NCBI Description
                  (Y11650) cyclic phosphodiesterase [Arabidopsis thaliana]
                  >gi 2832621 emb CAA16750 (AL021711) cyclic
                  phosphodiesterase [Arabidopsis thaliana]
Seq. No.
                  216350
                  LIB3147-037-Q1-K2-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174448
BLAST score
                  298
                  5.0e-27
E value
Match length
                  94
% identity
                   64
                  TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >qi 547391 (L32016) alpha-subunit; putative
                   [Arabidopsis thaliana]
Seq. No.
                  216351
                  LIB3147-037-Q1-K2-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1724100
BLAST score
                  285
E value
                  1.0e-25
                  111
Match length
                   53
% identity
                 (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
```

Seq. No. 216352

Seq. ID LIB3147-037-Q1-K2-H9

BLASTX Method NCBI GI g2431771 252 BLAST score E value 1.0e-21

Match length

% identity

40

100



```
113
Match length
% identity
                   48
                  (U62753) acidic ribosomal protein P2b [Zea mays]
NCBI Description
Seq. No.
                   216353
                   LIB3147-038-Q1-K2-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4467153
BLAST score
                   418
                   3.0e-41
E value
Match length
                   103
                   74
% identity
                   (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   216354
                   LIB3147-038-Q1-K2-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2225877
BLAST score
                   204
                   5.0e-16
E value
Match length
                   66
                   61
% identity
                   (AB002406) TIP49 [Rattus norvegicus], >gi 4106528 (AF100694)
NCBI Description
                   Pontin52 [Mus musculus] >gi 4521276 dbj BAA76313.1_
                   (AB001581) DNA helicase p50 [Rattus norvegicus]
Seq. No.
                   216355
                   LIB3147-038-Q1-K2-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1304227
BLAST score
                   185
                   8.0e-19
E value
Match length
                   107
                   46
% identity
                   (D63781) Epoxide hydrolase [Glycine max]
NCBI Description
                   >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase
                   [Glycine max]
                   216356
Seq. No.
                   LIB3147-038-Q1-K2-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4027891
BLAST score
                   532
                   1.0e-54
E value
Match length
                   116
% identity
                   82
                  (AF049350) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   216357
Seq. ID
                   LIB3147-038-Q1-K2-B1
Method
                   BLASTX
NCBI GI
                   q2493130
BLAST score
                   210
E value
                   9.0e-17
```

NCBI GI

E value

BLAST score

Match length

% identity

q2827536

8.0e-19

227

74

54



```
VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
NCBI Description
                  SUBUNIT) >qi 459200 (U07053) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
                  216358
Seq. No.
                  LIB3147-038-Q1-K2-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3165536
BLAST score
                  504
                  3.0e-51
E value
Match length
                  125
% identity
                  74
                  (AF067608) similar to DEAD-box helicases (Pfam: DEAD.hmm,
NCBI Description
                  score: 262.89) (Pfam: helicase C.hmm, score: 76.21)
                  [Caenorhabditis elegans]
Seq. No.
                  216359
Seq. ID
                  LIB3147-038-Q1-K2-B7
Method
                  BLASTX
NCBI GI
                  q132944
BLAST score
                  468
                  4.0e-47
E value
Match length
                  114
                  75
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  216360
                  LIB3147-038-Q1-K2-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3309243
BLAST score
                  330
                  5.0e-31
E value
                  103
Match length
                  67
% identity
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                  limon]
                  216361
Seq. No.
                  LIB3147-038-Q1-K2-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245098
BLAST score
                  584
E value
                  1.0e-60
Match length
                  120
                  90
% identity
NCBI Description (Z97343) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  216362
Seq. ID
                  LIB3147-038-Q1-K2-C10
Method
                  BLASTX
```



```
(AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216363
                  LIB3147-038-Q1-K2-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2792155
BLAST score
                  166
                  1.0e-11
E value
                  95
Match length
                  39
% identity
                  (AJ223291) chalcone reductase [Sesbania rostrata]
NCBI Description
                  216364
Seq. No.
                  LIB3147-038-Q1-K2-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2290400
BLAST score
                  221
                   4.0e-18
E value
                  52
Match length
                  83
% identity
                  (U91339) stearoyl-ACP desaturase [Helianthus annuus]
NCBI Description
Seq. No.
                  216365
                  LIB3147-038-Q1-K2-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3176709
                  164
BLAST score
E value
                   2.0e-11
Match length
                   95
                   38
% identity
                  (AC002392) putative anthranilate
NCBI Description
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   216366
                   LIB3147-038-Q1-K2-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g231660
BLAST score
                   270
E value
                   8.0e-24
                   120
Match length
                   50
% identity
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.
                   216367
                   LIB3147-038-Q1-K2-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3264759
BLAST score
                   513
                   2.0e-52
E value
Match length
                   109
% identity
                  (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
NCBI Description
Seq. No.
                   216368
```

Seq. ID LIB3147-038-Q1-K2-C7

Method BLASTX



```
NCBI GI
                      q131773
                      493
  BLAST score
                      5.0e-50
  E value
                      121
  Match length
                      83
  % identity
                      40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
  NCBI Description
                      >qi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
                      maize
                      216369
  Seq. No.
                      LIB3147-038-Q1-K2-C8
  Seq. ID
                      BLASTX
  Method
  NCBI GI
                      g2160322
  BLAST score
                      192
  E value
                      1.0e-14
                      59
  Match length
                      63
  % identity
                      (D16139) cytokinin binding protein CBP57 [Nicotiana
  NCBI Description
                      sylvestris]
                      216370
  Seq. No.
                      LIB3147-038-Q1-K2-D1
  Seq. ID
  Method
                      BLASTX
                      q1486472
  NCBI GI
                      510
  BLAST score
                      5.0e-52
  E value
                      109
  Match length
  % identity
                      87
                      (X99853) oxoglutarate malate translocator [Solanum
  NCBI Description
                      tuberosum]
                      216371
  Seq. No.
                      LIB3147-038-Q1-K2-D11
  Seq. ID
                      BLASTX
  Method
                      g541979
  NCBI GI
                       458
  BLAST score
                       6.0e-46
  E value
  Match length
                      113
                       80
  % identity
                      guanine nucleotide regulatory protein - fava bean
  NCBI Description
                      >gi_303744_dbj_BAA02113_ (D12545) GTP-binding protein
[Pisum sativum] >gi_452361_emb_CAA82709_ (Z29592) guanine
                      nucleotide regulatory protein [Vicia faba] >gi_738937_prf__2001457E GTP-binding protein [Pisum
                       satīvum] >\overline{gi_1098295_prf__2115367C small GTP-binding}
                       protein [Vicia faba]
  Seq. No.
                       216372
                       LIB3147-038-Q1-K2-D12
  Seq. ID
  Method
                       BLASTX
  NCBI GI
                       g3450889
                       493
  BLAST score
• E value
                       5.0e-50
  Match length
                       114
                       85
  % identity
```

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]



```
Seq. No.
                  216373
                  LIB3147-038-Q1-K2-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2947070
                  291
BLAST score
                  3.0e-26
E value
Match length
                  107
                  41
% identity
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  216374
                  LIB3147-038-Q1-K2-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2765837
BLAST score
                  247
                  4.0e-21
E value
Match length
                  81
                  69
% identity
                  (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
                  216375
Seq. No.
Seq. ID
                  LIB3147-038-Q1-K2-E1
Method
                  BLASTX
NCBI GI
                   g3182917
BLAST score
                   336
                   1.0e-31
E value
Match length
                  81
                   70
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi 2274920 emb CAA03896
NCBI Description
                   (AJ000063) ADP-ribosylation factor 1 [Dictyostelium
                   discoideum]
                   216376
Seq. No.
                  LIB3147-038-Q1-K2-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2792297
BLAST score
                   280
                   5.0e-25
E value
                   61
Match length
                   72
% identity
                  (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   216377
Seq. No.
                   LIB3147-038-Q1-K2-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1458245
BLAST score
                   191
E value
                   2.0e-14
                   119
Match length
                   34
% identity
                   (U64834) coded for by C. elegans cDNA cm17a1; coded for by
NCBI Description
                   C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                   CEMSE26F; similar to methyltransferases [Caenorhabditis
```

Seq. No. 216378

elegans]



```
LIB3147-038-Q1-K2-E6
Seq. ID
                  BLASTX
Method
                  g2244916
NCBI GI
                  189
BLAST score
                  3.0e-14
E value
                  113
Match length
                  32
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  216379
Seq. No.
                  LIB3147-038-Q1-K2-E7
Seq. ID
                  BLASTX
Method
                  g2950476
NCBI GI
                  167
BLAST score
                  1.0e-11
E value
Match length
                  79
                  46
% identity
                  (AL022070) vesicle transport v-snare protein
NCBI Description
                  [Schizosaccharomyces pombe]
                  216380
Seq. No.
                  LIB3147-038-Q1-K2-F11
Seq. ID
                  BLASTX
Method
                  q2911042
NCBI GI
BLAST score
                  475
                  7.0e-48
E value
Match length
                  104
                  86
% identity
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  216381
                  LIB3147-038-Q1-K2-F2
Seq. ID
Method
                  BLASTX
                   q3600031
NCBI GI
BLAST score
                   219
E value
                   2.0e-18
                   56
Match length
                   70
% identity
                  (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
NCBI Description
                   acid aldolases [Arabidopsis thaliana]
                   216382
Seq. No.
                   LIB3147-038-Q1-K2-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3123264
BLAST score
                   417
                   5.0e-41
E value
                   85
Match length
                   91
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   216383
Seq. No.
Seq. ID
                   LIB3147-038-Q1-K2-F6
```

30278

BLASTX

g4455203

Method NCBI GI

% identity



```
BLAST score
                  157
                  1.0e-10
E value
                  81
Match length
% identity
                  24
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
                  216384
Seq. No.
                  LIB3147-038-Q1-K2-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419789
BLAST score
                  241
E value
                  1.0e-20
Match length
                  70
                  66
% identity
NCBI Description hypothetical protein - potato
Seq. No.
                  216385
                  LIB3147-038-Q1-K2-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974782
BLAST score
                  454
                  1.0e-45
E value
Match length
                  95
                   94
% identity
NCBI Description
                  (Z49150) cobalamine-independent methionine synthase
                   [Solenostemon scutellarioides]
                  216386
Seq. No.
                  LIB3147-038-Q1-K2-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2909522
BLAST score
                   168
                   6.0e-12
E value
Match length
                  96
                   36
% identity
NCBI Description (AL021932) ufaAl [Mycobacterium tuberculosis]
Seq. No.
                   216387
                  LIB3147-038-Q1-K2-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2465434
BLAST score
                   367
E value
                   3.0e-35
Match length
                  88
% identity
                   80
NCBI Description (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
Seq. No.
                   216388
Seq. ID
                  LIB3147-038-Q1-K2-G11
Method
                  BLASTX
NCBI GI
                  g122006
BLAST score
                   404
E'value
                  1.0e-39
                  107
Match length
                   74
```

NCBI Description HISTONE H2A >gi_81906_pir__JQ1183 histone H2A - garden pea

NCBI Description

thaliana]



```
216389
Seq. No.
                    LIB3147-038-Q1-K2-G12
Seq. ID
                    BLASTX
Method
                    g464987
NCBI GI
BLAST score
                    549
                    1.0e-56
E value
                    108
Match length
                    94
% identity
                    UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                    LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                    >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana
                    >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                    conjugating enzyme [Arabidopsis thaliana]
                    216390
Seq. No.
                    LIB3147-038-Q1-K2-G2
Seq. ID
                    BLASTX
Method
                    g4309698
NCBI GI
                    337
BLAST score
                    1.0e-31
E value
                    122
Match length
                    62
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                    thaliana]
                    216391
Seq. No.
                    LIB3147-038-Q1-K2-G5
Seq. ID
                    BLASTN
Method
NCBI GI
                    g1777727
BLAST score
                    66
                    5.0e-29
E value
                    78
Match length
                    97
% identity
NCBI Description Gossypium hirsutum 18S ribosomal RNA gene, partial sequence
                    216392
Seq. No.
                    LIB3147-038-Q1-K2-H1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4510383
BLAST score
                    109
                    1.0e-09
E value
Match length
                    86
% identity
                    45
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                    216393
                    LIB3147-038-Q1-K2-H2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2583123
BLAST score
                    367
                    3.0e-35
E value
                    85
Match length
% identity
                    81
                    (AC002387) putative nucleotide sugar epimerase [Arabidopsis
```

Seq. ID

Method



```
216394
Seq. No.
Seq. ID
                   LIB3147-038-Q1-K2-H7
Method
                   BLASTX
NCBI GI
                   g4510383
BLAST score
                   515
                   1.0e-52
E value
Match length
                   111
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   216395
Seq. No.
                   LIB3147-039-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4063749
                   139
BLAST score
                   1.0e-08
E value
                   85
Match length
                   22
% identity
NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]
                   216396
Seq. No.
Seq. ID
                   LIB3147-039-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   q1769887
BLAST score
                   196
                   5.0e-17
E value
Match length
                   106
                   51
% identity
NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]
Seq. No.
                   216397
                   LIB3147-039-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130089
BLAST score
                   222
E value
                   1.0e-18
Match length
                   48
                   83
% identity
NCBI Description 2-oxoglutarate/malate translocator (clone OMT103),
                   mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                   translocator [Panicum miliaceum]
                   216398
Seq. No.
Seq. ID
                   LIB3147-039-Q1-K1-A4
                   BLASTX
Method
NCBI GI
                   g2632252
BLAST score
                   301
E value
                   2.0e-27
                   109
Match length
                   57
% identity
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                   216399
```

30281

LIB3147-039-Q1-K1-A7

BLASTX

E value

Match length

1.0e-18 53



```
NCBI GI
                  q4454464
                  464
BLAST score
                  1.0e-46
E value
Match length
                  99
                  85
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  216400
Seq. No.
                  LIB3147-039-Q1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4263712
BLAST score
                  427
                  3.0e-42
E value
Match length
                  111
                  70
% identity
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                  thaliana]
                  216401
Seq. No.
                  LIB3147-039-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g2642215
NCBI GI
BLAST score
                  317
                  2.0e-29
E value
Match length
                  75
% identity
                  80
                  (AF030386) NOI protein [Arabidopsis thaliana]
NCBI Description
                  216402
Seq. No.
                  LIB3147-039-Q1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g11244
BLAST score
                  111
                  1.0e-55
E value
Match length
                  187
% identity
                  90
NCBI Description A.thaliana chloroplast DNA for transfer RNA-Ile and
                  ribosomal protein
                  216403
Seq. No.
Seq. ID
                  LIB3147-039-Q1-K1-B4
Method
                  BLASTN
NCBI GI
                   g2687434
BLAST score
                  129
E value
                  1.0e-66
Match length
                  153
% identity
                   96
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                   216404
Seq. No.
                  LIB3147-039-Q1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567232
BLAST score
                  226
```



```
% identity
NCBI Description
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
                  thaliana]
                  216405
Seq. No.
                  LIB3147-039-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2738248
BLAST score
                  446
E value
                  1.0e-44
Match length
                  108
% identity
                   90
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                  216406
Seq. No.
                  LIB3147-039-Q1-K1-B9
Seq. ID
Method
                  BLASTX
                  q2583123
NCBI GI
BLAST score
                  183
                   5.0e-14
E value
Match length
                   69
                   59
% identity
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                   216407
                  LIB3147-039-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2829899
BLAST score
                   150
                   1.0e-09
E value
Match length
                   64
                   47
% identity
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                   216408
                   LIB3147-039-Q1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455159
                   150
BLAST score
E value
                   1.0e-09
Match length
                   39
% identity
                   67
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
Seq. No.
                   216409
                   LIB3147-039-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1351279
BLAST score
                   227
                   5.0e-19
E value
Match length
                   51
% identity
                   86
```

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)



>gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]

Seq. No. 216410

Seq. ID LIB3147-039-Q1-K1-D1

Method BLASTX
NCBI GI g2558962
BLAST score 301
E value 2.0e-27
Match length 107
% identity 62

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 216411

Seq. ID LIB3147-039-Q1-K1-D12

Method BLASTX
NCBI GI g4220529
BLAST score 400
E value 5.0e-39
Match length 130
% identity 63

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 216412

Seq. ID LIB3147-039-Q1-K1-D5

Method BLASTX
NCBI GI g1841870
BLAST score 243
E value 1.0e-20
Match length 59
% identity 81

NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No. 216413

Seq. ID LIB3147-039-Q1-K1-D6

Method BLASTX
NCBI GI g3851640
BLAST score 498
E value 2.0e-50
Match length 133
% identity 74

NCBI Description (AF098636) chaperone GrpE type 2 [Nicotiana tabacum]

Seq. No. 216414

Seq. ID LIB3147-039-Q1-K1-D7

Method BLASTN
NCBI GI g4204371
BLAST score 38
E value 6.0e-12
Match length 97
% identity 90

NCBI Description Zea mays acidic ribosomal protein P2a-2 (rpp2a-2) mRNA,

complete cds

Seq. No. 216415

Seq. ID LIB3147-039-Q1-K1-D8

Method BLASTX

NCBI GI

BLAST score



```
q3319355
NCBI GI
                  299
BLAST score
                  1.0e-30
E value
Match length
                  81
% identity
                  85
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                  gamma chain [Arabidopsis thaliana]
                  216416
Seq. No.
                  LIB3147-039-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                   g2924520
NCBI GI
                   600
BLAST score
                   2.0e-62
E value
Match length
                  133
% identity
                   86
NCBI Description
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
                   [Arabidopsis thaliana]
Seq. No.
                   216417
                   LIB3147-039-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131772
BLAST score
                   364
                   8.0e-35
E value
Match length
                   90
                   83
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                   maize
                   216418
Seq. No.
                   LIB3147-039-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1922251
BLAST score
                   580
E value
                   3.0e-60
Match length
                   121
                   92
% identity
                  (Y12072) farnesyl pyrophosphate synthase [Gossypium
NCBI Description
                   arboreum]
Seq. No.
                   216419
Seq. ID
                   LIB3147-039-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g3201969
BLAST score
                   593
E value
                   1.0e-61
                   118
Match length
                   86
% identity
                  (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
Seq. No.
                   216420
Seq. ID
                   LIB3147-039-Q1-K1-E4
                   BLASTX
Method
```

30285

g4220462



```
4.0e-23
E value
                  87
Match length
                  59
% identity
                  (AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8)
NCBI Description
                  gene from Arabidopsis thaliana containing Homeobox PF_00046
                  and bZIP PF 00170 domains. [Arabidopsis thaliana]
                  216421
Seq. No.
                  LIB3147-039-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  g2117168
NCBI GI
BLAST score
                  658
                  3.0e-69
E value
                  135
Match length
                   92
% identity
                  (Z73961) RAC1 [Lotus japonicus]
NCBI Description
Seq. No.
                   216422
                   LIB3147-039-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g3043428
NCBI GI
BLAST score
                   435
                   4.0e-43
E value
                   93
Match length
                   87
% identity
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
                   216423
Seq. No.
                   LIB3147-039-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g4105827
NCBI GI
                   158
BLAST score
                   3.0e-11
E value
                   34
Match length
                   85
% identity
NCBI Description (AF050090) nuclear alpha-tubulin [Guillardia theta]
                   216424
Seq. No.
                   LIB3147-039-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q1773014
NCBI GI
                   459
BLAST score
                   6.0e-46
E value
                   127
Match length
                   69
 % identity
NCBI Description (Y10338) chloride channel Stclc1 [Solanum tuberosum]
                   216425
 Seq. No.
                   LIB3147-039-Q1-K1-F7
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q3421413
                   457
 BLAST score
 E value
                    1.0e-45
                   134
 Match length
 % identity
                    71
                   (AF081922) protein phosphatase 2A 55 kDa B regulatory
 NCBI Description
```

subunit [Oryza sativa] >gi_3421415 (AF081923) protein

Seq. ID



```
phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
```

```
216426
Seq. No.
Seq. ID
                  LIB3147-039-Q1-K1-F8
Method
                  BLASTX
                  q3860257
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
                  45
Match length
                  73
% identity
                  (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  216427
Seq. No.
                  LIB3147-039-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q401043
                  176
BLAST score
                   7.0e-13
E value
                   34
Match length
                   97
% identity
                  40S RIBOSOMAL PROTEIN S15 >gi_218131_dbj_BAA01746_ (D10962)
NCBI Description
                  unnamed protein product [Oryza sativa]
                   216428
Seq. No.
                  LIB3147-039-Q1-K1-G10
Seq. ID
                   BLASTN
Method
                   g3241939
NCBI GI
                   47
BLAST score
                   2.0e-17
E value
                   147
Match length
                   54
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T26J13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   216429
Seq. No.
Seq. ID
                   LIB3147-039-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3913633
BLAST score
                   356
                   6.0e - 34
E value
Match length
                   108
% identity
                   68
NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown
                   protein [Arabidopsis thaliana]
                   216430
Seq. No.
                   LIB3147-039-Q1-K1-G4
Seq. ID
Method
                   BLASTX
                   q2078350
NCBI GI
BLAST score
                   565
E value
                   3.0e-58
Match length
                   124
                   91
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                   216431
Seq. No.
```

30287

LIB3147-039-Q1-K1-G8



BLASTN Method g2687434 NCBI GI 281 BLAST score 1.0e-157 E value 333 Match length 96 % identity Eucryphia lucida large subunit 26S ribosomal RNA gene, NCBI Description partial sequence 216432 Seq. No. LIB3147-039-Q1-K1-H10 Seq. ID Method BLASTX g3687251 NCBI GI 423 BLAST score 1.0e-41 E value Match length 109 74 % identity (AC005169) unknown protein [Arabidopsis thaliana] NCBI Description 216433 Seq. No. LIB3147-039-Q1-K1-H11 Seq. ID BLASTX Method g1706918 NCBI GI 167 BLAST score 3.0e-12E value 49 Match length 53 % identity NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi 498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis] 216434 Seq. No. LIB3147-039-Q1-K1-H5 Seq. ID BLASTX Method q464621 NCBI GI 222 BLAST score E value 4.0e-18 Match length 89 53 % identity 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 NCBI Description ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum] 216435 Seq. No. LIB3147-039-Q1-K1-H9 Seq. ID Method BLASTX NCBI GI g3914685 BLAST score 331 3.0e-31 E value 89 Match length

72 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal

protein L17 [Zea mays]

216436 Seq. No.

Seq. ID LIB3147-040-Q1-K1-A10

BLASTX Method



```
g3297815
NCBI GI
BLAST score
                   344
E value
                   2.0e-33
Match length
                  109
                   68
% identity
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                  216437
Seq. No.
                  LIB3147-040-Q1-K1-A4
Seq. ID
Method
                  BLASTN
                   g499059
NCBI GI
BLAST score
                   38
E value
                   6.0e-12
                   90
Match length
                   86
% identity
NCBI Description C.arietinum mRNA for open reading frame
                  216438
Seq. No.
                  LIB3147-040-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2497752
BLAST score
                   291
                   3.0e-26
E value
                  105
Match length
                   56
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                   >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                   [Prunus dulcis]
                   216439
Seq. No.
Seq. ID
                   LIB3147-040-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q3132696
BLAST score
                   660
                   2.0e-69
E value
Match length
                   146
% identity
                   88
NCBI Description
                  (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
Seq. No.
                   216440
Seq. ID
                   LIB3147-040-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g417360
BLAST score
                   307
E value
                   3.0e-28
Match length
                   100
% identity
                   58
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                   >gi 2131280 pir S67767 high mobility group-like protein
                   NHP2 - yeast (Saccharomyces cerevisiae)
                   >gi_666101_emb_CAA40885_ (X57714) high mobility group-like
```

nuclear protein 2 [Saccharomyces cerevisiae]

>gi 1429348 emb CAA67483 (X99000) high-mobility-group-like

protein [Saccharomyces cerevisiae]

>gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w

[Saccharomyces cerevisiae]



```
216441
Seq. No.
                  LIB3147-040-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  q4572671
NCBI GI
BLAST score
                  335
                   6.0e - 35
E value
                  92
Match length
                   84
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
```

 Seq. No.
 216442

 Seq. ID
 LIB3147-040-Q1-K1-B1

 Method
 BLASTX

NCBI GI g4539417 BLAST score 484 E value 6.0e-49 Match length 112 % identity 77

NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

 Seq. No.
 216443

 Seq. ID
 LIB3147-040-Q1-K1-B10

 Method
 BLASTX

 NCBI GI
 g2500376

 BLAST score
 469

 E value
 4.0e-47

E value 4.0e-4 Match length 98 % identity 93

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_

(AC005508) 23552 [Arabidopsis thaliana]

Seq. No. 216444

Seq. ID LIB3147-040-Q1-K1-B11

Method BLASTX
NCBI GI g3947448
BLAST score 149
E value 8.0e-10
Match length 82
% identity 43

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 216445

Seq. ID LIB3147-040-Q1-K1-B2

Method BLASTX
NCBI GI g730449
BLAST score 571
E value 4.0e-59
Match length 125



```
% identity
                  60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
NCBI Description
                  >gi_480647_pir__S37132 ribosomal protein L13.A - rape
                  >gi 398918 emb CAA80341 (Z22618) cold induced protein
                   (BnC24A) [Brassica napus]
                  216446
Seq. No.
                  LIB3147-040-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2492504
BLAST score
                  574
                  7.0e-60
E value
                  142
Match length
                   44
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                   >gi 1669660 emb CAA70565_ (Y09396) protein of AAA family
                   [Capsicum annuum]
                   216447
Seq. No.
                  LIB3147-040-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g2497752
NCBI GI
                   237
BLAST score
                   7.0e-20
E value
                   73
Match length
                   62
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                   >gi 1321911 emb_CAA65475_ (X96714) lipid transfer protein
                   [Prunus dulcis]
                   216448
Seq. No.
                   LIB3147-040-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q730449
BLAST score
                   341
E value
                   4.0e-32
Match length
                   139
% identity
                   55
                   60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
NCBI Description
                   >gi_480647_pir__S37132 ribosomal protein L13.A - rape
                   >gi 398918 emb CAA80341 (Z22618) cold induced protein
                   (BnC24A) [Brassica napus]
                   216449
Seq. No.
                   LIB3147-040-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172811
BLAST score
                   293
E value
                   2.0e-26
Match length
                   108
                   57
% identity
                   60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >qi 1076751 pir S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb CAA57339 (X81691) putative tumor
```

Seq. No. 216450

suppresser [Oryza satīva]

Seq. No.

Seq. ID



```
LIB3147-040-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1524121
BLAST score
                  385
E value
                  3.0e-37
Match length
                  93
% identity
                  74
NCBI Description
                  (X96539) malate dehydrogenase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  216451
                  LIB3147-040-Q1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
                  8.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  216452
Seq. No.
                  LIB3147-040-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g122106
BLAST score
                  375
E value
                  4.0e-36
Match length
                  76
                  100
% identity
                  HISTONE H4 >gi 70771 pir_ HSZM4 histone H4 - maize
NCBI Description
                  >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                  >gi 2119028 pir S60475 histone H4 - garden pea
                  >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
                  aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                  thaliana] >gi 166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                  >qi 168501 (M13370) histone H4 [Zea mays] >gi_168503
                   (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914_
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                  >gi 3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                  >gi 4580385 gb AAD24364.1 AC007184_4 (AC007184) histone H4
                   [Arabidopsis thaliana] >gi 225838_prf__1314298A histone H4
                   [Arabidopsis thaliana]
Seq. No.
                  216453
Seq. ID
                  LIB3147-040-Q1-K1-C8
Method
                  BLASTX
                  q3687235
NCBI GI
BLAST score
                  190
E value
                  2.0e-14
                  65
Match length
% identity
                  (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
```

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LIB3147-040-Q1-K1-C9

216454

E value

Match length

3.0e-17



```
Method
                  BLASTX
NCBI GI
                  g2500376
BLAST score
                  472
                  2.0e-47
E value
                  95
Match length
                  95
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
                  (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.
                  216455
Seq. ID
                  LIB3147-040-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2982243
BLAST score
                  340
E value
                  6.0e-32
Match length
                  113
% identity
                  58
NCBI Description (AF051204) hypothetical protein [Picea mariana]
Seq. No.
                  216456
Seq. ID
                  LIB3147-040-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4455364
BLAST score
                  467
E value
                  8.0e-47
Match length
                  140
% identity
                  57
                  (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  216457
Seq. ID
                  LIB3147-040-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2959324
BLAST score
                  261
E value
                  1.0e-22
Match length
                  64
                  80
% identity
NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
Seq. No.
                  216458
Seq. ID
                  LIB3147-040-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  669
                  2.0e-70
E value
                  142
Match length
% identity
                  86
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  216459
Seq. ID
                  LIB3147-040-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3747026
BLAST score
                  214
```

BLAST score

Match length

E value

326

102

9.0e - 46



```
% identity
                  (AF093244) import protein Tim9p [Saccharomyces cerevisiae]
NCBI Description
Seq. No.
                  216460
Seq. ID
                  LIB3147-040-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g508304
BLAST score
                  344
E value
                  2.0e-32
Match length
                  79
% identity
                  78
NCBI Description
                  (L22305) corC [Medicago sativa]
                  216461
Seq. No.
Seq. ID
                  LIB3147-040-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g114682
BLAST score
                  150
E value
                  8.0e-10
Match length
                  48
                  62
% identity
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi_168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                  216462
Seq. ID
                  LIB3147-040-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g461530
BLAST score
                  240
                  1.0e-20
E value
Match length
                  91
% identity
                   49
                  N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
NCBI Description
                   >qi 159365 (L11348) ARD1 protein homologue [Leishmania
                  donovani]
Seq. No.
                   216463
                  LIB3147-040-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2623680
BLAST score
                  279
                   2.0e-25
E value
                   55
Match length
% identity
NCBI Description (AF031482) calmodulin [Zea mays]
Seq. No.
                   216464
                  LIB3147-040-Q1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                  g3901012
```

E value

Match length

5.0e-15



```
% identity
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                  216465
                  LIB3147-040-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114682
BLAST score
                  474
E value
                  1.0e-47
Match length
                  137
                  70
% identity
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi 168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
                  216466
Seq. No.
Seq. ID
                  LIB3147-040-Q1-K1-E6
Method
                  BLASTX
                  g117952
NCBI GI
                  558
BLAST score
                  1.0e-57
E value
                  108
Match length
                  94
% identity
                  CYTOCHROME C >gi 65504 pir CCAB cytochrome c - China jute
NCBI Description
Seq. No.
                  216467
Seq. ID
                  LIB3147-040-Q1-K1-F1
Method
                  BLASTN
                  g2264305
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  86
% identity
                  92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   216468
                  LIB3147-040-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3785978
BLAST score
                  247
E value
                   3.0e-21
Match length
                  83
% identity
                  (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216469
Seq. ID
                  LIB3147-040-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  g3269284
BLAST score
                  193
```



87

% identity

```
% identity
                  (AL030978) histone H2A- like protein [Arabidopsis thaliana]
NCBI Description
                  216470
Seq. No.
                  LIB3147-040-Q1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2558962
BLAST score
                  279
                  7.0e-25
E value
Match length
                  57
                  98
% identity
                  (AF025667) histone H2B1 [Gossypium hirsutum]
NCBI Description
                  216471
Seq. No.
                  LIB3147-040-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  q4490743
NCBI GI
                   459
BLAST score
                   6.0e - 46
E value
                  122
Match length
                   70
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                  216472
Seq. No.
                  LIB3147-040-Q1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2129844
                   279
BLAST score
                   9.0e-25
E value
                   67
Match length
% identity
                   79
NCBI Description stress-induced protein stil - soybean
                   216473
Seq. No.
                   LIB3147-040-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2642648
BLAST score
                   688
E value
                   8.0e-73
Match length
                   137
% identity
                   99
                   (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                   shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                   cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.
                   216474
                   LIB3147-040-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q231496
BLAST score
                   478
                   3.0e-48
E value
                   107
Match length
```

>gi 21536 emb CAA39278_ (X55749) actin [Solanum tuberosum]

NCBI Description ACTIN 58 >gi 100421_pir__S20094 actin - potato



```
216475
Seq. No.
                  LIB3147-040-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g542190
NCBI GI
BLAST score
                  274
                  3.0e-24
E value
                  124
Match length
                  53
% identity
                  hypothetical protein 1087 - maize >gi 459269 emb CAA54960
NCBI Description
                  (X78029) transcribed sequence 1087 [Zea mays]
                  216476
Seq. No.
                  LIB3147-040-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  q4580390
NCBI GI
BLAST score
                  251
                  2.0e-21
E value
                  137
Match length
                  50
% identity
                  (AC007171) putative disease resistance response protein
NCBI Description
                   [Arabidopsis thaliana]
                  216477
Seq. No.
                  LIB3147-040-Q1-K1-G4
Seq. ID
Method
                  BLASTX
                  g1350777
NCBI GI
BLAST score
                   239
E value
                   3.0e-20
                   51
Match length
                   90
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi 971282_dbj BAA07209_ (D38012)
                   ribosomal protein L9 [Oryza sativa]
                   216478
Seq. No.
                   LIB3147-040-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2583134
BLAST score
                   163
E value
                   1.0e-11
Match length
                   65
% identity
                   (ACO02387) putative proline-rich protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   216479
Seq. ID
                   LIB3147-040-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   q135860
                   289
BLAST score
                   4.0e-26
E value
                   64
Match length
% identity
                   88
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi 99761_pir__S22202 tonoplast intrinsic
                   protein gamma - Arabidopsis thaliana
```

>gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic

protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732



(M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

```
Seq. No.
                   216480
                   LIB3147-040-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   q1351722
NCBI GI
                   145
BLAST score
                   5.0e-09
E value
                   62
Match length
                   50
% identity
                   HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I
NCBI Description
                   >gi_1122371_emb_CAA92386_ (Z68198) hypothetical protein
                   [Schizosaccharomyces pombe]
                   216481
Seq. No.
                   LIB3147-040-Q1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662341
BLAST score
                   653
                   1.0e-68
E value
                   131
Match length
                   96
 % identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   216482
 Seq. No.
 Seq. ID
                   LIB3147-040-Q1-K1-H3
 Method
                   BLASTX
 NCBI GI
                   g1296816
 BLAST score
                   250
                   2.0e-21
 E value
 Match length
                   63
                   79
 % identity
 NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]
                   216483
 Seq. No.
 Seq. ID
                   LIB3147-040-Q1-K1-H4
 Method
                   BLASTX
 NCBI GI
                   g4138137
 BLAST score
                   169
 E value
                   5.0e-12
 Match length
                   37
 % identity
                   81
 NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]
                   216484
 Seq. No.
                   LIB3147-040-Q1-K1-H6
 Seq. ID
                   BLASTX
 Method
                   g1706749
 NCBI GI
                   256
 BLAST score
E value
                   1.0e-22
```

54

94

Match length

% identity



3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR NCBI Description (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi 780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana] 216485 Seq. No. LIB3147-040-Q1-K1-H7 Seq. ID Method BLASTX NCBI GI q3927825 235 BLAST score E value 4.0e-20 Match length 70 71

% identity NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

216486 Seq. No. LIB3147-041-Q1-K1-A12 Seq. ID Method BLASTX NCBI GI g1173043 BLAST score 281

6.0e-25 E value Match length 68 79 % identity

60S RIBOSOMAL PROTEIN L38 >gi 479441 pir S33899 ribosomal NCBI Description

protein L38 - tomato (cv. Moneymaker)

>gi 313027 emb CAA49599 (X69979) ribosomal protein L38

[Lycopersicon esculentum]

216487 Seq. No.

Seq. ID LIB3147-041-Q1-K1-A6

Method BLASTX NCBI GI g2369714 BLAST score 455 E value ' 1.0e-45 Match length 98 % identity 88

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

216488 Seq. No.

Seq. ID LIB3147-041-Q1-K1-A9

Method BLASTX NCBI GI g3785977 BLAST score 141 1.0e-08 E value Match length 62 % identity 44

(AC005560) putative growth regulator protein [Arabidopsis NCBI Description

thaliana]

216489 Seq. No.

LIB3147-041-Q1-K1-B10 Seq. ID

BLASTX Method NCBI GI g2119278 BLAST score 624 E value 2.0e-65 125 Match length



```
% identity
                  95
NCBI Description tubulin beta-1 chain - rice
                  216490
Seq. No.
                  LIB3147-041-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548774
BLAST score
                  195
E value
                  2.0e-15
Match length
                  51
                  67
% identity
                  60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  216491
                  LIB3147-041-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3650030
BLAST score
                  245
E value
                   9.0e-21
                  79
Match length
                   56
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216492
                  LIB3147-041-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2352492
                   393
BLAST score
E value
                   2.0e-38
                   100
Match length
                   74
% identity
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   216493
Seq. ID
                   LIB3147-041-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                   q3334113
BLAST score
                   398
E value
                   6.0e-39
Match length
                   76
                   100
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                   acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                   216494
                   LIB3147-041-Q1-K1-C7
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2558962
BLAST score 230
E value 3.0e-19
Match length 49
% identity 96

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]



Seq. No.

Seq. ID

216495

LIB3147-041-Q1-K1-C9

```
BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
                  9.0e-11
E value
Match length
                  50
                  51
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  216496
Seq. No.
                  LIB3147-041-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023857
BLAST score
                   472
                  1.0e-47
E value
                  104
Match length
                   55
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN >gi_629591_pir__S48839 guanine nucleotide
                   regulatory protein - rape >gi_563335_emb_CAA83924_ (Z33643)
                   guanine nucleotide regulatory protein [Brassica napus]
                   216497
Seq. No.
                  LIB3147-041-Q1-K1-D8
Seq. ID
Method
                   BLASTN
                   g2267582
NCBI GI
BLAST score
                   68
                   1.0e-30
E value
Match length
                   68
% identity
                   100
                  Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA,
NCBI Description
                   complete cds
                   216498
Seq. No.
Seq. ID
                   LIB3147-041-Q1-K1-D9
                   BLASTX
Method
NCBI GI
                   q4325354
BLAST score
                   220
E value
                   8.0e-18
Match length
                   75
                   56
% identity
                   (AF128395) contains similarity to retrovirus-related
NCBI Description
                   polyproteins and to CCHC zinc finger protein (Pfam:
                   PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
Seq. No.
                   216499
Seq. ID
                   LIB3147-041-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   q1703380
BLAST score
                   219
                   2.0e-18
E value
Match length
                   48
                   94
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483 dbj_BAA04607 (D17760)
                   ADP-ribosylation factor [Oryza sativa]
```

NCBI Description



```
216500
Seq. No.
                  LIB3147-041-Q1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172977
BLAST score
                  145
                  3.0e-09
E value
Match length
                  95
                  40
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  216501
Seq. No.
                  LIB3147-041-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g82200
NCBI GI
BLAST score
                  433
                  4.0e-43
E value
                  96
Match length
                  82
% identity
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
                  216502
Seq. No.
                  LIB3147-041-Q1-K1-E7
Seq. ID
Method
                  BLASTX
                  g730583
NCBI GI
BLAST score
                  255
                  1.0e-22
E value
                   68
Match length
                   75
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267_emb_CAA55047_
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
                   216503
Seq. No.
Seq. ID
                   LIB3147-041-Q1-K1-F12
Method
                   BLASTN
NCBI GI
                   q2865522
BLAST score
                   38
                   7.0e-12
E value
Match length
                   103
% identity
                   92
NCBI Description Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
                   complete cds
                   216504
Seq. No.
                   LIB3147-041-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q20186
                   630
BLAST score
                   5.0e-66
E value
Match length
                   124
% identity
                   62
```

>gi_3336950_emb_CAA74307_ (Y13974) calmodulin [Zea mays]
>gi_4103961 (AF030034) calmodulin [Phaseolus vulgaris]

(X65016) calmodulin [Oryza sativa]



```
216505
Seq. No.
                  LIB3147-041-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  q1839188
NCBI GI
BLAST score
                  281
                  5.0e-25
E value
                  73
Match length
                  74
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                  216506
Seq. No.
                  LIB3147-041-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g2144186
NCBI GI
                  296
BLAST score
                   6.0e-36
E value
                  91
Match length
                  88
% identity
                  farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) 1 -
NCBI Description
                   Glycyrrhiza glabra L >gi 1449163 dbj_BAA13083_ (D86409)
                   squalene synthase [Glycyrrhiza glabra]
                  216507
Seq. No.
                  LIB3147-041-Q1-K1-H10
Seq. ID
                  BLASTX
Method ·
NCBI GI
                   g2245065
                   195
BLAST score
                   9.0e-30
E value
                   99
Match length
                   23
% identity
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   216508
Seq. No.
                   LIB3147-042-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3834302
BLAST score
                   321
                   8.0e-30
E value
                   65
Match length
                   92
% identity
                   (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
NCBI Description
                   from Oryza sativa. ESTs gb F14272 and gb F14273 come from
                   this gene. [Arabidopsis thaliana]
                   216509
Seq. No.
                   LIB3147-042-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4263704
BLAST score
                   327
E value
                   2.0e-30
```

Match length 128 % identity

(AC006223) putative sugar starvation-induced protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 216510

Seq. ID LIB3147-042-Q1-K1-A2



```
BLASTN
Method
NCBI GI
                  g409574
                  39
BLAST score
                  3.0e-13
E value
                 51
Match length
                  94
% identity
                 Atriplex nummularia glyceraldehyde-3-phosphate
NCBI Description
                  dehydrogenase (GAPDH) mRNA, complete cds.
                  >gi 414606 emb X75597 ANDAP3DH A.nummularia mRNA for
                  glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                 216511
                 LIB3147-042-Q1-K1-A3
Seq. ID
                 BLASTX
Method
                  g1552379
NCBI GI
BLAST score
                 185
                  2.0e-14
E value
Match length
                  53
                  62
% identity
                 (Y08155) pectin methylesterase [Silene latifolia ssp. alba]
NCBI Description
                  216512
Seq. No.
                  LIB3147-042-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  g505482
NCBI GI
                  548
BLAST score
                  2.0e-56
E value
Match length
                  119
                  88
% identity
                 (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                  photosystem II [Nicotiana tabacum]
                  216513
Seq. No.
                  LIB3147-042-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2935298
NCBI GI
BLAST score
                  109
E value
                  3.0e-10
                  110
Match length
                  44
% identity
                 (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                  1 [Gossypium hirsutum]
                  216514
Seq. No.
                  LIB3147-042-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501056
BLAST score
                  198
E value
                  2.0e-15
                  55
Match length
                  71
% identity
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                  Synthetase [Arabidopsis thaliana]
```

Seq. No. 216515

Method

NCBI GI

BLASTX g3426038



```
LIB3147-042-Q1-K1-B12
Seq. ID
Method
                   BLASTN
NCBI GI
                   a22441
BLAST score
                   42
E value
                   1.0e-14
Match length
                   78
                   90
% identity
NCBI Description
                   Maize pML2 gene for zein
Seq. No.
                   216516
                   LIB3147-042-Q1-K1-B2
Seq. ID
Method
                   BLASTX
                   g133939
NCBI GI
BLAST score
                   238
                   2.0e-20
E value
Match length
                   77
                   64
% identity
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70865 pir_R3NT3
NCBI Description
                   ribosomal protein S3 - common tobacco chloroplast
                   >gi_11865_emb_CAA77381_ (Z00044) ribosomal protein S3
[Nicotiana tabacum] >gi_225235_prf__1211235BT ribosomal
                   protein S3 [Nicotiana tabacum]
Seq. No.
                   216517
Seq. ID
                   LIB3147-042-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2270994
BLAST score
                   312
E value
                   1.0e-28
Match length
                   102
% identity
                   56
                   (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
                   216518
Seq. No.
Seq. ID
                   LIB3147-042-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   q1296816
BLAST score
                   426
E value
                   5.0e-42
Match length
                   105
% identity
                   80
NCBI Description
                   (X94995) naringenin-chalcone synthase [Juglans sp.]
Seq. No.
                   216519
                   LIB3147-042-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244740
BLAST score
                   403
E value
                   2.0e-39
Match length
                   105
                   72
% identity
NCBI Description
                  (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
Seq. No.
                   216520
                   LIB3147-042-Q1-K1-B7
Seq. ID
```



114

68

Match length

% identity

```
BLAST score
                   164
                   3.0e-11
E value
Match length
                   49
% identity
                   71
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216521
                  LIB3147-042-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16159
BLAST score
                   44
                   2.0e-15
E value
                   92
Match length
                   87
% identity
NCBI Description A.thaliana mRNA for adenosine nucleotide translocator
                   216522
Seq. No.
                  LIB3147-042-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1839022
BLAST score
                   166
                   1.0e-17
E value
Match length
                  72
                   67
% identity
                  (Y11121) amino acid carrier [Ricinus communis]
NCBI Description
Seq. No.
                   216523
                  LIB3147-042-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3075391
BLAST score
                   426
                   5.0e-42
E value
Match length
                   142
                   56
% identity
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                   216524
                   LIB3147-042-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455217
BLAST score
                   409
E value
                   5.0e-40
Match length
                   136
% identity
                   60
                  (AL035440) Avr9 elicitor response like protein [Arabidopsis
NCBI Description
                   thaliana]
                   216525
Seq. No.
                   LIB3147-042-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2736186
BLAST score
                   409
                   3.0e-40
E value ,
```

30306

NCBI Description (AF024623) galactose kinase [Arabidopsis thaliana]



```
216526
Seq. No.
                  LIB3147-042-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135449
BLAST score
                  741
                  6.0e-79
E value
                  144
Match length
                  97
% identity
NCBI Description
                  TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1
                  chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1
                  tubulin [Zea mays]
Seq. No.
                  216527
                  LIB3147-042-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1346675
                  598
BLAST score
                  3.0e-62
E value
Match length
                  122
                  93
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
NCBI Description
                  >gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                  bidentis]
Seq. No.
                  216528
Seq. ID
                  LIB3147-042-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g224293
                  409
BLAST score
                  5.0e-40
E value
Match length
                  86
                  95
% identity
NCBI Description histone H4 [Triticum aestivum]
                  216529
Seq. No.
Seq. ID
                  LIB3147-042-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  210
E value
                   5.0e-17
Match length
                  69
% identity
                   59
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   216530
Seq. ID
                  LIB3147-042-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4262226
BLAST score
                  168
E value
                  8.0e-12
                  106
Match length
% identity
                   43
NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]
```

Seq. No. 216531

Seq. ID LIB3147-042-Q1-K1-D10

Method BLASTX

% identity

50



```
NCBI GI
                  q1841464
BLAST score
                  729
                  2.0e-77
E value
                  150
Match length
                  58
% identity
NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
                  216532
Seq. No.
Seq. ID
                  LIB3147-042-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2262159
                  382
BLAST score
E value
                  5.0e-37
Match length
                  117
                  63
% identity
NCBI Description
                 (AC002329) predicted protein similar to S.pombe protein
                  C5H10.03 [Arabidopsis thaliana]
Seq. No.
                  216533
                  LIB3147-042-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  509
E value
                  9.0e-52
Match length
                  143
                  70
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  216534
Seq. ID
                  LIB3147-042-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  387
                  2.0e-37
E value
Match length
                  105
                  74
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  216535
                  LIB3147-042-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3766368
BLAST score
                  253
E value
                  1.0e-21
Match length
                  126
% identity
                  44
NCBI Description (AL031907) putative trascription factor, ccr4-associated
                  factor homolog [Schizosaccharomyces pombe]
Seq. No.
                  216536
                  LIB3147-042-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3861188
BLAST score
                  215
E value
                  2.0e-17
Match length
                  84
```



(AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia NCBI Description prowazekii] 216537 Seq. No.

LIB3147-042-Q1-K1-E7 Seq. ID BLASTX Method NCBI GI g3452497

BLAST score 643 2.0e-67 E value Match length 139 88 % identity

NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No. 216538

LIB3147-042-Q1-K1-E9 Seq. ID

BLASTX Method NCBI GI g2853219 BLAST score 301 5.0e-39 E value Match length 116 63 % identity

NCBI Description (AJ000923) glutathione transferase [Carica papaya]

Seq. No. 216539

Seq. ID LIB3147-042-Q1-K1-F2

Method BLASTX NCBI GI g1945440 BLAST score 189 E value 2.0e-14 47 Match length 85

% identity

NCBI Description (U93094) salt-inducible protein [Medicago sativa]

216540 Seq. No.

Seq. ID LIB3147-042-Q1-K1-F3

BLASTX Method NCBI GI q3928093 BLAST score 415 E value 7.0e-41Match length 114 73 % identity

NCBI Description (AC005770) IVR-like protein [Arabidopsis thaliana]

Seq. No. 216541

LIB3147-042-Q1-K1-F6 Seq. ID

Method BLASTX a2677830 NCBI GI BLAST score 541 E value 2.0e-55 116 Match length % identity 92

NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 216542

Seq. ID LIB3147-042-Q1-K1-F8

Method BLASTX NCBI GI g3914667



```
BLAST score
                   208
E value
                   7.0e-17
Match length
                  68
% identity
                   66
NCBI Description
                  50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
                  >gi 2459427 (AC002332) putative chloroplast 50S ribosomal
                  protein L28 [Arabidopsis thaliana]
Seq. No.
                  216543
Seq. ID
                  LIB3147-042-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  556
E value
                  3.0e-57
Match length
                  139
% identity
                  71
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  216544
Seq. ID
                  LIB3147-042-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g119354
BLAST score
                  523
E value
                  1.0e-53
Match length
                  116
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185
                  phosphopyruvate hydratase (EC 4.2.1.11) - tomato
                  >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon
                  esculentum]
Seq. No.
                  216545
Seq. ID
                  LIB3147-042-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q2827469
BLAST score
                  219
E value
                  4.0e-18
Match length
                  75
% identity
                  61
NCBI Description (AF044255) NOSA [Dictyostelium discoideum]
Seq. No.
                  216546
Seq. ID
                  LIB3147-042-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3176668
                  562
BLAST score
E value
                  6.0e-58
```

Match length 134 % identity

NCBI Description (AC004393) Similar to ribosomal protein L17 gb X62724 from

Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and

gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No. 216547

Seq. ID LIB3147-042-Q1-K1-H1

Method BLASTX



q2746719 NCBI GI BLAST score 386 1.0e-37 E value Match length 82 % identity 96

NCBI Description (AF038386) histone H2B [Capsicum annuum]

216548 Seq. No.

Seq. ID LIB3147-042-Q1-K1-H10

Method BLASTX NCBI GI q2129771 BLAST score 285 E value 7.0e-28Match length 75 % identity 79

NCBI Description xyloglucan endotransqlycosylase-related protein XTR-6 -

Arabidopsis thaliana >gi 1244758 (U43488) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299 emb CAB39602.1 (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No. 216549

Seq. ID LIB3147-042-Q1-K1-H11

Method BLASTX NCBI GI g2654122 BLAST score 283 E value 2.0e-25 97 Match length % identity 61

NCBI Description (AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No. 216550

Seq. ID LIB3147-042-Q1-K1-H12

Method BLASTX NCBI GI q4415930 BLAST score 183 E value 1.0e-13 Match length 64 % identity 61

(AC006418) unknown protein [Arabidopsis thaliana] NCBI Description

>gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 216551

Seq. ID LIB3147-042-Q1-K1-H2

Method BLASTX NCBI GI g2407802 BLAST score 156 E value 1.0e-10 33 Match length % identity

NCBI Description (Y12576) histone H2B [Arabidopsis thaliana]

216552 Seq. No.

Seq. ID LIB3147-042-Q1-K1-H4

Method BLASTX NCBI GI g485514



```
BLAST score
                  268
                  1.0e-23
E value
Match length
                  56
% identity
                  89
                  ADR11-2 protein - soybean (fragment)
NCBI Description
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
Seq. No.
                  216553
Seq. ID
                  LIB3147-042-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  427
                  4.0e-42
E value
Match length
                  104
                  79
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  216554
Seq. No.
Seq. ID
                  LIB3147-042-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q730463
BLAST score
                  314
E value
                  7.0e-29
Match length
                  105
% identity
                  57
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
Seq. No.
                  216555
Seq. ID
                  LIB3147-043-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2398679
BLAST score
                  719
E value
                  2.0e-76
Match length
                  140
                  96
% identity
NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                  synthase [Morinda citrifolia]
Seq. No.
                  216556
Seq. ID
                  LIB3147-043-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q2951777
BLAST score
                  207
E value
                  2.0e-16
                  118
Match length
% identity
                  41
NCBI Description (AB011823) translation initiation factor 3
                   [Schizosaccharomyces pombe]
```

216557

LIB3147-043-Q1-K1-A3

Seq. No.

Seq. ID

BLAST score

E value

498

1.0e-50



```
BLASTX
Method
                  q3868853
NCBI GI
BLAST score
                  229
E value
                  6.0e-19
                  68
Match length
                  65
% identity
                 (AB013853) GPI-anchored protein [Vigna radiata]
NCBI Description
                  216558
Seq. No.
                  LIB3147-043-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                  480
                  2.0e-48
E value
                  128
Match length
% identity
                  75
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                  (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  216559
                  LIB3147-043-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3098571
BLAST score
                  211
                  7.0e-17
E value
Match length
                  96
% identity
                  44
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
                  216560
Seq. No.
Seq. ID
                  LIB3147-043-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  682
E value
                  5.0e-72
Match length
                  140
% identity
                  10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  216561
Seq. ID
                  LIB3147-043-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g548852
BLAST score
                  361
E value
                  2.0e-34
Match length
                  82
% identity
                  80
                  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  216562
Seq. ID
                  LIB3147-043-Q1-K1-B2
                  BLASTX
Method
NCBI GI
                  g4206124
```



```
Match length
% identity
                  (AF097668) T-complex protein 1 epsilon subunit
NCBI Description
                  [Mesembryanthemum crystallinum]
Seq. No.
                  216563
                  LIB3147-043-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173043
                  301
BLAST score
E value
                  2.0e-27
Match length
                  65
% identity
                  91
                  60S RIBOSOMAL PROTEIN L38 >gi 479441 pir S33899 ribosomal
NCBI Description
                  protein L38 - tomato (cv. Moneymaker)
                  >gi_313027_emb_CAA49599_ (X69979) ribosomal protein L38
                  [Lycopersicon esculentum]
Seq. No.
                  216564
Seq. ID
                  LIB3147-043-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q1076670
BLAST score
                  749
E value
                  7.0e-80
Match length
                  144
% identity
                  96
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi_668985_emb_CAA59062_ (X84319) NADH dehydrogenase
                  [Solanum tuberosum]
Seq. No.
                  216565
Seq. ID
                  LIB3147-043-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g82200
BLAST score
                  217
E value
                   2.0e-17
Match length
                  137
% identity
                   39
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
Seq. No.
                   216566
Seq. ID
                  LIB3147-043-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2661422
BLAST score
                   499
E value
                   1.0e-50
Match length
                  118
                  83
% identity
                  (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                   [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
```

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3147-043-Q1-K1-C1

216567

BLASTX Method NCBI GI g82537



```
BLAST score
                  130
E value
                  1.0e-13
Match length
                  59
% identity
                  66
                  hypothetical 8K protein (rps12-trnN intergenic region) -
NCBI Description
                  rice chloroplast >gi_12039_emb_CAA33943_ (X15901) ORF72
                  [Oryza sativa] >gi_12063_emb_CAA33917_ (X15901) ORF72
                  [Oryza sativa] >gi_226659_prf__1603356CK ORF 71 [Oryza
                  sativa]
Seq. No.
                  216568
Seq. ID
                  LIB3147-043-Q1-K1-C12
Method
                  BLASTX
                  q2116599
```

Method BLASTX
NCBI GI g2116599
BLAST score 223
E value 3.0e-18
Match length 64
% identity 69

NCBI Description (AB003779) leucoanthocyanidin dioxygenase [Perilla

frutescens]

Seq. No. 216569

Seq. ID LIB3147-043-Q1-K1-C4

Method BLASTX
NCBI GI g3913416
BLAST score 500
E value 1.0e-50
Match length 135
% identity 72

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_2129920_pir__S68990 adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle

>gi_758695 (U12573) S-adenosyl-L-methionine decarboxylase
proenzyme [Catharanthus roseus] >gi_1094441_prf__2106177A

Met(S-adenosyl) decarboxylase [Catharanthus roseus]

Seq. No. 216570

Seq. ID LIB3147-043-Q1-K1-C7

Method BLASTX
NCBI GI g1408471
BLAST score 165
E value 2.0e-11
Match length 36
% identity 92

NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis

thaliana] >gi_3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 216571

Seq. ID LIB3147-043-Q1-K1-C8

Method BLASTX
NCBI GI g1346806
BLAST score 150
E value 1.0e-09
Match length 35
% identity 74

NCBI Description PROFILIN 3 >gi 1008445 emb CAA61945 (X89827) profilin



[Triticum aestivum]

```
216572
Seq. No.
Seq. ID
                   LIB3147-043-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q4105798
BLAST score
                   253
                   9.0e-22
E value
                   131
Match length
% identity
                   34
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   216573
Seq. No.
                   LIB3147-043-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4249662
                   535
BLAST score
                   7.0e-55
E value
                   124
Match length
                   84
% identity
                   (AF089810) Altered Response to Gravity [Arabidopsis
NCBI Description
                   thaliana]
                   216574
Seq. No.
                   LIB3147-043-Q1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3421109
BLAST score
                   354
E valué
                   5.0e-47
Match length
                   110
                   88
% identity
NCBI Description
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
                   thaliana]
                   216575
Seq. No.
Seq. ID
                   LIB3147-043-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g1724114
BLAST score
                   175
                    9.0e-13
E value
                    38
Match length
% identity
                    92
NCBI Description
                   (U80041) Af10-protein [Avena fatua]
                    216576
Seq. No.
Seq. ID
                   LIB3147-043-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g125887
                    232
BLAST score
E value
                    3.0e-19
Match length
                   133
% identity
                   ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                   >gi_82092_pir__S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
```

esculentum]



```
Seq. No.
                  216577
Seq. ID
                  LIB3147-043-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q585960
BLAST score
                  211
                  6.0e-17
E value
Match length
                  43
                   93
% identity
NCBI Description
                  PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
                  >gi_433665_emb_CAA81412_ (Z26753) Sec61 beta-subunit
                  homolog [Arabidopsis thaliana]
Seq. No.
                  216578
                  LIB3147-043-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539545
BLAST score
                  458
                   9.0e-46
E value
                  97
Match length
% identity
                  90
NCBI Description (Y16644) PRCI [Nicotiana tabacum]
                  216579
Seq. No.
                  LIB3147-043-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q166867
                   340
BLAST score
                   3.0\dot{e} - 32
E value
Match length
                  88
                   76
% identity
NCBI Description (J05216) ribosomal protein S11 (probable start codon at bp
                   67) [Arabidopsis thaliana]
                   216580
Seq. No.
Seq. ID
                  LIB3147-043-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   q1694976
BLAST score
                   382
E value
                   7.0e-37
Match length
                  107
% identity
                   67
                  (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
Seq. No.
                   216581
                  LIB3147-043-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350680
BLAST score
                  213
E value
                   4.0e-17
Match length
                  47
                   83
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
```

Seq. No. 216582

Seq. ID LIB3147-043-Q1-K1-E6

Seq. No.

216587



```
Method
                  BLASTX
                  g4263704
NCBI GI
BLAST score
                  205
E value
                  3.0e-16
Match length
                  82
                  50
% identity
                  (AC006223) putative sugar starvation-induced protein
NCBI Description
                  [Arabidopsis thaliana]
                  216583
Seq. No.
                  LIB3147-043-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82308
BLAST score
                  591
E value
                  2.0e-61
Match length
                  107
                  99
% identity
NCBI Description myb protein 308 - garden snapdragon
                  216584
Seq. No.
                  LIB3147-043-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133867
                  566
BLAST score
                 ~2.0e-58
E value
Match length
                  127
% identity
                  85
                 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                  216585
                  LIB3147-043-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262233
BLAST score
                  240
E value
                  3.0e-20
Match length
                  129
% identity
NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216586
Seq. ID
                  LIB3147-043-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g135535
BLAST score
                  367
E value
                  4.0e-35
                  78
Match length
                  92
% identity
                  T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                  (CCT-ALPHA) >gi 322602 pir JN0448 t-complex polypeptide
                  Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
                  (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                  thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                  alpha/TCP-1 [Arabidopsis thaliana]
```

NCBI Description



```
Seq. ID
                   LIB3147-043-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   q3980396
BLAST score
                   190
                   2.0e-14
E value
Match length
                   35
                   100
% identity
NCBI Description
                   (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                   thaliana]
Seq. No.
                   216588
Seq. ID
                   LIB3147-043-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g1800281
BLAST score
                   539
                   3.0e-55
E value
Match length
                   116
                   20
% identity
                   (U82086) polyubiquitin [Fragaria x ananassa]
NCBI Description
Seq. No.
                   216589
                   LIB3147-043-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3513727
BLAST score
                   609
E value
                   2.0e-63
Match length
                   140
                   89
% identity
                   (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                   TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                   kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                   thaliana] >gi 4539358 emb CAB40052.1 (AL049525) putative
                   protein [Arabidopsis thaliana]
Seq. No.
                   216590
Seq. ID
                   LIB3147-043-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g141597
BLAST score
                   330
E value
                   1.0e-30
Match length
                   132
% identity
                   56
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   216591
Seq. ID
                   LIB3147-043-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   q3128168
BLAST score
                   153
E value
                   5.0e-10
                   29
Match length
                   79
% identity
```

[Arabidopsis thaliana]

(AC004521) putative carboxyl-terminal peptidase

Method

BLASTX



```
216592
Seq. No.
Seq. ID
                  LIB3147-043-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                   q2583123
                   331
BLAST score
                   7.0e-31
E value
Match length
                   88
                   70
% identity
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                   216593
                  LIB3147-043-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4098129
BLAST score
                   467
E value
                   5.0e-61
                  127
Match length
% identity
                   94
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   216594
                  LIB3147-043-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2129842
                  144
BLAST score
                 .4.0e-09
E value
Match length
                   71
% identity
                   41
NCBI Description
                  SE60 protein - soybean >gi_509769_emb_CAA79164_ (Z18359)
                   seed-specific low molecular weight sulfur-rich protein
                   [Glycine max]
Seq. No.
                   216595
Seq. ID
                   LIB3147-043-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   q3757519
BLAST score
                   374
E value
                   5.0e-36
Match length
                  142
% identity
                   53
NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   216596
Seq. ID
                  LIB3147-043-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3269289
BLAST score
                  195
E value
                   3.0e-15
                  84
Match length
% identity
                   48
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   216597
Seq. No.
Seq. ID
                  LIB3147-043-Q1-K1-H11
```



```
q3292831
NCBI GI
BLAST score
                     503
                     4.0e-51
E value
Match length
                     132
% identity
                     70
NCBI Description
                     (AL031018) putative serine/threonine kinase [Arabidopsis
                     thaliana]
                     216598
Seq. No.
Seq. ID
                     LIB3147-043-Q1-K1-H12
Method
                     BLASTX
NCBI GI
                     q508545
BLAST score
                     204
E value
                     2.0e-22
Match length
                     85
% identity
                     72
NCBI Description (L34340) zein [Zea mays]
                     216599
Seq. No.
                     LIB3147-043-Q1-K1-H2
Seq. ID
Method
                     BLASTN
NCBI GI
                     q433664
BLAST score
                     42
E value
                     2.0e-14
Match length
                     136
% identity
                     87
NCBI Description A.thaliana for Sec61 beta-subunit homolog
                     216600
Seq. No.
                     LIB3147-043-Q1-K1-H3
Seq. ID
Method
                     BLASTX
NCBI GI
                     q232041
BLAST score
                     162
E value
                     3.0e-13
Match length
                     68
% identity
                     68
NCBI Description
                     1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
                     (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN AP4 OR PAE12)
                     >gi_81731_pir__S22513 ethylene-forming enzyme - apple tree >gi_19545_emb_CAA43662_ (X61390) ethylene related [Malus
                     domestica] >gi_168337 (M81794) ripening-related protein
                     [Malus sylvestris] >gi_3153159_emb_CAA74328_ (Y14005) ACC oxidase [Malus domestica] >gi_3641491 (AF030859) ACC oxidase [Malus domestica] >gi_384329_prf_1905416A
                     aminocyclopropane carboxylate oxidase [Malus domestica]
Seq. No.
                     216601
Seq. ID
                     LIB3147-043-Q1-K1-H4
Method
                     BLASTX
```

Method BLASTX
NCBI GI g543867
BLAST score 543
E value 9.0e-56
Match length 140
% identity 81

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1076684_pir__A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato



>gi 303626 dbj BAA03526 (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No. 216602

LIB3147-043-Q1-K1-H5 Seq. ID

Method BLASTX NCBI GI g4090533 BLAST score 509 E value 9.0e-52 Match length 132 % identity 74

NCBI Description (U68215) ACC oxidase [Carica papaya]

216603 Seq. No.

LIB3147-043-Q1-K1-H7 Seq. ID

Method BLASTX NCBI GI g3522936 BLAST score 345 E value 2.0e-32 Match length 139 % identity 52

NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis

thaliana]

Seq. No. 216604

LIB3147-044-Q1-K1-A10 Seq. ID

Method BLASTX NCBI GI g3420057 197 BLAST score E value 2.0e-15 Match length 58

57 % identity

NCBI Description (AC004680) putative ABC transporter [Arabidopsis thaliana]

216605 Seq. No.

Seq. ID LIB3147-044-Q1-K1-A2

Method BLASTX NCBI GI q2829899 BLAST score 292 E value 3.0e-26 Match length 129 % identity 43

NCBI Description (AC002311) similar to ripening-induced protein,

gp AJ001449 2465015 and major#latex protein,

gp X91961 1107495 [Arabidopsis thaliana]

Seq. No. 216606

Seq. ID LIB3147-044-Q1-K1-A9

Method BLASTX NCBI GI g1931619 BLAST score 639 E value 5.0e-67 Match length 133 95 % identity

NCBI Description (U93208) glyceraldehyde 3-phosphate dehydrogenase

[Lycopersicon esculentum]



```
216607
Seq. No.
Seq. ID
                  LIB3147-044-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g4106388
BLAST score
                  150
                  1.0e-09
E value
Match length
                  67
                  49
% identity
NCBI Description (AF074849) unknown [Arabidopsis thaliana]
Seq. No.
                  216608
                  LIB3147-044-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170508
BLAST score
                  567
                  1.0e-58
E value
Match length
                  111
                  98
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
                  >gi_2119931_pir__S60244 translation initiation factor
                  eIF-4A.8, anther-specific - common tobacco
                  >gi_475219_emb_CAA55639_ (X79004) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
                  >gi_475221_emb_CAA55640_ (X79005) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
Seq. No.
                  216609
Seq. ID
                  LIB3147-044-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3608127
BLAST score
                  351
E value
                  3.0e - 33
Match length
                  70
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                  216610
                  LIB3147-044-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1815759
BLAST score
                  245
E value
                  8.0e-21
Match length
                  127
% identity
NCBI Description (U85499) pollen-specific protein [Phalaris coerulescens]
Seq. No.
                  216611
Seq. ID
                  LIB3147-044-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  9.0e-11
E value
Match length
                  48
                  67
% identity
```

Seq. No. 216612

NCBI Description Xenopus laevis cDNA clone 27A6-1



Seq. ID LIB3147-044-Q1-K1-B6 Method BLASTX

NCBI GI q2828147 BLAST score 310 E value 2.0e-28 Match length 124 52 % identity

NCBI Description (AF042384) BC-2 protein [Homo sapiens]

Seq. No. 216613

Seq. ID LIB3147-044-Q1-K1-B7

Method BLASTX NCBI GI q3759184 BLAST score 576 E value 1.0e-59 Match length 145 73 % identity

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 216614

LIB3147-044-Q1-K1-B8 Seq. ID

Method BLASTX NCBI GI q1841464 BLAST score 525 E value 1.0e-53 Match length 119 % identity 51

NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 216615

Seq. ID LIB3147-044-Q1-K1-C10

Method BLASTN NCBI GI q3821780 BLAST score 36 E value 8.0e-11 Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 216616

Seq. ID LIB3147-044-Q1-K1-C3

Method BLASTX NCBI GI g3913008 BLAST score 636 E value 1.0e-66 Match length 143 % identity 85

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description

>gi_3021338_emb_CAA06308_ (AJ005041) cytosolic
fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No. 216617

Seq. ID LIB3147-044-Q1-K1-C5

Method BLASTX NCBI GI g2879811 BLAST score 392 E value 3.0e-38



```
Match length
                  80
% identity
                  95
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
Seq. No.
                  216618
                  LIB3147-044-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1842188
BLAST score
                  581
E value
                  3.0e-60
Match length
                  121
% identity
                  91
NCBI Description
                  (Y08499) mitochondrial phosphate translocator [Betula
                  pendula]
Seq. No.
                  216619
                  LIB3147-044-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3551958
BLAST score
                  190
E value
                  2.0e-14
Match length
                  63
                  56
% identity
NCBI Description
                  (AF082032) senescence-associated protein 12 [Hemerocallis
                  hybrid cultivar]
Seq. No.
                  216620
Seq. ID
                  LIB3147-044-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2317901
BLAST score
                  330
E value
                  1.0e-30
Match length
                  150
% identity
                  51
NCBI Description (U89959) Similar to vesicle transport protein, PIR
                  Accession Number A55931 [Arabidopsis thaliana]
Seq. No.
                  216621
Seq. ID
                  LIB3147-044-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1076793
BLAST score
                  736
E value
                  2.0e-78
Match length
                  145
% identity
                  65
NCBI Description
                  calmodulin cam2 - maize >gi 747917 emb CAA54583 (X77397)
                  calmodulin [Zea mays]
Seq. No.
                  216622
Seq. ID
                  LIB3147-044-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g3834307
BLAST score
                  361
E value
                  2.0e-34
Match length
                  125
% identity
```

30325

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi 2832679



putative protein from Arabidopsis thaliana BAC gb AL021712. ESTs gb N65887 and gb N65627 come from this gene. [Arabidopsis thaliana]

216623 Seq. No. Seq. ID LIB3147-044-Q1-K1-D10 Method BLASTX NCBI GI g2431769 BLAST score 257 E value 2.0e-22 Match length 61 % identity 84 NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays] Seq. No. 216624 Seq. ID LIB3147-044-Q1-K1-D11 Method BLASTX NCBI GI g3402693 BLAST score 195 E value 4.0e-15 Match length 92 50 % identity NCBI Description (AC004697) unknown protein [Arabidopsis thaliana] Seq. No. 216625 Seq. ID LIB3147-044-Q1-K1-D2 Method BLASTX

NCBI GI g3023189 BLAST score 233 E value 2.0e-19 Match length 49 % identity 94

14-3-3-LIKE PROTEIN C (14-3-3-LIKE PROTEIN B) NCBI Description

>gi_1848208_emb_CAA72094_ (Y11211) 14-3-3-like protein B
[Nicotiana tabacum] >gi_2689475 (U91724) 14-3-3 isoform c

[Nicotiana tabacum]

Seq. No. 216626

Seq. ID LIB3147-044-Q1-K1-D3

Method BLASTX NCBI GI g3123274 BLAST score 287 E value 7.0e-26 77 Match length 73 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L32 (RP49) >gi 1928968 (U92431)

ribosomal protein 49 [Drosophila melanogaster]

>gi_2739301_emb_CAA74278_ (Y13939) ribosomal protein 49
[Drosophila melanogaster]

Seq. No. 216627

Seq. ID LIB3147-044-Q1-K1-D4

Method BLASTX NCBI GI g3024148 BLAST score 550 9.0e-57 E value Match length 110



% identity S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi 1655580 emb CAA95858 (Z71273) S-adenosyl-L-methionine synthetase 3 [Catharanthus roseus] 216628 Seq. No. LIB3147-044-Q1-K1-D5 Seq. ID Method BLASTX NCBI GI g4193388 BLAST score 302 E value 1.0e-27 Match length 62 90 % identity (AF091455) translationally controlled tumor protein [Hevea NCBI Description brasiliensis] 216629 Seq. No. LIB3147-044-Q1-K1-D8 Seq. ID Method BLASTX g2984225 NCBI GI BLAST score 311 2.0e-28 E value Match length 129 % identity 47 NCBI Description (AE000766) enolase-phosphatase E-1 [Aquifex aeolicus] 216630 Seq. No. LIB3147-044-Q1-K1-D9 Seq. ID Method BLASTX NCBI GI g549010 BLAST score 399 E value 7.0e-39 Match length 81 % identity 90 NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1
homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast
omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis
thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic
early release factor subunit 1-like protein [Arabidopsis thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No. 216631

Seq. ID LIB3147-044-Q1-K1-E1

Method BLASTX NCBI GI g544861 BLAST score 356 E value 8.0e-34 Match length 69 100 % identity

NCBI Description (S68003) actin [Striga asiatica=witchweed, Kuntze, Peptide

Partial, 114 aa] [Striga asiatica]



```
216632
Seq. No.
                  LIB3147-044-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3522938
NCBI GI
                  228
BLAST score
                  5.0e-19
E value
                  92
Match length
                  53
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216633
                  LIB3147-044-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                  g1483218
NCBI GI
                  241
BLAST score
                  3.0e-20
E value
                  47
Match length
                  89
% identity
                  (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                  thaliana]
                  216634
Seq. No.
                  LIB3147-044-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129248
                  184
BLAST score
E value
                  1.0e-13
                  100
Match length
                  23
% identity
                  ORGAN SPECIFIC PROTEIN S2 >gi 72318 pir KNPMS2 protein S2
NCBI Description
                  - garden pea >gi_295831_emb_CAA35944_ (X51595) S2 protein
                   [Pisum sativum]
                  216635
Seq. No.
                  LIB3147-044-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1439609
BLAST score
                  517
                  8.0e-53
E value
Match length
                  104
                   99
% identity
NCBI Description
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
                  hirsutum]
                   216636
Seq. No.
Seq. ID
                  LIB3147-044-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   g2129578
BLAST score
                   423
E value
                   8.0e-42
                  87
Match length
% identity
                  89
                  dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                   thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
```

30328

[Arabidopsis thaliana]

dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene

Seq. No.

Seq. ID

216642

LIB3147-044-Q1-K1-F11



```
216637
Seq. No.
Seq. ID
                  LIB3147-044-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3123264
BLAST score
                  415
                  5.0e-41
E value
                  86
Match length
                  90
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                  216638
Seq. No.
                  LIB3147-044-Q1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241939
BLAST score
                  47
                  3.0e-17
E value
Match length
                  147
% identity
                  60
                  Arabidopsis thaliana chromosome II BAC T26J13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  216639
                  LIB3147-044-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220462
                   610
BLAST score
                  1.0e-63
E value
Match length
                  142
% identity
                  85
                  (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
NCBI Description
                   gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF 00170 domains. [Arabidopsis thaliana]
Seq. No.
                   216640
                  LIB3147-044-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128175
BLAST score
                  144
E value
                   5.0e-09
                  83
Match length
                   40
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   216641
                  LIB3147-044-Q1-K1-F10
Seq. ID
                  BLASTN
Method
NCBI GI
                   g473216
BLAST score
                  36
E value
                   6.0e-11
                   44
Match length
                   95
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
```



Method BLASTX NCBI GI g3122785 230 BLAST score E value 3.0e-19Match length 97 % identity 52 NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal protein S14 [Lupinus luteus] Seq. No. 216643 LIB3147-044-Q1-K1-F2 Seq. ID Method BLASTN NCBI GI q3449313 BLAST score 34 E value 1.0e-09 Match length 62 % identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana] Seq. No. 216644 Seq. ID LIB3147-044-Q1-K1-F6 BLASTX Method NCBI GI g1350707 BLAST score 222 E value 4.0e-18 Match length 52 77 % identity 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal NCBI Description protein 17K - mouse >gi_404766 (L08651) ribosomal protein [Mus musculus] Seq. No. 216645 Seq. ID LIB3147-044-Q1-K1-F7 Method BLASTX NCBI GI g3687243 BLAST score 245 E value 8.0e-21 Match length 61 % identity 79 NCBI Description (AC005169) putative ribosomal protein [Arabidopsis thaliana] Seq. No. 216646 Seq. ID LIB3147-044-Q1-K1-F8 Method BLASTX NCBI GI g4204300 BLAST score 310 E value 9.0e-29 Match length 91

% identity

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

216647 Seq. No.

Seq. ID LIB3147-044-Q1-K1-G11

Method BLASTX NCBI GI q4006878



```
BLAST score
                   384
                   3.0e-37
E value
Match length
                   122
% identity
                   60
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
                   216648
Seq. No.
                   LIB3147-044-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3776013
BLAST score
                   254
E value
                   2.0e-22
Match length
                   67
                   70
% identity
NCBI Description (AJ010470) RNA helicase [Arabidopsis thaliana]
                   216649
Seq. No.
                   LIB3147-044-Q1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729480
BLAST score
                   336
E value
                   5.0e - 32
Match length
                   70
                   87
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
                   >gi_435647_dbj_BAA04232 (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479 (D38445)
                   root ferredoxin-NADP+ reductase [Oryza sativa]
                   >gi 1096932 prf 2113196A ferredoxin-NADP oxidoreductase
                   [Oryza sativa]
Seq. No.
                   216650
                   LIB3147-044-Q1-K1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   36
E value
                   9.0e-11
Match length
                   36
% identity
                   38
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   216651
Seq. ID
                   LIB3147-044-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   g3024697
BLAST score
                   638
E value
                   6.0e-67
Match length
                   128
% identity
                   92
                  T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
NCBI Description
                   (CCT-EPSILON) >gi 2213618 (AC000103) F21J9.12 [Arabidopsis
```

thaliana]

Seq. No. 216652

Seq. ID LIB3147-044-Q1-K1-G8

Method BLASTX NCBI GI g1899025

NCBI GI

E value

BLAST score

g3668097

3.0e-53

521



```
BLAST score
                   343
                   1.0e-32
E value
Match length
                  81
% identity
                   79
NCBI Description
                 (U28215) hexokinase 2 [Arabidopsis thaliana] >qi 3687232
                   (AC005169) hexokinase [Arabidopsis thaliana]
                  216653
Seq. No.
Seq. ID
                  LIB3147-044-Q1-K1-H10
Method
                  BLASTN
NCBI GI
                  q1658196
BLAST score
                  54
                  2.0e-21
E value
Match length
                  110
% identity
                  87
NCBI Description Ricinus communis calreticulin mRNA, complete cds
                  216654
Seq. No.
Seq. ID
                  LIB3147-044-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3559805
BLAST score
                  582
E value
                  2.0e-60
Match length
                  120
% identity
                  82
NCBI Description
                  (AJ006787) putative phytochelatin synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  216655
                  LIB3147-044-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548437
BLAST score
                  171
E value
                   3.0e-12
Match length
                  90
% identity
                   41
NCBI Description
                  OSH1 PROTEIN >gi_1078479_pir__S53463 SWH1 protein (version
                  1) - yeast (Saccharomyces cerevisiae) >gi 456143 (L28920)
                  Oshlp [Saccharomyces cerevisiae]
Seq. No.
                  216656
Seq. ID
                  LIB3147-044-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1665817
BLAST score
                  142
E value
                  7.0e-09
Match length
                  47
                  57
% identity
NCBI Description
                 (D87466) Similar to S.cerevisiae hypothetical protein L3111
                   (S59316) [Homo sapiens]
Seq. No.
                  216657
Seq. ID
                  LIB3147-044-Q1-K1-H6
                BLASTX
Method
```



Match length 128 79 % identity NCBI Description

(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

216658 Seq. No. Seq. ID

LIB3147-044-Q1-K1-H8

Method BLASTX NCBI GI q3947448 BLAST score 207 1.0e-16 E value Match length 93 44 % identity

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3

comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 216659

Seq. ID LIB3147-044-Q1-K1-H9

Method BLASTN NCBI GI q3821780 BLAST score 36 6.0e-11 E value Match length 48

% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

216660 Seq. No.

Seq. ID LIB3147-045-Q1-K1-A10

Method BLASTX NCBI GI g1213629 BLAST score 390 E value 9.0e-38 127 Match length

% identity 57

NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 216661

Seq. ID LIB3147-045-Q1-K1-A11

Method BLASTN NCBI GI g12292 BLAST score 229 E value 1.0e-126 353 Match length % identity 91

NCBI Description Spinach chloroplast DNA homologous to ARS and ARC elements

upstream of rDNA operon

Seq. No. 216662

Seq. ID LIB3147-045-Q1-K1-A4

Method BLASTX



```
NCBI GI
                    q3157922
 BLAST score
                    272
 E value
                    4.0e-24
 Match length
                    65
                    77
 % identity
                   (AC002131) Contains similarity to proline-rich protein,
 NCBI Description
                   gb S68113 from Brassica napus. [Arabidopsis thaliana]
 Seq. No.
                   216663
 Seq. ID
                   LIB3147-045-Q1-K1-B1
 Method
                   BLASTX
 NCBI GI
                   g2213867
 BLAST score
                   368
                   1.0e-35
 E value
 Match length
                   82
                   87
 % identity
                   (AF003124) fructose-biphosphate aldolase [Mesembryanthemum
 NCBI Description
                   crystallinum]
 Seq. No.
                   216664
                   LIB3147-045-Q1-K1-B10
 Seq. ID
 Method
                   BLASTX
                   g1103712
, NCBI GI
 BLAST score
                   597
 E value
                    4.0e-62
 Match length
                   138
                    87
 % identity
 NCBI Description (X83729) inorganic pyrophosphatase [Nicotiana tabacum]
 Seq. No.
                    216665
 Seq. ID
                   LIB3147-045-Q1-K1-B12
 Method
                   BLASTX
 NCBI GI
                    g4218120
 BLAST score
                    381
 E value
                    1.0e-36
 Match length
                   101
 % identity
                    68
                    (AL035353) Proline-rich APG-like protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    216666
 Seq. ID
                   LIB3147-045-Q1-K1-B2
 Method
                   BLASTX
 NCBI GI
                    g3193292
 BLAST score
                    456
 E value
                    1.0e-45
                   134
 Match length
 % identity
                    65
                   (AF069298) similar to ATPases associated with various
 NCBI Description
                    cellular activites (Pfam: AAA.hmm, score: 230.91)
                    [Arabidopsis thaliana]
                    216667
 Seq. No.
 Seq. ID
                   LIB3147-045-Q1-K1-B4
```

BLASTX Method NCBI GI g508304 BLAST score 287



```
1.0e-25
E value
Match length
                  64
% identity
                  81
NCBI Description
                  (L22305) corC [Medicago sativa]
Seq. No.
                  216668
Seq. ID
                  LIB3147-045-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4567249
BLAST score
                  587
E value
                   7.0e-61
Match length
                  133
% identity
                  81
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216669
                  LIB3147-045-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2052383
BLAST score
                  256
E value
                   5.0e-22
Match length
                  53
% identity
                   83
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                   216670
                  LIB3147-045-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3924612
BLAST score
                   341
E value
                   6.0e - 32
Match length
                  74
                  89
% identity
NCBI Description
                  (AF069442) mitochondrial elongation factor Tu [Arabidopsis
                   thaliana] >gi 4263511 gb AAD15337 (AC004044) mitochondrial
                   elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                   216671
Seq. ID
                  LIB3147-045-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                  36
E value
                   1.0e-10
Match length
                  36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   216672
Seq. ID
                  LIB3147-045-Q1-K1-C2
                  BLASTX
Method
NCBI GI
                   q485514
BLAST score
                   243
E value
                   1.0e-20
                   59
Match length
% identity
                   75
```

>gi 296443 emb CAA49341 (X69640) auxin down regulated

NCBI Description ADR11-2 protein - soybean (fragment)

Seq. No.

Seq. ID

216678

LIB3147-045-Q1-K1-C8



[Glycine max]

```
Seq. No.
                   216673
Seq. ID
                   LIB3147-045-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   q2979547
BLAST score
                   542
E value
                   2.0e-55
Match length
                   165
% identity
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   216674
Seq. ID
                  LIB3147-045-Q1-K1-C4
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   6.0e-11
Match length
                   48
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   216675
Seq. ID
                  LIB3147-045-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                   q2583108
BLAST score
                   423
E value
                   1.0e-41
Match length
                  118
% identity
                   71
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                   216676
Seq. ID
                  LIB3147-045-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4376203
BLAST score
                  275
E value
                   2.0e-24
Match length
                  139
% identity
                   40
NCBI Description
                  (U35226) putative cytochrome P-450 [Nicotiana
                  plumbaginifolia]
Seq. No.
                  216677
Seq. ID
                  LIB3147-045-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4115918
BLAST score
                  235
E value
                  1.0e-19
Match length
                  56
% identity
                  80
NCBI Description
                  (AF118222) similar to nascent polypeptide associated
                  complex alpha chain [Arabidopsis thaliana]
```

BLAST score

E value

659

3.0e-69



```
Method
                   BLASTX
NCBI GI
                   q4539408
BLAST score
                   160
E value
                   7.0e-11
Match length
                   50
% identity
                   62
NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]
Seq. No.
                   216679
Seq. ID
                  LIB3147-045-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                   q3024126
BLAST score
                   573
E value
                   3.0e-59
Match length
                  138
% identity
                   83
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
Seq. No.
                   216680
Seq. ID
                  LIB3147-045-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2583133
BLAST score
                  474
E value
                  1.0e-47
Match length
                  112
% identity
                   85
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
Seq. No.
                  216681
Seq. ID
                  LIB3147-045-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  713
E value
                  1.0e-75
Match length
                  145
                   90
% identity
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
Seq. No.
                  216682
Seq. ID
                  LIB3147-045-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g4049400
BLAST score
                  41
E value
                  8.0e-14
Match length
                  69
                  90
% identity
NCBI Description Arabidopsis thaliana mRNA for glutathione transferase AtGST
Seq. No.
                  216683
Seq. ID
                  LIB3147-045-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1524121
```



```
Match length
                   148
                   82
% identity
                   (X96539) malate dehydrogenase [Mesembryanthemum
NCBI Description
                   crystallinum]
                   216684
Seq. No.
                   LIB3147-045-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3236235
BLAST score
                   355
                   1.0e-33
E value
Match length
                   127
                   51
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4056501 (AC005896) unknown protein [Arabidopsis
                   thaliana]
                   216685
Seq. No.
                   LIB3147-045-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g231660
                   463
BLAST score
                   7.0e-64
E value
                   143
Match length
% identity
                   78
                  HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
NCBI Description
Seq. No.
                   216686
                   LIB3147-045-Q1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                    g4033430
BLAST score
                    152
E value
                    5.0e-10
                    99
Match length
                    40
% identity
                   PYRUVATE KINASE (PK) >gi_3108349 (AF061507) pyruvate kinase [Drosophila melanogaster] >gi_3128475 (AF062478) pyruvate
NCBI Description
                    kinase [Drosophila melanogaster]
                    216687
Seq. No.
                    LIB3147-045-Q1-K1-E5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4567203
BLAST score
                    222
E value
                    4.0e-18
Match length
                    48
% identity
                    90
                    (AC007168) putative beta-hydroxyacyl-ACP dehydratase
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    216688
                    LIB3147-045-Q1-K1-E8
Seq. ID
```

Method BLASTX NCBI GI g126896 BLAST score 550 2.0e-56 E value Match length 132

% identity



```
% identity
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)
                  precursor, mit\overline{oc}hondrial - watermelon
                  >gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27
                  to 320) [Citrullus lanatus]
                  216689
Seq. No.
Seq. ID
                  LIB3147-045-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3551257
BLAST score
                  333
E value
                  4.0e-31
Match length
                  139
                  24
% identity
NCBI Description (AB012708) 98b [Daucus carota]
                  216690
Seq. No.
                  LIB3147-045-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g2695931
NCBI GI
                  354
BLAST score
                  2.0e-33
E value
                  119
Match length
                  61
% identity
NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.
                  216691
                  LIB3147-045-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3202042
                  320
BLAST score
                   1.0e-29
E value
Match length
                  116
                   59
% identity
NCBI Description (AF069324) 26S proteasome regulatory subunit S5A
                   [Mesembryanthemum crystallinum]
                   216692
Seq. No.
                  LIB3147-045-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4406819
BLAST score
                   476
E value
                   6.0e-48
Match length
                  134
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.
                   216693
                  LIB3147-045-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1408473
                   355
BLAST score
E value
                   1.0e-33
                  76
Match length
```

NCBI Description (U48939) actin depolymerizing factor 2 [Arabidopsis

% identity

94



thaliana]

```
Seq. No.
                  216694
                  LIB3147-045-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500341
BLAST score
                  155
                  3.0e-10
E value
                  38
Match length
                  74
% identity
                  50S RIBOSOMAL PROTEIN L36 >gi_1652406_dbj_BAA17328
NCBI Description
                  (D90905) 50S ribosomal protein L36 [Synechocystis sp.]
                  216695
Seq. No.
                  LIB3147-045-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  q2558962
NCBI GI
                  192
BLAST score
                  2.0e-19
E value
                  73
Match length
                  84
% identity
                  (AF025667) histone H2B1 [Gossypium hirsutum]
NCBI Description
                  216696
Seq. No.
                  LIB3147-045-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3122060
                  707
BLAST score
                  6.0e - 75
E value
                  146
Match length
                  93
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_2598657_emb_CAA10847_ (AJ222579) elongation factor
                  1-alpha (EFI-a) [Vicia faba]
Seq. No.
                  216697
Seq. ID
                  LIB3147-045-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q2129726
BLAST score
                   686
                  2.0e-72
E value
Match length
                  168
                   79
% identity
NCBI Description
                  RNA polymerase II third largest chain RPB35.5A -
                  Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi 4544370 gb AAD22281.1_AC006920_5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
Seq. No.
                   216698
                  LIB3147-045-Q1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g755147
BLAST score
                  232
                  1.0e-128
E value
Match length
                  289
```



NCBI Description Gossypium hirsutum vacuolar H+-ATPase proteolipid (16 kDa) subunit (cva16-2) mRNA, complete cds Seq. No. 216699 LIB3147-045-Q1-K1-H11 Seq. ID Method BLASTX

NCBI GI g120669 BLAST score 597 E value 5.0e-62 Match length 138 83 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde

3-phosphate dehydrogenase [Magnolia liliiflora]

216700 Seq. No.

LIB3147-045-Q1-K1-H3 Seq. ID

Method BLASTX NCBI GI g3176668 BLAST score 475 E value 6.0e - 49Match length 127 % identity 75

NCBI Description (AC004393) Similar to ribosomal protein L17 gb X62724 from ^

Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and

gb Z33937 come from this gene. [Arabidopsis thaliana]

216701 Seq. No.

Seq. ID LIB3147-046-Q1-K1-A2

Method BLASTX NCBI GI q4490728 BLAST score 211 E value 6.0e-17 Match length 50 72

% identity

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 216702

Seq. ID LIB3147-046-Q1-K1-A6

Method BLASTN NCBI GI g12434 BLAST score 38 E value 4.0e-12 Match length 46 % identity 96

NCBI Description Maize chloroplast psbB-psbF-petB-petD gene cluster

Seq. No. 216703

Seq. ID LIB3147-046-Q1-K1-B1

Method BLASTX NCBI GI g3176668 BLAST score 383 E value 3.0e-37 Match length 80 93 % identity



NCBI Description (AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No. 216704

Seq. ID LIB3147-046-Q1-K1-B11

Method BLASTX
NCBI GI g3885884
BLAST score 249
E value 2.0e-21
Match length 53
% identity 89

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 216705

Seq. ID LIB3147-046-Q1-K1-B12

Method BLASTX
NCBI GI g950299
BLAST score 559
E value 1.0e-57
Match length 116
% identity 88

NCBI Description (L46792) xyloglucan endotransglycosylase precursor

[Actinidia deliciosa]

Seq. No. 216706

Seq. ID LIB3147-046-Q1-K1-B2

Method BLASTX
NCBI GI g1351834
BLAST score 306
E value 5.0e-28
Match length 94
% identity 62

NCBI Description PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi_1016162

(U30821) ABC transporter subunit [Cyanophora paradoxa]

Seq. No. 216707

Seq. ID LIB3147-046-Q1-K1-B3

Method BLASTX
NCBI GI g1173027
BLAST score 384
E value 3.0e-37
Match length 108
% identity 71

NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal

protein L31 [Nicotiana glutinosa]

Seq. No. 216708

Seq. ID LIB3147-046-Q1-K1-B4

Method BLASTX
NCBI GI g2467274
BLAST score 199
E value 2.0e-15
Match length 84
% identity 52

NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]



```
Seq. No.
                   216709
Seq. ID
                   LIB3147-046-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g548774
BLAST score
                   314
E value
                   4.0e-29
Match length
                   92
% identity
                   68
NCBI Description
                  60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal
                   protein L7a - rice >gi_303855_dbj_BAA02156 (D12631)
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   216710
Seq. ID
                  LIB3147-046-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q4417271
BLAST score
                   600
E value
                   2.0e-62
Match length
                  141
% identity
                   81
NCBI Description
                  (AC007019) putative cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   216711
                  LIB3147-046-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2511570
BLAST score
                  260
E value
                  1.0e-22
Match length
                  66
% identity
                  76
NCBI Description
                  (Y13174) multicatalytic endopeptidase [Arabidopsis
                  thaliana]
Seq. No.
                  216712
Seq. ID
                  LIB3147-046-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q2500378
BLAST score
                  162
E value
                  3.0e-11
Match length
                  38
% identity
                  84
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                  216713
Seq. ID
                  LIB3147-046-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g3287270
BLAST score
                  693
E value
                  2.0e-73
Match length
                  137
% identity
                  93
```

Seq. No. 216714

NCBI Description

Seq. ID LIB3147-046-Q1-K1-C12

Method BLASTX

30343

(Y09533) involved in starch metabalism [Solanum tuberosum]

BLAST score

E value

570

6.0e-59



```
NCBI GI
                  q4321399
                   506
BLAST score
E value
                  2.0e-51
Match length
                  119
% identity
                  74
NCBI Description
                   (AF047039) omega-3 fatty acid desaturase [Perilla
                  frutescens]
Seq. No.
                  216715
                  LIB3147-046-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829899
                  295
BLAST score
E value
                  1.0e-26
Match length
                  123
% identity
                  46
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                  216716
                  LIB3147-046-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3287270
NCBI GI
                  375
BLAST score
E value
                  3.0e-36
                  105
Match length
                  72
% identity
NCBI Description
                  (Y09533) involved in starch metabalism [Solanum tuberosum]
Seq. No.
                  216717
                  LIB3147-046-Q1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2828187
BLAST score
                  40
E value
                   4.0e-13
Match length
                   48
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21C13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  216718
Seq. ID
                  LIB3147-046-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2407800
BLAST score
                  352
E value
                  2.0e-33
                  79
Match length
                  89
% identity
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                  216719
Seq. ID
                  LIB3147-046-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g425194
```

30344-

BLAST score

E value

431

1.0e-42



```
Match length
                   118
% identity
                   (L26243) heat shock protein [Spinacia oleracea] >qi 2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                  oleracea]
Seq. No.
                   216720
                  LIB3147-046-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g126896
BLAST score
                   283
E value
                   3.0e-25
Match length
                   83
                   72
% identity
NCBI Description
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                  >gi 319831 pir DEPUMW malate dehydrogenase (EC 1.1.1.37)
                  precursor, mitochondrial - watermelon
                   >gi 18297 emb CAA35239 (X17362) precursor protein (AA -27
                   to 320) [Citrullus lanatus]
Seq. No.
                   216721
                  LIB3147-046-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g967125
BLAST score
                   365
                   3.0e - 35
E value
Match length
                   83
                   62
% identity
NCBI Description
                  (U08140) calcium dependent protein kinase [Vigna radiata]
                   216722
Seq. No.
                  LIB3147-046-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3721926
BLAST score
                   204
E value
                   3.0e-16
Match length
                   98
% identity
NCBI Description
                  (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
Seq. No.
                   216723
Seq. ID
                   LIB3147-046-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g2708749
BLAST score
                   325
E value
                   3.0e-30
Match length
                   103
% identity
                   59
NCBI Description
                   (AC003952) putative senescence-assoc. rhodanese-like
                   protein [Arabidopsis thaliana]
Seq. No.
                   216724
Seq. ID
                  LIB3147-046-Q1-K1-E4
                  BLASTX
Method
NCBI GI
                   g4508078
```

Match length

NCBI Description

% identity

53

49

thaliana]



```
Match length
                   90
 % identity
                   87
                   (AC005882) 64134 [Arabidopsis thaliana]
 NCBI Description
                   216725
 Seq. No.
                   LIB3147-046-Q1-K1-E7
 Seq. ID
                   BLASTX
 Method
                   g1169546
 NCBI GI
                    202
 BLAST score
                   7.0e-16
 E value
                    96
 Match length
                    43
 % identity
                   PUTATIVE ER LUMEN PROTEIN RETAINING RECEPTOR C28H8.4
 NCBI Description
                    >qi 669010 (U20861) similar to endoplasmic reticulum lumen
                   protein retaining receptor [Caenorhabditis elegans]
                    216726
 Seq. No.
                   LIB3147-046-Q1-K1-F11
 Seq. ID
                    BLASTX
 Method
                    g4538993
 NCBI GI
                    341
 BLAST score
                    2.0e-32
. E value
 Match length
                    81
                    79
 % identity
                   (AL049481) putative host response protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    216727
                    LIB3147-046-Q1-K1-F12
 Seq. ID
                    BLASTN
 Method
                    g3821780
 NCBI GI
 BLAST score
                    36
 E value
                    7.0e-11
                    45
 Match length
                    65
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                    216728
                    LIB3147-046-Q1-K1-F2
 Seq. ID
 Method
                    BLASTX
                    q1350680
 NCBI GI
 BLAST score
                    308
                    3.0e-28
 E value
                    84
 Match length
                    71
 % identity
 NCBI Description 60S RIBOSOMAL PROTEIN L1
 Seq. No.
                    216729
 Seq. ID
                    LIB3147-046-Q1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    q4559358
 BLAST score
                    150
 E value
                    4.0e-10
```

30346

(AC006585) putative steroid binding protein [Arabidopsis

Seq. No.

216735



```
Seq. No.
                  216730
Seq. ID
                  LIB3147-046-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g544077
BLAST score
                  170
E value
                  4.0e-12
Match length
                  101
% identity
                  40
NCBI Description
                  COATOMER ZETA SUBUNIT (ZETA-COAT PROTEIN) (ZETA-COP)
                  >gi_539742_pir__A49465 coatomer zeta chain - bovine
                  >gi_441486_emb_CAA53539_ (X75935) coatomer [Bos taurus]
                  >gi_740139_prf__2004374A coatomer zeta [Bos taurus]
Seq. No.
                  216731
Seq. ID
                  LIB3147-046-01-K1-G7
Method
                  BLASTX
NCBI GI
                  q2408103
BLAST score
                  211
E value
                  6.0e-17
Match length
                  110
% identity
                  46
NCBI Description
                 (AJ001587) sid3 [Schizosaccharomyces pombe]
                  216732
Seq. No.
Seq. ID
                  LIB3147-046-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3702340
BLAST score
                  140
E value
                  1.0e-08
                  99
Match length
% identity
                  38
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216733
                  LIB3147-046-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1546692
BLAST score
                  250
E value
                   4.0e-23
Match length
                  102
                   55
% identity
NCBI Description
                 (X98805) peroxidase ATP19a [Arabidopsis thaliana]
Seq. No.
                  216734
Seq. ID
                  LIB3147-046-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                  558
E value
                  2.0e-57
Match length
                  108
                  99
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
```



```
Seq. ID
                  LIB3147-046-Q1-K1-H8
                  BLASTX
Method
NCBI GI
                  q1350707
BLAST score
                  212
E value
                  6.0e-17
Match length
                  52
                  73
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal
                  protein 17K - mouse >gi 404766 (L08651) ribosomal protein
                  [Mus musculus]
                  216736
Seq. No.
Seq. ID
                  LIB3147-047-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4098323
BLAST score
                  622
E value
                  3.0e-69
Match length
                  139
% identity
NCBI Description (U76746) beta-tubulin 3 [Triticum aestivum]
                  216737
Seq. No.
Seq. ID
                  LIB3147-047-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2129605
BLAST score
                  319
E value
                  1.0e-32
                  73
Match length
                  87
% identity
NCBI Description
                  GTP-binding protein 2 - Arabidopsis thaliana
                  >gi_2129702_pir__S71585 Rab2 homolog GTP-binding protein
                  ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2
                  [Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986)
                  GTP-binding protein GB2 [Arabidopsis thaliana]
Seq. No.
                  216738
Seq. ID
                  LIB3147-047-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                  g3435196
BLAST score
                  328
E value
                  1.0e-30
Match length
                  126
% identity
                  62
NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                  216739
Seq. ID
                  LIB3147-047-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2854070
BLAST score
                  157
E value
                  2.0e-10
                  43
```

Match length % identity

NCBI Description (AF044914) putative histone deacetylase [Arabidopsis

thaliana]

Seq. No. 216740

Seq. No.

Seq. ID

216745

LIB3147-047-Q1-K1-D5



```
Seq. ID
                   LIB3147-047-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   q1332579
BLAST score
                   369
E value
                   2.0e-35
Match length
                   125
% identity
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   216741
                   LIB3147-047-Q1-K1-C4
Seq. ID
Method
                   BLASTX
                   g2493494
NCBI GI
BLAST score
                   274
                   5.0e-37
E value
Match length
                   124
                   65
% identity
                   SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
NCBI Description
                   >gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase
                   [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                   aa]
Seq. No.
                   216742
                   LIB3147-047-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454480
                   163
*BLAST score
E value
                   3.0e-11
Match length
                   76
                   41
% identity
NCBI Description
                  (AC006234) putative (1-4)-beta-mannan endohydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   216743
                   LIB3147-047-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2506139
BLAST score
                   142
E value
                   2.0e-09
Match length
                   46
% identity
                   65
NCBI Description
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi_1314049_emb CAA91901 (Z67962)
                   archain/delta-COP [Oryza sativa]
Seq. No.
                   216744
Seq. ID
                   LIB3147-047-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   q4510345
BLAST score
                   145
E value
                   3.0e-16
Match length
                   110
% identity
                   45
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
```



```
BLASTX
Method
                   g2760349
NCBI GI
                   372
BLAST score
                   6.0e-38
E value
                  97
Match length
                  18
% identity
                  (U84969) ubiquitin [Arabidopsis thaliana]
NCBI Description
                  216746
Seq. No.
                  LIB3147-047-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  g4115925
NCBI GI
                  135
BLAST score
                  1.0e-21
E value
                  81
Match length
                  80
% identity
                  (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  216747
                  LIB3147-047-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g4510377
NCBI GI
BLAST score
                  179
                   4.0e-13
E value
Match length
                   47
                   72
% identity
                  (AC007017) putative RNA helicase A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216748
                  LIB3147-047-Q1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2828187
BLAST score
                   34
E value
                   1.0e-09
                   38
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21C13, complete sequence [Arabidopsis thaliana]
                   216749
Seq. No.
Seq. ID
                   LIB3147-047-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   q2911075
BLAST score
                   203
E value
                   7.0e-16
Match length
                   63
% identity
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                   216750
```

Seq. ID LIB3147-049-Q1-K1-A11

MethodBLASTXNCBI GIg2623295BLAST score370

E value

Match length

3.0e-12 49



```
2.0e-35
 E value
 Match length
                    146
 % identity
                    51
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    216751
 Seq. No.
                    LIB3147-049-Q1-K1-A3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2982331
 BLAST score
                    226
 E value
                    9.0e-19
 Match length
                    45
 % identity
                    98
                   (AF051251) TAT-binding protein homolog [Picea mariana]
 NCBI Description
 Seq. No.
                    216752
                    LIB3147-049-Q1-K1-A7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q266944
 BLAST score
                    431
 E value
                    7.0e-43
 Match length
                    85
                    93
 % identity
                    60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
 NCBI Description
                    >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic -
                    tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein
                   L2 [Lycopersicon esculentum]
 Seq. No.
                    216753
                    LIB3147-049-Q1-K1-A8
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2264315
 BLAST score
                    39
 E value
                    2.0e-12
 Match length
                    79
 % identity
                    87
y NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MRN17, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    216754
 Seq. ID
                    LIB3147-049-Q1-K1-A9
 Method
                    BLASTX
 NCBI GI
                    g3915847
 BLAST score
                    219
 E value
                    5.0e-18
 Match length
                    50
 % identity
                    80
                    40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
 NCBI Description
                    40S ribosomal protein S2 [Arabidopsis thaliana]
                    216755
 Seq. No.
 Seq. ID
                    LIB3147-049-Q1-K1-B1
 Method
                    BLASTX
 NCBI GI
                    g2791806
 BLAST score
                    173
```



```
% identity
                   65
NCBI Description
                   (AF041433) bet3 [Mus musculus]
                  216756
Seq. No.
                  LIB3147-049-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g4468218
NCBI GI
                  188
BLAST score
                   4.0e-14
E value
                  115
Match length
                  23
% identity
                  (AJ010025) unr-interacting protein [Homo sapiens]
NCBI Description
Seq. No.
                  216757
                  LIB3147-049-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                   q3063392
NCBI GI
BLAST score
                   250
                   3.0e-21
E value
Match length
                   66
                   70
% identity
                  (AB012932) Ca2+/H+ exchanger [Vigna radiata]
NCBI Description
Seq. No.
                   216758
                   LIB3147-049-Q1-K1-B12
Seq. ID
Method
                   BLASTX
                   q974782
NCBI GI
BLAST score
                   503
E value
                   5.0e-51
                   102
Match length
                   98
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   216759
Seq. No.
                   LIB3147-049-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122818
                   171
BLAST score
                   4.0e-12
E value
Match length
                   73
                   45
% identity
                   30S RIBOSOMAL PROTEIN S6 >qi 2196757 (AF003196) ribosomal
NCBI Description
                   protein S6 [Neisseria gonorrhoeae]
                   216760
Seq. No.
                   LIB3147-049-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464849
BLAST score
                   808
                   9.0e-87
E value
Match length
                   155
                   99
% identity
                   TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
```

alpha-tubulin [Prunus dulcis]

chain - almond >gi 20413 emb CAA47635 (X67162)



216761 Seq. No. Seq. ID LIB3147-049-Q1-K1-C2 Method BLASTX NCBI GI q4115918 290 BLAST score 5.0e-26 E value Match length 74 74 % identity (AF118222) similar to nascent polypeptide associated NCBI Description complex alpha chain [Arabidopsis thaliana] 216762 Seq. No. LIB3147-049-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI g461944 BLAST score 274 3.0e-24 E value Match length 108 56 % identity NCBI Description DNAJ PROTEIN HOMOLOG (DNAJ-1) >gi 18260 emb_CAA47925 (X67695) cs DnaJ-1 [Cucumis sativus] Seq. No. 216763 LIB3147-049-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI g4115918 BLAST score 313 1.0e-28 E value Match length 92 67 % identity NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana] 216764 Seq. No. LIB3147-049-Q1-K1-D1 Seq. ID Method BLASTX NCBI GI g3334138 BLAST score 299 E value 4.0e-27 Match length 103 % identity 58 NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin [Glycine max] Seq. No. 216765 Seq. ID LIB3147-049-Q1-K1-D10 Method BLASTX NCBI GI g3341685 BLAST score 461 E value 4.0e-46 Match length 135 71 % identity NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 216766

Seq. ID LIB3147-049-Q1-K1-D2

Method BLASTX



```
g1766048
NCBI GI
                   692
BLAST score
E value
                   4.0e-73
Match length
                   169
% identity
                   82
                   (U81994) NAD+ dependent isocitrate dehydrogenase subunit 2
NCBI Description
                   [Arabidopsis thaliana]
                   216767
Seq. No.
Seq. ID
                   LIB3147-049-Q1-K1-D3
Method
                   BLASTX
                   g2660673
NCBI GI
BLAST score
                   169
                   7.0e-12
E value
                   131
Match length
                   17
% identity
                  (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
                   216768
Seq. No.
                   LIB3147-049-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1483563
BLAST score
                   501
                   8.0e-51
E value
Match length
                   127
                   75
% identity
NCBI Description
                  (X99825) leucine aminopeptidase [Petroselinum crispum]
                   216769
Seq. No.
                   LIB3147-049-Q1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3024516
BLAST score
                   717
                   4.0e-76
E value
Match length
                   142
% identity
                   99
NCBI Description
                   RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong
                   similarity to A. thaliana ara-\overline{2} (gb_ATHARA2). ESTs
                   gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene.
                   [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related
                   small GTPase [Arabidopsis thaliana]
                   216770
Seq. No.
Seq. ID
                   LIB3147-049-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                   g4107099
BLAST score
                   391
E value
                   8.0e-38
Match length
                   117
% identity
                   (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                   >gi 4156245 dbj BAA37112 (AB012570) ATHP3 [Arabidopsis
                   thaliana]
```

Seq. No. 216771

Seq. ID LIB3147-049-Q1-K1-E2

Method BLASTX

Method

NCBI GI

BLAST score

BLASTX

467

g170920



```
NCBI GI
                  g1212921
BLAST score
                  224
                  6.0e-19
E value
                  63
Match length
                  70
% identity
NCBI Description
                  (X95953) aquaporin [Helianthus annuus]
                  216772
Seq. No.
                  LIB3147-049-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g974782
BLAST score
                  249
                  3.0e-21
E value
Match length
                  51
                  98
% identity
NCBI Description
                  (Z49150) cobalamine-independent methionine synthase
                  [Solenostemon scutellarioides]
                  216773
Seq. No.
                  LIB3147-049-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3360289
                  330
BLAST score
                  1.0e-30
E value
                  98
Match length
% identity
                  65
NCBI Description
                  (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
                  216774
Seq. No.
                  LIB3147-049-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  282
                  5.0e-25
E value
Match length
                  74
% identity
                  76
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                  [Gossypium hirsutum]
Seq. No.
                  216775
Seq. ID
                  LIB3147-049-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q2832675
BLAST score
                  252
E value
                  2.0e-21
Match length
                  111
% identity
NCBI Description
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  216776
Seq. ID
                  LIB3147-049-Q1-K1-F12
```



```
7.0e-47
E value
Match length
                  86
                  100
% identity
NCBI Description
                  (M62396) ribosomal protein L41 [Candida maltosa]
                  216777
Seq. No.
                  LIB3147-049-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567279
BLAST score
                  350
                   4.0e-33
E value
Match length
                  109
                   65
% identity
                  (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   216778
Seq. No.
                  LIB3147-049-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827637
BLAST score
                   278
E value
                   1.0e-24
                   70
Match length
                   70
% identity
NCBI Description
                  (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                   216779
                  LIB3147-049-Q1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2323410
BLAST score
                   363
E value
                   9.0e-35
Match length
                   117
% identity
                   64
                  (AF015913) Skb1Hs [Homo sapiens]
NCBI Description
Seq. No.
                   216780
Seq. ID
                   LIB3147-049-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   q3687249
BLAST score
                   162
E value
                   2.0e-11
Match length
                   35
                   83
% identity
NCBI Description
                   (AC005169) putative copia-like transposable element
                   [Arabidopsis thaliana]
Seq. No.
                   216781
Seq. ID
                   LIB3147-049-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3024013
BLAST score
                   306
```

E value 7.0e-28 Match length 160 % identity 41

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA) >gi_2706460_emb_CAA15918.1_ (AL021046)





translational initiation factor 2 alpha

[Schizosaccharomyces pombe] 216782 Seq. No. LIB3147-049-Q1-K1-G7 Seq. ID Method BLASTX NCBI GI g2224911 BLAST score 264 3.0e-23 E value Match length 69 74 % identity NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus carota] 216783 Seq. No. Seq. ID LIB3147-049-Q1-K1-H10 Method BLASTX NCBI GI g1531758 BLAST score 250 E value 4.0e-34 Match length 96 73 % identity (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) NCBI Description unknown protein [Arabidopsis thaliana] Seq. No. 216784 Seq. ID LIB3147-049-Q1-K1-H2 Method BLASTN NCBI GI q3399678 BLAST score 43 E value 7.0e-15 Match length 103 85 % identity Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 216785 Seq. ID LIB3147-049-Q1-K1-H4 Method BLASTX NCBI GI a732893 BLAST score 385 E value 2.0e - 37Match length 81

% identity

NCBI Description (X85382) tobacco calretulin [Nicotiana tabacum]

Seq. No. 216786

Seq. ID LIB3147-049-Q1-K1-H9

Method BLASTX NCBI GI q3894389 BLAST score 350 E value 4.0e-33 Match length 145 % identity 10

(AF053996) Hcr2-2A [Lycopersicon pimpinellifolium] NCBI Description

Seq. No. 216787



```
LIB3147-050-Q1-K1-A11
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3962377
 BLAST score
                   331
 E value
                   8.0e-31
                   77
 Match length
                   79
 % identity
                  (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   216788
                   LIB3147-050-Q1-K1-A12
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q3821780
 BLAST score
                   36
                   7.0e-11
 E value
 Match length
                   43
                   63
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                   216789
                   LIB3147-050-Q1-K1-A2
 Seq. ID
Method
                   BLASTX
                   g1351014
 NCBI GI
 BLAST score
                   312
 E value
                   1.0e-28
 Match length
                   64
 % identity
                   92
 NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                   ribosomal protein S8 [Oryza sativa]
                   216790
 Seq. No.
                   LIB3147-050-Q1-K1-A4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4263790
 BLAST score
                    383
 E value
                    7.0e-37
 Match length
                   88
 % identity
                   84
 NCBI Description (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
                    216791
 Seq. No.
 Seq. ID
                   LIB3147-050-Q1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   g1946368
 BLAST score
                    420
                    2.0e-41
 E value
 Match length
                   126
 % identity
 NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    216792
 Seq. ID
                   LIB3147-050-Q1-K1-B2
 Method
                   BLASTX
 NCBI GI
                   g2662343
 BLAST score
                   716
```

30358

6.0e-76

138

E value Match length



```
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   216793
Seq. No.
                   LIB3147-050-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   q2147966
NCBI GI
                   180
BLAST score
                   2.0e-27
E value
                   95
Match length
                   65
% identity
                   probable 1-acyl-sn-glycerol-3-phosphate acyltransferase -
NCBI Description
                   Limnanthes douglasii >gi_1067138_emb_CAA88620_ (Z48730)
                   1-acyl-sn-glycerol-3-phosphate acyltransferase (putative)
                   [Limnanthes douglasii]
                   216794
Seq. No.
                   LIB3147-050-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   q3914685
NCBI GI
                   712
BLAST score
                   2.0e-75
E value
                   147
Match length
                   90
% identity
                   60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
NCBI Description
                   protein L17 [Zea mays]
Seq. No.
                   216795
                   LIB3147-050-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g732893
NCBI GI
BLAST score
                   443
                   6.0e-44
E value
                   94
Match length
                   82
% identity
                   (X85382) tobacco calretulin [Nicotiana tabacum]
NCBI Description
Seq. No.
                   216796
                   LIB3147-050-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q416662
BLAST score
                   194
                   4.0e-15
E value
                   88
Match length
                   52
% identity
                   21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin inhibitor homolog - soybean >gi_21909_emb_CAA39860_
NCBI Description
                   (X56509) 21 kDa seed protein [Theobroma cacao]
Seq. No.
                   216797
                   LIB3147-050-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2431769
BLAST score
                   190
```

30359

1.0e-14

56

66

E value Match length

% identity

Seq. ID Method

BLASTX



```
(U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
                  216798
Seq. No.
                  LIB3147-050-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3123745
                  196
BLAST score
                   3.0e-17
E value
                   64
Match length
                  78
% identity
                  (AB013447) aluminum-induced [Brassica napus]
NCBI Description
                  216799
Seq. No.
                  LIB3147-050-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  q294668
NCBI GI
BLAST score
                   413
                   2.0e-40
E value
                  96
Match length
                   85
% identity
                  (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
NCBI Description
                   216800
Seq. No.
                  LIB3147-050-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1435021
BLAST score
                   156
                   2.0e-12
E value
                   143
Match length
                   44
% identity
                  (D26575) DNA-binding protein [Daucus carota]
NCBI Description
                   216801
Seq. No.
                   LIB3147-050-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454484
BLAST score
                   151
                   2.0e-10
E value
Match length
                   41
                   66
% identity
                  (AC006234) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                   thaliana]
                   216802
Seq. No.
                   LIB3147-050-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2982268
BLAST score
                   495
E value
                   4.0e-50
Match length
                   105
% identity
                   92
NCBI Description
                  (AF051217) probable 40S ribosomal protein S15 [Picea
                   mariana]
                   216803
Seq. No.
                   LIB3147-050-Q1-K1-E1
```



```
g1351279
NCBI GI
BLAST score
                  200
                  1.0e-15
E value
Match length
                  44
                  89
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase
                   [Petunia x hybrida]
                  216804
Seq. No.
                  LIB3147-050-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2072393
                  217
BLAST score
                   2.0e-17
E value
                   82
Match length
                   54
% identity
                   (U29168) similar to human Xeroderma pigmentosum group B DNA
NCBI Description
                   repair protein, Swiss-Prot Accession Number P19447
                   [Arabidopsis thaliana]
                   216805
Seq. No.
Seq. ID
                   LIB3147-050-Q1-K1-E3
                   BLASTX
Method
                   q4415992
NCBI GI
                   784
BLAST score
                   6.0e-84
E value
                   162
Match length
% identity
                   91
                  (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                   216806
Seq. No.
                   LIB3147-050-Q1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129915
BLAST score
                   438
                   2.0e-43
E value
Match length
                   118
                   69
% identity
                   ferredoxin precursor - sweet orange
NCBI Description
                   >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
                   216807
Seq. No.
                   LIB3147-050-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g3193303
NCBI GI
                   127
BLAST score
                   6.0e-10
E value
                   60
Match length
                   63
% identity
                   (AF069298) similar to several proteins containing a tandem
NCBI Description
                   repeat region such as Plasmodium falciparum GGM tandem
```

repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No.



```
Seq. ID
                  LIB3147-050-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g119354
BLAST score
                  489
E value
                  2.0e-49
                  101
Match length
                  94
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185
                  phosphopyruvate hydratase (EC 4.2.1.11) - tomato
                  >gi 19281 emb CAA41115 (X58108) enolase [Lycopersicon
                  esculentum]
                  216809
Seq. No.
Seq. ID
                  LIB3147-050-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3445201
BLAST score
                  173
E value
                  3.0e-12
Match length
                  105
                  42
% identity
                  (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216810
                  LIB3147-050-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1314711
BLAST score
                   788
E value
                   2.0e-84
Match length
                  163
                   91
% identity
                  (U54615) calcium-dependent protein kinase [Arabidopsis
NCBI Description
                   thaliana] >gi 3068712 (AF049236) calcium dependent protein
                   kinase [Arabidopsis thaliana]
Seq. No.
                   216811
                  LIB3147-050-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   q2507421
NCBI GI
                   530
BLAST score
                   4.0e-54
E value
                   113
Match length
                   89
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                   thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                   translation initiation factor [Arabidopsis thaliana]
                   216812
Seq. No.
Seq. ID
                   LIB3147-050-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g1176081
```

Method BLASTX
NCBI GI g1176081
BLAST score 274
E value 4.0e-24
Match length 141
% identity 43

NCBI Description HYPOTHETICAL PROTEIN HI0671 >gi 1074478 pir F64156

BLAST score

E value Match length 170 1.0e-16

153



hypothetical protein HI0671 - Haemophilus influenzae (strain Rd KW20) >gi_1573672 (U32750) conserved hypothetical protein [Haemophilus influenzae Rd]

```
216813
Seq. No.
                  LIB3147-050-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                  g320558
NCBI GI
                  281
BLAST score
                  6.0e-25
E value
                  85
Match length
                  72
% identity
                  DNA-binding protein - Arabidopsis thaliana >gi_601843
NCBI Description
                   (M25268) DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  216814
                  LIB3147-050-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                   q461736
NCBI GI
                   753
BLAST score
                   3.0e-80
E value
                   164
Match length
                   92
% identity
                  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
NCBI Description
                   >gi_478786_pir__S29316 chaperonin 60 - cucurbit
                   >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                   sp.]
                   216815
Seq. No.
                   LIB3147-050-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g575605
NCBI GI
                   406
BLAST score
                   1.0e-39
E value
                   140
Match length
                   59
% identity
                   (D42065) cationic peroxidase isozyme 40K precursor
NCBI Description
                   [Nicotiana tabacum]
                   216816
Seq. No.
                   LIB3147-050-Q1-K1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q575603
                   180
BLAST score
                   4.0e-13
E value
                   138
Match length
                   36
% identity
                   (D42064) cationic peroxidase isozyme 38K precursor
NCBI Description
                   [Nicotiana tabacum]
                   216817
 Seq. No.
                   LIB3147-050-Q1-K1-G6
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2065021
```



% identity (Y12555) alanyl t-RNA synthetase [Arabidopsis thaliana] NCBI Description Seq. No. 216818 LIB3147-050-Q1-K1-G8 Seq. ID Method BLASTX NCBI GI q4056469 BLAST score 613 7.0e-64E value Match length 126 96 % identity (AC005990) Strong similarity to gb_M95166 ADP-ribosylation NCBI Description factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb AA712956, gb T46403, gb T46050, gb AI100391 and gb Z25043 come from t 216819 Seq. No. Seq. ID LIB3147-050-Q1-K1-H11 BLASTX Method NCBI GI g2980770 BLAST score 759 5.0e-81E value Match length 161 88 % identity (AL022198) putative protein kinase [Arabidopsis thaliana] NCBI Description Seq. No. 216820 Seq. ID LIB3147-050-Q1-K1-H3 Method BLASTX q2829899 NCBI GI 209 BLAST score 1.0e-16 E value 131 Match length 38 % identity (AC002311) similar to ripening-induced protein, NCBI Description gp AJ001449_2465015 and major#latex protein, gp X91961 1107495 [Arabidopsis thaliana] Seq. No. 216821 LIB3147-050-Q1-K1-H7 Seq. ID BLASTX Method NCBI GI g3152572 687

BLAST score 1.0e-72 E value 152 Match length 82 % identity

NCBI Description (AC002986) Contains homology to DNAJ heatshock protein

gb U32803 from Haemophilus influenzae. [Arabidopsis

thaliana]

216822 Seq. No.

LIB3147-050-Q1-K1-H8 Seq. ID

Method BLASTN g2264309 NCBI GI 40 BLAST score E value 5.0e-13



```
195
Match length
% identity
                  83
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  216823
                  LIB3147-051-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g4090257
NCBI GI
                  125
BLAST score
                  2.0e-15
E value
                  79
Match length
                  53
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
Seq. No.
                  216824
                  LIB3147-051-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q3152660
NCBI GI
                  207
BLAST score
                  3.0e-16
E value
Match length
                  139
                  35
% identity
                  (AF064603) GA17 protein [Homo sapiens]
NCBI Description
Seq. No.
                  216825
                  LIB3147-051-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g3860020
NCBI GI
BLAST score
                  229
                  5.0e-19
E value
Match length
                  104
                   45
% identity
                  (AF091091) unknown [Homo sapiens]
NCBI Description
                  216826
Seq. No.
Seq. ID
                  LIB3147-051-Q1-K1-A5
Method
                  BLASTX
                  g2500378
NCBI GI
BLAST score
                   434
                   6.0e-43
E value
Match length
                  95
                   83
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
                   216827
Seq. No.
Seq. ID
                  LIB3147-051-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                   q3023187
BLAST score
                   591
                   2.0e-61
E value
Match length
                   127
% identity
                   91
NCBI Description 14-3-3-LIKE PROTEIN (G-BOX BINDING FACTOR) >gi_1773328
```

30365

crystallinum]

(U80070) 14-3-3-like protein [Mesembryanthemum



```
Seq. No.
                   216828
                   LIB3147-051-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703275
BLAST score
                   212
                   6.0e-17
E value
Match length
                   45
% identity
                   82
                   METHIONINE AMINOPEPTIDASE 2 (METAP 2) (PEPTIDASE M 2)
NCBI Description
                   (INITIATION FACTOR 2 ASSOCIATED 67 KD GLYCOPROTEIN) (P67)
Seq. No.
                   216829
                   LIB3147-051-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q310587
BLAST score
                   110
                   4.0e-09
E value
Match length
                   57
                   67
% identity
                   (L20864) ascorbate peroxidase [Spinacia oleracea]
NCBI Description
                   >qi 1384110 dbj BAA12890 (D85864) cytosolic ascorbate
                   peroxidase [Spinacia oleracea]
                   216830
Seq. No.
                   LIB3147-051-Q1-K1-B2
Seq. ID
Method
                   BLASTX
                   g2429280
NCBI GI
BLAST score
                   630
E value
                   9.0e-66
Match length
                   137
                   90
% identity
                   (AF014055) asparagine synthetase [Triphysaria versicolor]
NCBI Description
                   >gi_2429282 (AF014056) asparagine synthetase [Triphysaria
                   versicolor] >gi_2429284 (AF014057) asparagine synthetase
                    [Triphysaria versicolor]
                   216831
Seq. No.
                   LIB3147-051-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4056469
BLAST score
                   621
                   7.0e-65
E value
Match length
                   124
% identity
                   (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                   factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                    gb AA712956, gb T46403, gb T46050, gb AI100391 and
                    gb Z25043 come from t
```

216832 Seq. No.

Seq. ID LIB3147-051-Q1-K1-B4

Method BLASTX NCBI GI g2827709 BLAST score 429 E value 2.0e-42 Match length 98

Method

BLASTX



% identity (AL021684) predicted protein [Arabidopsis thaliana] NCBI Description Seq. No. 216833 LIB3147-051-Q1-K1-B6 Seq. ID Method BLASTX NCBI GI q3702343 BLAST score 298 4.0e-27 E value Match length 118 % identity 56 (AC005397) putative homeotic gene regulator [Arabidopsis NCBI Description thaliana] Seq. No. 216834 Seq. ID LIB3147-051-Q1-K1-B7 Method BLASTX NCBI GI g2335099 BLAST score 367 3.0e-35 E value Match length 114 % identity 61 (AC002339) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 216835 LIB3147-051-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI g3860321 BLAST score 330 6.0e-31 E value Match length 75 73 % identity (AJ012687) beta-galactosidase [Cicer arietinum] NCBI Description 216836 Seq. No. LIB3147-051-Q1-K1-C1 Seq. ID Method BLASTX NCBI GI g2230757 BLAST score 145 4.0e-09 E value 108 Match length 39 % identity (Y11969) dnaJ-like protein [Arabidopsis thaliana] NCBI Description 216837 Seq. No. LIB3147-051-Q1-K1-C10 Seq. ID Method BLASTX NCBI GI g2662343 BLAST score 186 7.0e-14E value 38 Match length 95 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 216838 LIB3147-051-Q1-K1-C2 Seq. ID



NCBI GI q516124 390 BLAST score 9.0e-38 E value Match length 152 53 % identity (X78712) glycerol kinase [Homo sapiens] NCBI Description 216839 Seq. No. LIB3147-051-Q1-K1-C3 Seq. ID BLASTX Method g3763933 NCBI GI BLAST score 167 9.0e-12 E value 46 Match length % identity 67 (AC004450) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 216840 LIB3147-051-Q1-K1-C7 Seq. ID Method BLASTX q4314388 NCBI GI BLAST score 489 E value 2.0e-49 Match length 111 % identity 83 (AC006232) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 216841 LIB3147-051-Q1-K1-D10 Seq. ID BLASTX Method q3318615 NCBI GI BLAST score 638 7.0e-67 E value 143 Match length 85 % identity (AB016065) mitochondrial phosphate transporter [Oryza NCBI Description sativa] 216842 Seq. No. LIB3147-051-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI q3914535 209 BLAST score 1.0e-16 E value 49 Match length 84 % identity 60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ NCBI Description (AJ223363) ribosomal protein L13a [Lupinus luteus] 216843 Seq. No. LIB3147-051-Q1-K1-D3

Seq. ID

Method BLASTX NCBI GI q1703380 BLAST score 480 2.0e-48 E value Match length 94 % identity 98

Seq. No.

Seq. ID

216849

LIB3147-051-Q1-K1-F11



```
ADP-RIBOSYLATION FACTOR >gi_1132483_dbj BAA04607_ (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
Seq. No.
Seq. ID
                  LIB3147-051-Q1-K1-D8
                  BLASTX
Method
                  q3860321
NCBI GI
BLAST score
                  330
                  1.0e-30
E value
                  75
Match length
                  73
% identity
                  (AJ012687) beta-galactosidase [Cicer arietinum]
NCBI Description
                  216845
Seq. No.
                  LIB3147-051-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2431769
                  249
BLAST score
E value
                  3.0e-21
                  107
Match length
% identity
                  52
                  (U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
Seq. No.
                  216846
                  LIB3147-051-Q1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1514643
BLAST score
                  571
                  6.0e-59
E value
Match length
                  144
% identity
                  43
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
Seq. No.
                  216847
                  LIB3147-051-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g1843527
NCBI GI
                  438
BLAST score
E value
                  2.0e-43
Match length
                  100
                  44
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  216848
                  LIB3147-051-Q1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g464980
BLAST score
                  247
                  2.0e-21
E value
                  64
Match length
                  73
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 (L06967)
                  ubiquitin carrier protein [Medicago satīva]
```



```
Method
                  BLASTX
NCBI GI
                  q4376815
BLAST score
                  194
E value
                  8.0e-15
Match length
                  101
                  42
% identity
                  (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia
NCBI Description
                  pneumoniae]
                  216850
Seq. No.
                  LIB3147-051-Q1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982465
BLAST score
                  260
                  2.0e-22
E value
                  72
Match length
% identity
                  71
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                  216851
Seq. No.
                  LIB3147-051-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q3548818
NCBI GI
BLAST score
                   556
E value
                   3.0e-57
                  119
Match length
                  82
% identity
NCBI Description
                  (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  216852
                  LIB3147-051-Q1-K1-F5
Seq. ID
Method
                  BLASTX
                   q1402912
NCBI GI
BLAST score
                   605
                   5.0e-63
E value
Match length
                   145
% identity
                   78
                  (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216853
                  LIB3147-051-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                   g2244979
NCBI GI
BLAST score
                   371
                   1.0e-35
E value
Match length
                   113
                   66
% identity
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                   thaliana]
                   216854
Seq. No.
                   LIB3147-051-Q1-K1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2924247
BLAST score
                   357
```

30370

7.0e-34

86

E value Match length



```
% identity
                  (Y07782) expansin [Oryza sativa]
NCBI Description
                  216855
Seq. No.
                  LIB3147-051-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g2829923
NCBI GI
                  299
BLAST score
                   4.0e-27
E value
                  146
Match length
                   46
% identity
                   (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                   thaliana]
                   216856
Seq. No.
                  LIB3147-051-Q1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2982322
                   180
BLAST score
                   9.0e-14
E value
                   40
Match length
                   85
% identity
                   (AF051246) probable proteasome subunit [Picea mariana]
NCBI Description
                   216857
Seq. No.
                   LIB3147-051-Q1-K1-G7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4309719
BLAST score
                   38
                   5.0e-12
E value
                   70
Match length
                   89
% identity
                   Arabidopsis thaliana chromosome II BAC T30D6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   216858
Seq. No.
                   LIB3147-051-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g2493144
NCBI GI
                   402
BLAST score
                   2.0e-39
E value
                   96
Match length
                   56
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                   16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132
                   H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                   (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (L44585)
                   vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                   thaliana]
                   216859
Seq. No.
                   LIB3147-051-Q1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4455207
                   440
BLAST score
                   1.0e-43
E value
```

95

Match length

NCBI Description



```
% identity
                  (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  216860
                  LIB3147-051-Q1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q113232
BLAST score
                  148
                  2.0e-20
E value
                  56
Match length
                  96
% identity
                  ACTIN 2 >gi 100150 pir S07003 actin 2 - carrot
NCBI Description
                  216861
Seq. No.
                  LIB3147-051-Q1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4406777
                   228
BLAST score
                   6.0e-19
E value
                   102
Match length
                   48
% identity
                   (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   216862
Seq. No.
                   LIB3147-051-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g1173218
NCBI GI
BLAST score
                   326
                   2.0e-30
E value
Match length
                   62
                   100
% identity
                   40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                   protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                   216863
Seq. No.
                   LIB3147-051-Q1-K1-H7
Seq. ID
Method
                   BLASTX
                   g2058456
NCBI GI
                   429
BLAST score
                   2.0e-42
E value
                   88
Match length
                   92
% identity
                   (U66408) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2345150_gb_AAB67830_ (AF014822) developmentally
                   regulated GTP binding protein [Arabidopsis thaliana]
                   216864
Seq. No.
                   LIB3147-051-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3885515
                   429
BLAST score
E value
                   2.0e-42
                   99
Match length
                   80
% identity
                  (AF084202) similar to ribosomal protein S26 [Medicago
```



sativa]

```
Seq. No.
                  216865
                  LIB3147-051-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  q4220519
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
                   47
Match length
                   66
% identity
                   (AL035356) putative protein binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   216866
Seq. No.
Seq. ID
                  LIB3147-052-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2583108
BLAST score
                   585
                   1.0e-60
E value
Match length
                   146
                   79
% identity
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216867
                   LIB3147-052-Q1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3047082
BLAST score
                   577
E value
                   1.0e-59
Match length
                   156
                   67
% identity
                  (AF058914) similar to Vigna radiata pectinacetylesterase
NCBI Description
                   precursor (GB:X99348) [Arabidopsis thaliana]
                   216868
Seq. No.
                   LIB3147-052-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g2160166
NCBI GI
                   219
BLAST score
                   4.0e-18
E value
                   125
Match length
                   44
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   216869
Seq. No.
                   LIB3147-052-Q1-K1-A4
Seq. ID
Method
                   BLASTX
                   g1255954
NCBI GI
                   458
BLAST score
                   1.0e-45
E value
                   114
Match length
                   73
% identity
                  (Z70677) thioredoxin [Ricinus communis]
NCBI Description
                   216870
Seq. No.
                   LIB3147-052-Q1-K1-A9
Seq. ID
Method
                   BLASTX
```

E value

Match length

% identity

64

75



```
q4508068
NCBI GI
BLAST score
                  188
                  3.0e-14
E value
                  114
Match length
                  43
% identity
                  (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
                  216871
Seq. No.
                  LIB3147-052-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g4154352
NCBI GI
BLAST score
                  107
E value
                  5.0e-09
                  108
Match length
                  38
% identity
                  (AF110333) PrMC3 [Pinus radiata]
NCBI Description
                  216872
Seq. No.
                  LIB3147-052-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                   q4335724
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
                   66
Match length
                   64
% identity
                   (AC006248) putative RING-H2 finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   216873
Seq. No.
Seq. ID
                   LIB3147-052-Q1-K1-C2
                   BLASTX
Method
                   q4580513
NCBI GI
                   622
BLAST score
                   6.0e-65
E value
Match length
                   155
                   75
% identity
                  (AF036300) scarecrow-like 1 [Arabidopsis thaliana]
NCBI Description
                   216874
Seq. No.
                   LIB3147-052-Q1-K1-C4
Seq. ID
                   BLASTN
Method
                   g2618602
NCBI GI
                   37
BLAST score
                   3.0e-11
E value
Match length
                   157
 % identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   216875
 Seq. No.
                   LIB3147-052-Q1-K1-C6
 Seq. ID
                   BLASTX
Method
                   g2431769
 NCBI GI
                   248
 BLAST score
                   1.0e-21
```



```
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                   216876
Seq. No.
                   LIB3147-052-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   q1350944
NCBI GI
                   391
BLAST score
                   7.0e-38
E value
                   80
Match length
                   96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S17
                   216877
Seq. No.
Seq. ID
                   LIB3147-052-Q1-K1-D11
                   BLASTX
Method
                   q2499819
NCBI GI
BLAST score
                   259
                    2.0e-22
E value
Match length
                    56
                    82
% identity
                   ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                   >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
                    rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                    protease [Oryza sativa]
                    216878
Seq. No.
                   LIB3147-052-Q1-K1-D3
Seq. ID
Method
                    BLASTX
                    q2789664
NCBI GI
                    154
BLAST score
                    5.0e-10
E value
                    82
Match length
                    38
% identity
                   (AF040629) macrophage migration inhibitory factor
NCBI Description
                    [Wuchereria bancrofti]
                    216879
 Seq. No.
                    LIB3147-052-Q1-K1-D5
 Seq. ID
                    BLASTX
 Method
                    g3687243
 NCBI GI
                    245
 BLAST score
                    8.0e-21
 E value
                    61
 Match length
                    79
 % identity
                    (AC005169) putative ribosomal protein [Arabidopsis
 NCBI Description
                    thaliana]
                    216880
 Seq. No.
                    LIB3147-052-Q1-K1-D9
 Seq. ID
                    BLASTX
 Method
                    q112863
 NCBI GI
                    619
 BLAST score
                    1.0e-64
 E value
                    122
 Match length
                    89
 % identity
 NCBI Description STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
```



>gi_100227_pir__S12209 hypothetical protein - tomato
>gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon esculentum]

Seq. No. 216881

Seq. ID LIB3147-052-Q1-K1-E10

Method BLASTX
NCBI GI g3386608
BLAST score 144
E value 6.0e-09
Match length 81
% identity 46

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 216882

Seq. ID LIB3147-052-Q1-K1-E11

Method BLASTN
NCBI GI g3869075
BLAST score 35
E value 4.0e-10

E value 4.0e-10
Match length 155
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 216883

Seq. ID LIB3147-052-Q1-K1-E2

Method BLASTX
NCBI GI g2288887
BLAST score 375
E value 6.0e-36
Match length 124
% identity 59

NCBI Description (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis

thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate

diphosphate decarboxylase [Arabidopsis thaliana]

>gi 3786002 (AC005499) mevalonate diphosphate decarboxylase

[Arabidopsis thaliana]

Seq. No. 216884

Seq. ID LIB3147-052-Q1-K1-E3

Method BLASTX
NCBI GI g3269284
BLAST score 252
E value 8.0e-22
Match length 89
- % identity 61

NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No. 216885

Seq. ID LIB3147-052-Q1-K1-E4

Method BLASTX
NCBI GI g543905
BLAST score 571
E value 6.0e-59
Match length 140
% identity 77



```
BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
                  216886
Seq. No.
                  LIB3147-052-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244990
BLAST score
                  476
                  8.0e-48
E value
Match length
                  123
                  79
% identity
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
                  Caenorhabditis [Arabidopsis thaliana]
Seq. No.
                  216887
Seq. ID
                  LIB3147-052-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2829899
BLAST score
                  263
                  5.0e-23
E value
Match length
                  109
                  46
% identity
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
                  216888
Seq. No.
Seq. ID
                  LIB3147-052-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3702338
BLAST score
                  206
                  4.0e-16
E value
                  120
Match length
% identity
                  46
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  216889
Seq. No.
                  LIB3147-052-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1420887
                  213
BLAST score
                   6.0e-17
E value
                  89
Match length
                   45
% identity
                  (U34334) non-specific lipid transfer-like protein
NCBI Description
                   [Phaseolus vulgaris]
                   216890
Seq. No.
                  LIB3147-052-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1694976
                   390
BLAST score
                   1.0e-37
E value
Match length
                  116
% identity
                   66
                  (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
```



thaliana]

```
216891
Seq. No.
                  LIB3147-052-Q1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q117188
BLAST score
                  396
                  1.0e-38
E value
                  136
Match length
                  57
% identity
                  CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)
NCBI Description
                  >gi 81423 pir A35867 cytochrome P450 71A1 - avocado
                  216892
Seq. No.
                  LIB3147-052-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206155
BLAST score
                  149
                  2.0e-09
E value
                  73
Match length
                  37
% identity
                  (AF109219) Mcd4p homolog [Homo sapiens]
NCBI Description
                  216893
Seq. No.
                  LIB3147-052-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2780194
BLAST score
                  257
                  2.0e-22
E value
                  86
Match length
                  65
% identity
                  (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
                  216894
Seq. No.
                  LIB3147-052-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169534
BLAST score
                   678
E value
                  1.0e-71
Match length
                  141
                   91
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                  phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                   >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus
                   communis]
Seq. No.
                   216895
                   LIB3147-052-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2894592
BLAST score
                   584
E value
                   2.0e-60
Match length
                   140
% identity
                   78
```

NCBI Description (AL021889) predicted protein [Arabidopsis thaliana]



```
216896
Seq. No.
                  LIB3147-052-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q116908
                  737
BLAST score
E value
                  2.0e-78
Match length
                  157
                  85
% identity
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi_166420 (M63853)
                  S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase
                   [Medicago sativa]
                  216897
Seq. No.
                  LIB3147-052-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2935416
BLAST score
                  515
                  2.0e-52
E value
Match length
                  131
                  79
% identity
                  (AF047896) isoflavone reductase homolog [Betula pendula]
NCBI Description
                  216898
Seq. No.
                  LIB3147-052-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g1732411
NCBI GI
BLAST score
                  371
E value
                   2.0e-35
Match length
                  154
% identity
                   51
                  (U47924) isopeptidase T [Homo sapiens]
NCBI Description
                  216899
Seq. No.
Seq. ID
                  LIB3147-052-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                   g3860277
BLAST score
                   621
E value
                   8.0e-65
Match length
                   150
% identity
                   81
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb AAD15604 (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                   216900
                   LIB3147-052-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1362093
                   233
BLAST score
E value
                   1.0e-19
Match length
                   95
                   49
% identity
```

>qi 924632 (U20595) unknown [Solanum lycopersicum]

NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)



```
      Seq. No.
      216901

      Seq. ID
      LIB3147-052-Q1-K1-H5

      Method
      BLASTX

      NCBI GI
      g464524

      BLAST score
      161

      E value
      3.0e-11

      Match length
      34
```

% identity 88
NCBI Description
NCBI Description
RAS-RELATED PROTEIN RAB-1A >gi_345404_pir__S32206 RAB1
protein - great pond snail >gi_481217_pir__S38339 rab1
protein - great pond snail >gi_288934_emb_CAA51233_

(X72688) RAB1 [Lymnaea stagnalis]

216902 Seq. No. LIB3147-052-Q1-K1-H9 Seq. ID BLASTX Method NCBI GI q122085 BLAST score 522 E value 3.0e-53 Match length 122 86 % identity

NCBI Description HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21)

- rice >gi_1362194_pir__S57626 histone H3 - maize
>gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136)
[Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3
(AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3
(H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]

>gi 168497 (M13379) histone H3 [Zea mays] >gi 168506

(M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3

homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana]

>gi 225459 prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

 Seq. No.
 216903

 Seq. ID
 LIB3147-054-Q1-K1-A1

 Method
 BLASTX

 NCBI GI
 g2583108

BLAST score 416
E value 8.0e-41
Match length 110
% identity 72

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 216904

NCBI GI

E value

BLAST score

361

1.0e-63



```
LIB3147-054-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  q1480008
NCBI GI
                  221
BLAST score
                   4.0e-18
E value
                   46
Match length
                   98
% identity
                  (D78490) human immunodeficiency virus Tat binding protein 1
NCBI Description
                   [Brassica rapa]
                   216905
Seq. No.
                  LIB3147-054-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1332579
                   555
BLAST score
                   4.0e-59
E value
                   130
Match length
                   10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   216906
Seq. No.
Seq. ID
                   LIB3147-054-Q1-K1-A6
                   BLASTX
Method
                   g3608485
NCBI'GI
BLAST score
                   186
                   4.0e-14
E value
                   44
Match length
                   84
% identity
                  (AF088915) proteasome beta subunit [Petunia x hybrida]
NCBI Description
                   216907
Seq. No.
Seq. ID
                   LIB3147-054-Q1-K1-A9
                   BLASTX
Method
                   q4262250
NCBI GI
BLAST score
                   283
                   9.0e-29
E value
                   86
Match length
                   75
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   216908
Seq. No.
                   LIB3147-054-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   q2495365
NCBI GI
BLAST score
                   354
                   8.0e - 34
E value
                   104
Match length
                   70
% identity
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B
NCBI Description
                   heat shock protein HSP81-2 [Arabidopsis thaliana]
                   216909
Seq. No.
                   LIB3147-054-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g3024020
```



```
Match length
                  133
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 2225881_dbj_BAA20877 (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                  216910
Seq. No.
Seq. ID
                  LIB3147-054-Q1-K1-B12
                  BLASTX
Method
                  g2398829
NCBI GI
                  361
BLAST score
                  7.0e-58
E value
Match length
                  128
% identity
                  (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                  tuberosum]
                  216911
Seq. No.
Seq. ID
                  LIB3147-054-Q1-K1-B7
Method
                  BLASTX
                  q1408473
NCBI GI
                  500
BLAST score
                  9.0e-51
E value
Match length
                  130
                  75
% identity
                  (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  216912
                  LIB3147-054-Q1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2960069
BLAST score
                   247
E value
                   1.0e-44
Match length
                   141
                   65
% identity
                  (Y12777) acyl-CoA synthetase-like protein [Homo sapiens]
NCBI Description
Seq. No.
                   216913
                  LIB3147-054-Q1-K1-C10
Seq. ID
Method
                   BLASTN
                   q3985958
NCBI GI
                   40
BLAST score
                   4.0e-13
E value
                   92
Match length
                   86
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                   216914
Seq. No.
                   LIB3147-054-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g3334323
NCBI GI
BLAST score
                   278
                   6.0e-47
E value
```

30382

116

82

Match length

% identity

Method NCBI GI

BLAST score



```
NCBI Description GTP-BINDING PROTEIN SAR1A >gi 1314860 (U56929) Sar1 homolog
                  [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1
                  (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis
                  thaliana] >qi 2104550 (AF001535) AGAA.4 [Arabidopsis
                  thaliana]
Seq. No.
                  216915
                  LIB3147-054-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  g3176668
NCBI GI
                  460
BLAST score
                  5.0e-46
E value
                  102
Match length
% identity
                  84
                  (AC004393) Similar to ribosomal protein L17 gb X62724 from
NCBI Description
                  Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                  gb_Z33937 come from this gene. [Arabidopsis thaliana]
                  216916
Seq. No.
                  LIB3147-054-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  g465820
NCBI GI
BLAST score
                  387
                  2.0e-37
E value
                  108
Match length
                  64
% identity
NCBI Description
                  HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
                  >gi 280536 pir__S28301 hypothetical protein C40H1.6 -
                  Caenorhabditis elegans >gi 3874819 emb CAA79557 (Z19154)
                  C40H1.6 [Caenorhabditis elegans]
                  216917
Seq. No.
                  LIB3147-054-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g2213871
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
Match length
                   99
                   74
% identity
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                   216918
                  LIB3147-054-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1477428
BLAST score
                   722
E value
                   9.0e-77
Match length
                   138
                   95
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
Seq. No.
                   216919
                   LIB3147-054-Q1-K1-D10
Seq. ID
                   BLASTX
```

30383

g1170508



E value 2.0e-66
Match length 138
% identity 95

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)

>gi_2119931_pir__S60244 translation initiation factor

eIF-4A.8, anther-specific - common tobacco

>gi 475219 emb_CAA55639_ (X79004) translation initiation

factor (eIF-4A) [Nicotiana tabacum]

>gi 475221 emb CAA55640 (X79005) translation initiation

factor (eIF-4A) [Nicotiana tabacum]

Seq. No. 216920

Seq. ID LIB3147-054-Q1-K1-D12

Method BLASTX
NCBI GI g1350680
BLAST score 210
E value 1.0e-16
Match length 66
% identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 216921

Seq. ID LIB3147-054-Q1-K1-D2

Method BLASTX
NCBI GI g974294
BLAST score 318
E value 2.0e-29
Match length 108
% identity 57

NCBI Description (U31309) LP6 [Pinus taeda]

Seq. No. 216922

Seq. ID LIB3147-054-Q1-K1-D6

Method BLASTX
NCBI GI g4510345
BLAST score 158
E value 1.0e-10
Match length 78
% identity 68

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 216923

Seq. ID LIB3147-054-Q1-K1-D7

Method BLASTX
NCBI GI g2244939
BLAST score 407
E value 9.0e-40
Match length 150
% identity 58

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 216924

Seq. ID LIB3147-054-Q1-K1-D8

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 5.0e-11



```
38
Match length
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  216925
Seq. No.
                  LIB3147-054-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g2935342
NCBI GI
                  201
BLAST score
                  8.0e-21
E value
                  137
Match length
                   45
% identity
                   (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1
NCBI Description
                   [Arabidopsis thaliana]
                   216926
Seq. No.
Seq. ID
                  LIB3147-054-Q1-K1-E7
                  BLASTX
Method
                   q3821280
NCBI GI
BLAST score
                   701
                   3.0e-74
E value
                   147
Match length
                   86
% identity
                   (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
                   216927
Seq. No.
                   LIB3147-054-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3377797
                   584
BLAST score
                   2.0e-60
E value
                   140
Match length
                   82
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
Seq. No.
                   216928
                   LIB3147-054-Q1-K1-F1
Seq. ID
Method
                   BLASTX
                   q484656
NCBI GI
BLAST score
                   153
                   5.0e-10
E value
                   45
Match length
                   67
% identity
                   monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
NCBI Description
                   cucumber >gi 452165 dbj_BAA05408_ (D26392)
```

monodehydroascorbate reductase [Cucumis sativus]

Seq. No. 216929

Seq. ID LIB3147-054-Q1-K1-F10

Method BLASTX NCBI GI g398994 BLAST score 335

Method

NCBI GI

BLAST score

BLASTX

281

q4467121



```
1.0e-63
E value
                   144
Match length
                   86
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                   (ETHYLENE-FORMING ENZYME) (EFE) >gi 166313 (M97961) tomato
                   and apple ACC oxidase homologue [Actinidia deliciosa]
                   216930
Seq. No.
                   LIB3147-054-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2497752
NCBI GI
                   211
BLAST score
                   8.0e-17
E value
                   67
Match length
                   60
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                   >gi 1321911_emb_CAA65475_ (X96714) lipid transfer protein
                   [Prunus dulcis]
                   216931
Seq. No.
                   LIB3147-054-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g1765899
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
                   39
Match length
                   74
 % identity
                   (Y07917) Spot 3 protein [Arabidopsis thaliana] >gi 1839244
NCBI Description
                   (U86700) EGF receptor like protein [Arabidopsis thaliana]
 Seq. No.
                   216932
                   LIB3147-054-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   q4490705
NCBI GI
 BLAST score
                   170
                   4.0e-12
 E value
                   61
Match length
 % identity
                   (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   216933
 Seq. No.
 Seq. ID
                   LIB3147-054-Q1-K1-G1
                   BLASTX
 Method
                   q3236242
 NCBI GI
 BLAST score
                   306
                   6.0e-28
 E value
                   102
 Match length
 % identity
                   69
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   216934
                   LIB3147-054-Q1-K1-G12
 Seq. ID
```



```
1.0e-51
E value
                  147
Match length
                  32
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  216935
Seq. No.
                  LIB3147-054-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g4558659
NCBI GI
                  496
BLAST score
                  3.0e-50
E value
                  137
Match length
                  68
% identity
                  (AC007063) unknown protein [Arabidopsis thaliana]
NCBI Description
                  216936
Seq. No.
                  LIB3147-054-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                   g3080427
NCBI GI
BLAST score
                   340
                   6.0e-32
E value
                   126
Match length
                   58
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   216937
Seq. No.
                   LIB3147-054-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   q3075398
NCBI GI
BLAST score
                   273
                   4.0e-24
E value
                   79
Match length
                   65
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                   216938
Seq. No.
Seq. ID
                   LIB3147-054-Q1-K1-G6
                   BLASTX
Method
                   q4558659
NCBI GI
BLAST score
                   490
                   2.0e-49
E value
Match length
                   140
                   67
% identity
                   (AC007063) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216939
Seq. ID
                   LIB3147-054-Q1-K1-G7
                   BLASTX
Method
NCBI GI
                   g2623311
BLAST score
                   334
                   3.0e-31
E value
Match length
                   67
 % identity
                   96
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3402720 (AC004261) unknown protein [Arabidopsis
```

thaliana]

Method

NCBI GI

BLASTX

q126985



```
Seq. No.
                  216940
                  LIB3147-054-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q485742
                  591
BLAST score
                  2.0e-61
E value
Match length
                  141
% identity
                  82
                  (L32791) pyrophosphatase [Beta vulgaris]
NCBI Description
                  216941
Seq. No.
                  LIB3147-054-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1222552
BLAST score
                  327
                  6.0e-52
E value
Match length
                  121
% identity
                  78
                  (U49330) pectin methylesterase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  216942
                  LIB3147-054-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334115
BLAST score
                  388
                  6.0e-67
E value
Match length
                  147
                   61
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                   216943
Seq. No.
                  LIB3147-054-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                   g3868758
NCBI GI
BLAST score
                   390
                   7.0e-38
E value
Match length
                   94
                   76
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                   216944
Seq. No.
                   LIB3147-054-Q1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1771780
BLAST score
                   286
E value
                   1.0e-25
                   67
Match length
                   81
% identity
                  (Y10024) ubiquitin extension protein [Solanum tuberosum]
NCBI Description
                   216945
Seq. No.
                   LIB3147-054-Q1-K1-H4
Seq. ID
```



```
BLAST score
                  537
                  5.0e-55
E value
Match length
                  118
                  82
% identity
                  MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis
NCBI Description
                  thaliana]
                  216946
Seq. No.
                  LIB3147-054-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                   g4210451
NCBI GI
BLAST score
                  160
                  7.0e-11
E value
                   66
Match length
                   56
% identity
                  (AB016472) ARR2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216947
                   LIB3147-055-Q1-K1-A10
Seq. ID
                   BLASTN
Method
                   g2687439
NCBI GI
BLAST score
                   41
                   7.0e-14
E value
Match length
                   41
                   100
% identity
                  Peltoboykinia tellimoides large subunit 26S ribosomal RNA
NCBI Description
                   gene, partial sequence
Seq. No.
                   216948
                   LIB3147-055-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g3176668
NCBI GI
                   543
BLAST score
                   9.0e-56
E value
                   115
Match length
                   90
% identity
                   (ACO04393) Similar to ribosomal protein L17 gb X62724 from
NCBI Description
                   Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                   gb Z33937 come from this gene. [Arabidopsis thaliana]
                   216949
Seq. No.
                   LIB3147-055-Q1-K1-A2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2687434
                   88
BLAST score
                   2.0e-42
E value
                   116
Match length
                   94
 % identity
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                   partial sequence
                   216950
 Seq. No.
                   LIB3147-055-Q1-K1-A6
```

Seq. ID

BLASTX Method g2935450 NCBI GI 300 BLAST score 3.0e-27 E value

NCBI Description



```
Match length
                   61
% identity
                   98
                  (AF048824) histone H2B [Malus domestica]
NCBI Description
Seq. No.
                   216951
                  LIB3147-055-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4090257
BLAST score
                   461
                   4.0e-46
E value
                   91
Match length
                   96
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   216952
Seq. No.
Seq. ID
                   LIB3147-055-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g2924520
BLAST score
                   559
                   1.0e-57
E value
Match length
                   123
                   87
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   216953
Seq. No.
                   LIB3147-055-Q1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3643602
BLAST score
                   465
                   1.0e-46
E value
Match length
                   147
                   63
% identity
                  (AC005395) putative tonoplast intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   216954
Seq. No.
Seq. ID
                   LIB3147-055-Q1-K1-B4
Method
                   BLASTX
                   g4206122
NCBI GI
                   578
BLAST score
                   7.0e-60
E value
Match length
                   127
                   83
% identity
                  (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                   crystallinum]
                   216955
Seq. No.
                   LIB3147-055-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464986
                   592
BLAST score
E value
                   2.0e-61
Match length
                   112
                   98
% identity
```

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN



>gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
>gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
ubiquitin conjugating enzyme [Arabidopsis thaliana]
>gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
enzyme E2 [Arabidopsis thaliana]
>gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
ligase UBC9 [Arabidopsis thaliana]

216956 Seq. No. LIB3147-055-Q1-K1-C11 Seq. ID BLASTX Method g1351279 NCBI GI 169 BLAST score 4.0e-12 E value 38 Match length % identity TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]

 Seq. No.
 216957

 Seq. ID
 LIB3147-055-Q1-K1-C2

 Method
 BLASTX

 NCBI GI
 g586004

 BLAST score
 628

BLAST score 628
E value 1.0e-65
Match length 128
% identity 89
NCRI Description SUPPROV

NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)

superoxide dismutase [Ipomoea batatas]

Seq. No. 216958

Seq. ID LIB3147-055-Q1-K1-C3

Method BLASTN
NCBI GI g1771779
BLAST score 38
E value 3.0e-12
Match length 66
% identity 89

NCBI Description S.tuberosum mRNA for ubiquitin extension protein

Seq. No. 216959

Seq. ID LIB3147-055-Q1-K1-C6

Method BLASTX
NCBI GI g1498338
BLAST score 709
E value 3.0e-75
Match length 141
% identity 97

NCBI Description (U60502) actin [Glycine max]

Seq. No. 216960



```
Seq. ID
                  LIB3147-055-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q1103712
BLAST score
                  674
                  4.0e-71
E value
                  140
Match length
                  99
% identity
                  (X83729) inorganic pyrophosphatase [Nicotiana tabacum]
NCBI Description
                  216961
Seq. No.
                  LIB3147-055-Q1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1173256
BLAST score
                  653
                  1.0e-68
E value
Match length
                  129
% identity
                  97
                  40S RIBOSOMAL PROTEIN S4 >qi 629496 pir S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                  216962
Seq. No.
                  LIB3147-055-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                  g4193382
NCBI GI
                  383
BLAST score
                   6.0e - 37
E value
Match length
                  86
% identity
                  81
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
                   216963
Seq. No.
                  LIB3147-055-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                   g4101568
NCBI GI
                   220
BLAST score
                   7.0e-18
E value
                   75
Match length
                   57
% identity
                  (AF004816) unknown [Triticum aestivum]
NCBI Description
                   216964
Seq. No.
                   LIB3147-055-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g3913927
NCBI GI
                   568
BLAST score
                   1.0e-58
E value
                   146
Match length
                   75
% identity
                  ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
NCBI Description
                   SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                   (VACUOLAR INVERTASE) >gi 1084382 pir__S55521
```

beta-fructofuranosidase (EC 3.2.1.26) - fava bean >gi 861159 emb_CAA89992_ (Z49831) vacuolar invertase;



beta-fructofuranosidase [Vicia faba]

```
216965
Seq. No.
Seq. ID
                  LIB3147-055-Q1-K1-D3
                  BLASTX
Method
                  g2501182
NCBI GI
BLAST score
                  158
                  1.0e-10
E value
                  73
Match length
                  41
% identity
                  OSMOTIN-LIKE PROTEIN PRECURSOR >gi 2129934 pir JC5237
NCBI Description
                  osmotin-like protein - tomato >gi_1220537 (L76632)
                  osmotin-like protein [Lycopersicon esculentum]
                  216966
Seq. No.
                  LIB3147-055-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  q2286153
NCBI GI
BLAST score
                   448
                   8.0e-45
E value
                  105
Match length
                   81
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   216967
Seq. No.
                   LIB3147-055-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q3643608
NCBI GI
BLAST score
                   525
                   1.0e-53
E value
                   141
Match length
                   76
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   216968
                   LIB3147-055-Q1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g416662
BLAST score
                   486
E value
                   5.0e-49
                   145
Match length
% identity
                   63
                   21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin
NCBI Description
                   inhibitor homolog - soybean >gi 21909 emb CAA39860
                   (X56509) 21 kDa seed protein [Theobroma cacao]
                   216969
Seq. No.
                   LIB3147-055-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g3080395
NCBI GI
                   286
BLAST score
                   9.0e-26
E value
                   99
Match length
                   57
% identity
NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]
                   216970
Seq. No.
```

NCBI Description



```
LIB3147-055-Q1-K1-E7
Seq. ID
Method
                  BLASTX
                  q1778143
NCBI GI
BLAST score
                  498
                  1.0e-50
E value
                  123
Match length
                  80
% identity
                  (U66401) phosphate/phosphoenolpyruvate translocator
NCBI Description
                  precursor [Nicotiana tabacum]
                  216971
Seq. No.
                  LIB3147-055-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  q4539452
NCBI GI
                  327
BLAST score
                  2.0e-30
E value
                  139
Match length
                  45
% identity
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                  216972
Seq. No.
                  LIB3147-055-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                   q584794
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
Match length
                   40
                   90
% identity
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                   >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
                   - curled-leaved tobacco >gi_170289 (M80489) plasma membrane
                   H+ ATPase [Nicotiana plumbaginifolia]
Seq. No.
                   216973
                   LIB3147-055-Q1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g136057
BLAST score
                   237
                   6.0e-20
E value
Match length
                   58
                   79
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >qi 99499 pir A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi 556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
                   216974
Seq. No.
                   LIB3147-055-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   g2244750
NCBI GI
                   453
BLAST score
                   2.0e-45
E value
                   88
Match length
                   97
% identity
```

(Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

Method



[Arabidopsis thaliana]

```
216975
Seq. No.
Seq. ID
                  LIB3147-055-Q1-K1-F7
Method
                  BLASTX
                  g3786001
NCBI GI
                  574
BLAST score
                   2.0e-59
E value
                   142
Match length
                   77
% identity
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                   216976
Seq. No.
                   LIB3147-055-Q1-K1-F8
Seq. ID
                   BLASTN
Method
                   g2668747
NCBI GI
                   41
BLAST score
                   1.0e-13
E value
Match length
                   77
                   88
% identity
                  Zea mays ribosomal protein L17 (rpl17) mRNA, complete cds
NCBI Description
                   216977
Seq. No.
Seq. ID
                   LIB3147-055-Q1-K1-F9
                   BLASTX
Method
                   g2961343
NCBI GI
                   279
BLAST score
                   9.0e-25
E value
                   99 ့
Match length
% identity
                   53
                   (AL022140) symbiosis-related like protein [Arabidopsis
NCBI Description
                   thaliana]
                   216978
Seq. No.
                   LIB3147-055-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g3063465
NCBI GI
BLAST score
                   329
                   1.0e-30
E value
Match length
                   136
                   55
 % identity
NCBI Description (AC003981) F22013.27 [Arabidopsis thaliana]
                   216979
 Seq. No.
                   LIB3147-055-Q1-K1-G2
 Seq. ID
                   BLASTX
 Method
                   g3033380
 NCBI GI
                   356
 BLAST score
                   8.0e-34
 E value
                   83
 Match length
                   84
 % identity
                   (AC004238) putative coatomer epsilon subunit [Arabidopsis
 NCBI Description
                   thaliana]
                   216980
 Seq. No.
                   LIB3147-055-Q1-K1-G3
 Seq. ID
                   BLASTX
```



g3600033 NCBI GI BLAST score 170 5.0e-12E value 40 Match length 82 % identity (AF080119) contains similarity to the N terminal domain of NCBI Description the E1 protein (Pfam: E1 N.hmm, score: 12.36) [Arabidopsis thaliana] 216981 Seq. No. Seq. ID LIB3147-055-Q1-K1-G4 BLASTX Method NCBI GI g629483 357 BLAST score 6.0e - 34E value 142 Match length 53 % identity gene 1-Sc3 protein - European white birch NCBI Description >qi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula] >gi 1584322_prf 2122374C allergen Bet v 1-Sc3 [Betula pendula] 216982 Seq. No. Seq. ID LIB3147-055-Q1-K1-G7 Method BLASTX NCBI GI g115525 677 BLAST score 2.0e-71 E value Match length 133 % identity 67 CALMODULIN >gi 71685 pir MCSP calmodulin - spinach NCBI Description 216983 Seq. No. LIB3147-055-Q1-K1-G9 Seq. ID Method BLASTN NCBI GI g3821780 BLAST score 36 1.0e-10 E value Match length 36 % identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1 216984 Seq. No. LIB3147-055-Q1-K1-H11 Seq. ID Method BLASTX NCBI GI g2815246 217 BLAST score 1.0e-17 E value Match length 51 % identity 76 (X95709) class I type 2 metallothionein [Cicer arietinum] NCBI Description 216985 Seq. No. LIB3147-055-Q1-K1-H3

Seq. ID

Method BLASTX NCBI GI g1172977 BLAST score 602

Match length

% identity

134 69



```
1.0e-62
E value
                  134
Match length
                  87
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
                  216986
Seq. No.
                  LIB3147-055-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  g3023816
NCBI GI
                  206
BLAST score
                  3.0e-16
E value
                   41
Match length
                  95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
                   216987
Seq. No.
                   LIB3147-055-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   g280961
NCBI GI
                   178
BLAST score
                   6.0e-13
E value
                   41
Match length
                   90
% identity
                  histone H2B, testis - mouse (fragment) >gi_556310 (M25487)
NCBI Description
                   spermatid-specific [Mus musculus]
                   216988
Seq. No.
                   LIB3147-056-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   q3269301
NCBI GI
                   336
BLAST score
                   2.0e-31
E value
                   144
Match length
                   44
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   216989
Seq. No.
                   LIB3147-056-Q1-K1-A10
Seq. ID
                   BLASTX
Method
                   q1407705
NCBI GI
                   554
BLAST score
                   5.0e-57
E value
Match length
                   143
                   73
 % identity
NCBI Description (U60202) lipoxygenase [Solanum tuberosum]
                   216990
 Seq. No.
                   LIB3147-056-Q1-K1-A2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q1708191
 BLAST score
                   494
                   5.0e-50
 E value
```



```
NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose
                  carrier protein [Ricinus communis]
                  216991
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-A3
                  BLASTX
Method
                  g2829894
NCBI GI
                  140
BLAST score
                  1.0e-08
E value
                  62
Match length
                  52
% identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
                  216992
Seq. No.
                  LIB3147-056-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                   g4539350
NCBI GI
                   209
BLAST score
                   9.0e-17
E value
                   47
Match length
                   79
% identity
NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]
                   216993
Seq. No.
                   LIB3147-056-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g2827143
NCBI GI
                   359
BLAST score
                   4.0e-34
E value
                   70
Match length
                   91
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   216994
Seq. No.
                   LIB3147-056-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   q3021355
NCBI GI
                   305
BLAST score
                   6.0e-58
E value
                   121
Match length
                   88
 % identity
                   (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
 NCBI Description
                   tetragonoloba]
                   216995
 Seq. No.
                   LIB3147-056-Q1-K1-B10
 Seq. ID
                   BLASTX
 Method
                   g3157922
 NCBI GI
 BLAST score
                   388
                   1.0e-37
 E value
 Match length
                   111
                   70
 % identity
                   (AC002131) Contains similarity to proline-rich protein,
 NCBI Description
                   gb S68113 from Brassica napus. [Arabidopsis thaliana]
```

30398

216996

Seq. No.

```
LIB3147-056-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  g730463
NCBI GI
BLAST score
                  314
                  6.0e-29
E value
Match length
                  105
                  58
% identity
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi_1420537_emb CAA99454_ (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                  216997
Seq. No.
                  LIB3147-056-Q1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1293835
BLAST score
                  235
                  1.0e-19
E value
                  107
Match length
                   47
% identity
NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]
                   216998
Seq. No.
                  LIB3147-056-Q1-K1-B5
Seq. ID
                  BLASTN
Method
                   g2924257
NCBI GI
BLAST score
                   66
E value
                   1.0e-28
                   125
Match length
                   94
% identity
                  Tobacco chloroplast genome DNA
NCBI Description
Seq. No.
                   216999
                   LIB3147-056-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   q508304
NCBI GI
                   275
BLAST score
                   3.0e-24
E value
                   111
Match length
% identity
                   53
                  (L22305) corC [Medicago sativa]
NCBI Description
Seq. No.
                   217000
                   LIB3147-056-Q1-K1-C12
Seq. ID
                   BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
                   8.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

30399

217001

BLASTX

LIB3147-056-Q1-K1-C2

Seq. No.

Seq. ID

Method

Method

NCBI GI

BLASTX

g2618704



```
NCBI GI
                  q730934
BLAST score
                  225
                  2.0e-18
E value
Match length
                  129
% identity
                  38
                  QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
NCBI Description
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)
                  >gi 2137015 pir S68430 queuine tRNA-ribosyltransferase (EC
                  2.4.2.29), 60K chain - rabbit >gi_623547 (L37420) queuine
                  tRNA-ribosyltransferase [Oryctolagus cuniculus]
                  217002
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-C3
                  BLASTX
Method
                  g2980770
NCBI GI
BLAST score
                  179
                  3.0e-13
E value
Match length
                  93
% identity
                  47
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  217003
Seq. ID
                  LIB3147-056-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2326372
BLAST score
                  577
                  1.0e-59
E value
Match length
                  148
                  74
% identity
NCBI Description (Y14404) putative arabinose kinase [Arabidopsis thaliana]
Seq. No.
                  217004
                  LIB3147-056-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g322750
BLAST score
                  658
E value
                  3.0e-69
Match length
                  128
% identity
                  99
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
                  >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
Seq. No.
                  217005
Seq. ID
                  LIB3147-056-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  q3582340
                  157
BLAST score
E value
                  2.0e-10
Match length
                  149
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
                  217006
                  LIB3147-056-Q1-K1-C9
Seq. ID
```



BLAST score 542 E value 1.0e-55 Match length 137 % identity 74

NCBI Description (AC002510) putative thioredoxin reductase [Arabidopsis

thaliana]

Seq. No. 217007

Seq. ID LIB3147-056-Q1-K1-D10

Method BLASTN
NCBI GI g22531
BLAST score 50
E value 3.0e-19
Match length 192
% identity 84

NCBI Description Zea mays mRNA encoding a zein (clone pZ22.1)

>gi_270688_gb_I03336_ Sequence 10 from Patent US 4885357

>gi_270741_gb_I03273 Sequence 2 from Patent US

Seq. No. 217008

Seq. ID LIB3147-056-Q1-K1-D2

Method BLASTX
NCBI GI g133867
BLAST score 643
E value 2.0e-67
Match length 141
% identity 86

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

protein S11 - maize >gi 22470 emb CAA39438 (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 217009

Seq. ID LIB3147-056-Q1-K1-D4

Method BLASTX
NCBI GI g1707998
BLAST score 220
E value 8.0e-18
Match length 56
% identity 75

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 481944 pir S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082 (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 217010

Seq. ID LIB3147-056-Q1-K1-D5

Method BLASTX
NCBI GI g126770
BLAST score 362
E value 2.0e-34
Match length 69
% identity 100

NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate

synthase (EC 4.1.3.2) - upland cotton

>gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)



[Gossypium hirsutum]

```
Seq. No.
                  217011
Seq. ID
                  LIB3147-056-Q1-K1-D6
                  BLASTX
Method
NCBI GI
                  g2500380
                  477
BLAST score
                  6.0e-48
E value
                  88
Match length
                  100
% identity
                  60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal
NCBI Description
                  protein RL44 - upland cotton >gi 1553129 (U64677) ribosomal
                  protein L44 isoform a [Gossypium hirsutum] >gi_1553131
                  (U64678) ribosomal protein L44 isoform b [Gossypium
                  hirsutum]
                  217012
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-D7
Method
                  BLASTX
                  a974782
NCBI GI
BLAST score
                  441
                  9.0e-44
E value
                  88
Match length
                  99
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                  217013
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-D8
Method
                  BLASTX
                  q2961300
NCBI GI
BLAST score
                   495
                   3.0e-50
E value
                  105
Match length
% identity
                   90
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
                   217014
Seq. No.
                  LIB3147-056-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2129820
BLAST score
                   336
                   2.0e-31
E value
                   128
Match length
% identity
                   48
                  chitinase (EC 3.2.1.14) class II - peanut
NCBI Description
                   >gi 1237025_emb_CAA57773_ (X82329) chitinase (class II)
                   [Arachis hypogaea]
                   217015
Seq. No.
                  LIB3147-056-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g541954
NCBI GI
                   518
BLAST score
                   8.0e-53
E value
```

131

82

Match length

% identity

Seq. ID



```
NCBI Description ubiquitin extension protein - white lupine
                  >gi 438111 emb_CAA80334_ (Z22613) ubiquitin extension
                  protein [Lupinus albus]
                  217016
Seq. No.
                  LIB3147-056-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2970051
NCBI GI
                  147
BLAST score
                  7.0e-10
E value
                  32
Match length
                  88
% identity
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
                  217017
Seq. No.
                  LIB3147-056-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                  g218157
NCBI GI
                   389
BLAST score
                   4.0e-51
E value
                  126
Match length
                 . 87
% identity
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
                   217018
Seq. No.
                   LIB3147-056-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2735256
NCBI GI
                   389
BLAST score
                   1.0e-37
E value
Match length
                   74
                   97
% identity
NCBI Description (U89683) protein kinase [Lycopersicon esculentum]
                   217019
Seq. No.
Seq. ID
                   LIB3147-056-Q1-K1-E6
                   BLASTX
Method
                   q3687250
NCBI GI
                   531
BLAST score
                   2.0e-54
E value
                   127
Match length
% identity
                   80
                  (AC005169) putative arginine n-methyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   217020
                   LIB3147-056-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   g467324
NCBI GI
BLAST score
                   35
                   2.0e-10
E value
                   87
Match length
                   85
% identity
NCBI Description Nicotiana tabacum (clone 6.2.1) mRNA, complete cds
Seq. No.
                   217021
```

30403

LIB3147-056-Q1-K1-F11



```
BLASTN
Method
NCBI GI
                  q19212
BLAST score
                  54
                  1.0e-21
E value
                  120
Match length
                  20
% identity
NCBI Description Tomato extensin mRNA (clone w17-1)
                  217022
Seq. No.
                  LIB3147-056-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  g2392895
NCBI GI
BLAST score
                  513
                  3.0e-52
E value
                  113
Match length
                  88
% identity
                 (AF017056) brassinosteroid insensitive 1 [Arabidopsis
NCBI Description
                  thaliana]
                  217023
Seq. No.
                  LIB3147-056-Q1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2500376
                  472
BLAST score
E value
                  2.0e-47
                  95
Match length
                  95
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177 gb_AAD14494
                  (AC005508) 23552 [Arabidopsis thaliana]
                  217024
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-F6
                  BLASTX
Method
                  q3915000
NCBI GI
BLAST score
                  434
                   6.0e-43
E value
Match length
                  90
                  88
% identity
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi 2305109 (AF009734) Cu/Zn
                  superoxide dismutase [Capsicum annuum]
Seq. No.
                   217025
Seq. ID
                  LIB3147-056-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  g1439609
BLAST score
                   681
                  7.0e-72
E value
Match length
                   136
                   58
% identity
NCBI Description (U62778) delta-tonoplast intrinsic protein [Gossypium
                  hirsutum]
                   217026
Seq. No.
                   LIB3147-056-Q1-K1-F9
Seq. ID
```

30404

BLASTX

245

g2996166

Method

NCBI GI

BLAST score



```
7.0e-21
E value
                  71
Match length
                  68
% identity
                  (AF051757) putative 60S ribosomal protein L15 [Picea
NCBI Description
                  mariana] >gi_2996168 (AF051758) putative 60S ribosomal
                  protein L15 [Picea mariana] >gi_2996170 (AF051759) putative
                  60S ribosomal protein L15 [Picea mariana]
                  217027
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-G11
Method
                  BLASTX
                  q167367
NCBI GI
                  349
BLAST score
                  4.0e-33
E value
                  67
Match length
                  100
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  217028
Seq. No.
                  LIB3147-056-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244816
                   335
BLAST score
                   2.0e-31
E value
                  113
Match length
% identity
                   69
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   217029
Seq. No.
                  LIB3147-056-Q1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3860277
                   482
BLAST score
                   1.0e-48
E value
                   128
Match length
                   75
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   217030
Seq. No.
Seq. ID
                   LIB3147-056-Q1-K1-G5
                   BLASTX
Method
                   q1173043
NCBI GI
                   259
BLAST score
                   2.0e-22
E value
                   69
Match length
                   77
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi_479441_pir__S33899 ribosomal
NCBI Description
                   protein L38 - tomato (cv. Moneymaker)
                   >qi 313027 emb CAA49599 (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
```

Seq. No. 217031

Seq. ID LIB3147-056-Q1-K1-G7

Method BLASTX NCBI GI g2961300



540

BLAST score

```
2.0e-55
E value
                  112
Match length
                  94
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                  217032
Seq. No.
                  LIB3147-056-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  q3924596
NCBI GI
                  181
BLAST score
                  3.0e-13
E value
                   56
Match length
                   66
% identity
                   (AF069442) putative phospho-ser/thr phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                   217033
Seq. No.
                  LIB3147-056-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                   g1946331
NCBI GI
BLAST score
                   389
                   9.0e-38
E value
                   114
Match length
                   73
% identity
                  (U69155) prohibitin [Arabidopsis thaliana] >gi_4097692
NCBI Description
                   (U66593) prohibitin 3 [Arabidopsis thaliana]
                   217034
Seq. No.
Seq. ID
                   LIB3147-056-Q1-K1-H12
Method
                   BLASTX
                   q4544399
NCBI GI
                   433
BLAST score
E value
                   5.0e-43
                   111
Match length
% identity
                   (ACO07047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   217035
Seq. No.
                   LIB3147-056-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   q2829899
NCBI GI
BLAST score
                   349
                   5.0e-33
E value
Match length
                   144
                   47
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449_2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
                   217036
Seq. No.
                   LIB3147-056-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   q1362107
NCBI GÌ
BLAST score
                   204
                   2.0e-16
E value
```



```
Match length
                  44
                  89
% identity
NCBI Description GUT8-2a protein - common tobacco
                  217037
Seq. No.
                  LIB3147-056-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  g543905
NCBI GI
                  362
BLAST score
                  2.0e-59
E value
                  115
Match length
                  95
% identity
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
                  217038
Seq. No.
                  LIB3147-056-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g746510
NCBI GI
BLAST score
                  373
                  9.0e-36
E value
                  110
Match length
                  58
% identity
                  (U23517) similar to ubiquitin conjugating enzyme
NCBI Description
                   [Caenorhabditis elegans]
                  217039
Seq. No.
Seq. ID
                  LIB3147-056-Q1-K1-H7
                  BLASTX
Method
                  g2760325
NCBI GI
BLAST score
                  503
                   5.0e-51
E value
                  146
Match length
                   68
% identity
NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]
                   217040
Seq. No.
                  LIB3147-056-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2494144
                   121
BLAST score
                   1.0e-15
E value
Match length
                   85
                   52
% identity
NCBI Description (AC002329) predicted leucine-rich protein [Arabidopsis
                   thaliana]
                   217041
Seq. No.
Seq. ID
                   LIB3147-056-Q1-K1-H9
                   BLASTX
Method
NCBI GI
                   q119748
BLAST score
                   219
                   6.0e-18
E value
Match length
                   48
% identity
                   83
NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
```

(D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)



>gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11),
cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690)
fructose-bisphosphatase [Spinacia oleracea]

Seq. No. 217042

Seq. ID LIB3147-057-Q1-K1-B4

Method BLASTX
NCBI GI g3212610
BLAST score 155
E value 2.0e-10
Match length 55
% identity 56

NCBI Description Chain A, Sulfite Oxidase From Chicken Liver

>gi_3212611_pdb_1SOX_B Chain B, Sulfite Oxidase From

Chicken Liver

Seq. No. 217043

Seq. ID LIB3147-057-Q1-K1-B6

Method BLASTX
NCBI GI g3421164
BLAST score 550
E value 1.0e-56
Match length 126
% identity 84

NCBI Description (AF045675) arginine decarboxylase [Sisymbrium altissimum]

>gi 3421166 (AF045676) arginine decarboxylase [Stanleya

pinnata]

Seq. No. 217044

Seq. ID LIB3147-057-Q1-K1-C2

Method BLASTX
NCBI GI g2961346
BLAST score 307
E value 4.0e-28
Match length 72
% identity 78

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis

thaliana]

Seq. No. 217045

Seq. ID LIB3147-057-Q1-K1-C5

Method BLASTX
NCBI GI g2196466
BLAST score 137
E value 3.0e-15
Match length 72
% identity 64

NCBI Description (Y13673) TATA binding protein-associated factor

[Arabidopsis thaliana]

Seq. No. 217046

Seq. ID LIB3147-057-Q1-K1-D3

Method BLASTX
NCBI GI g2736288
BLAST score 575
E value 2.0e-59
Match length 128

Seq. ID

Method



```
% identity
                  (AF031080) isopentenyl diphosphate isomerase II
NCBI Description
                  [Camptotheca acuminata]
                  217047
Seq. No.
Seq. ID
                  LIB3147-057-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g730463
BLAST score
                  312
                  9.0e-29
E value
                  102
Match length
                  59
% identity
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi 1420537 emb CAA99454 (Z75142) ORF YOR234c
                  [Saccharomyces cerevisiae]
Seq. No.
                  217048
                  LIB3147-057-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q974782
                  300
BLAST score
                  1.0e-27
E value
                  65
Match length
                  91
% identity
                 (Z49150) cobalamine-independent methionine synthase
NCBI Description
                  [Solenostemon scutellarioides]
                  217049
Seq. No.
                  LIB3147-057-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  a2244841
NCBI GI
BLAST score
                  186
                  5.0e-14
E value
                  113
Match length
% identity
                  42
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                  217050
Seq. No.
                  LIB3147-057-Q1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1350988
BLAST score
                  291
E value
                  3.0e-35
Match length
                  116
                  74
% identity
                  40S RIBOSOMAL PROTEIN S3B (S1B) >gi_2119058_pir__I51635
NCBI Description
                   ribosomal protein S1 - African clawed frog
                   >gi 587600 emb CAA84291 (Z34530) ribosomal protein S1
                   [Xenopus laevis] >gi 587602 emb CAA84290 (Z34529)
                   ribosomal protein [Xenopus laevis]
                   217051
Seq. No.
```

30409

LIB3147-057-Q1-K1-H2

BLASTX



```
g1169421
NCBI GI
                   172
BLAST score
                   5.0e-13
E value
                   56
Match length
                   68
% identity
                   DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG (XDRG)
NCBI Description
                   >gi_2120159_pir__I51426 GTP-binding protein DRG - African
clawed frog >gi_433422_dbj_BAA02978_ (D13865) GTP-binding
                   protein DRG [Xenopus laevis]
Seq. No.
                   217052
                   LIB3147-057-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g1169534
NCBI GI
                   591
BLAST score
                   2.0e-61
E value
                   125
Match length
                    89
% identity
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                    phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                    >gi 433609 emb CAA82232_ (Z28386) enolase [Ricinus
                    communis]
                    217053
Seq. No.
                    LIB3147-057-Q1-K1-H6
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2961300
                    473
BLAST score
                    1.0e-47
E value
                    118
Match length
                    79
% identity
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
                    217054
Seq. No.
                    LIB3147-058-Q1-K1-A3
Seq. ID
                    BLASTX
Method
                    g585973
NCBI GI
                    406
BLAST score
                    1.0e-39
E value
                    103
Match length
                    76
% identity
NCBI Description FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC
                    2.7.1.4) - potato >gi 2\overline{9}701\overline{5} emb CAA78283 (Z12823)
                    fructokinase [Solanum tuberosum] >gi 1095321_prf 2108342A
                    fructokinase [Solanum tuberosum]
                    217055
Seq. No.
                    LIB3147-058-Q1-K1-A4
Seq. ID
                    BLASTX
Method
                    g2244740
NCBI GI
                    286
BLAST score
                    1.0e-25
E value
                    54
Match length
```

NCBI Description (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

100

% identity



```
217056
Seq. No.
                  LIB3147-058-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g3135264
NCBI GI
                  297
BLAST score
                  4.0e-27
E value
                  67
Match length
                  81
% identity
                  (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                  217057
Seq. No.
                  LIB3147-058-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  q4580395
NCBI GI
                  291
BLAST score
                  3.0e-26
E value
                  110
Match length
                  52
% identity
                  (AC007171) putative kinesin-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  217058
Seq. No.
                  LIB3147-058-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                   q2982297
NCBI GI
                   588
BLAST score
                   5.0e-61
E value
                   129
Match length
                   88
% identity
                  (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
                   217059
Seq. No.
                   LIB3147-058-Q1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1706329
BLAST score
                   508
                   8.0e-52
E value
                   97
Match length
                   97
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                   >gi_2146788_pir__S65471 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC2) - Garden pea (fragment)
                   >gi 1177605_emb_CAA91445_ (Z66544) pyruvate decarboxylase
                   [Pisum sativum]
                   217060
Seq. No.
                   LIB3147-058-Q1-K1-B1
Seq. ID
                   BLASTN
Method
                   g3869074
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
                   74
Match length
                   88
 % identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MMI9, complete sequence [Arabidopsis thaliana]
```

Seq. No. 217061



```
LIB3147-058-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g3023857
NCBI GI
                  525
BLAST score
                  1.0e-53
E value
                  113
Match length
                  87
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi_629591_pir__S48839 guanine nucleotide
                  regulatory protein - rape >gi_563335_emb_CAA83924_ (Z33643)
                  guanine nucleotide regulatory protein [Brassica napus]
                  217062
Seq. No.
                  LIB3147-058-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g4530591
NCBI GI
                  374
BLAST score
                  6.0e-36
E value
                  89
Match length
                  78
% identity
                  (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
NCBI Description
                  >qi 4530593 gb AAD22108.1_ (AF132476) heme oxygenase 1
                   [Arabidopsis thaliana]
                   217063
Seq. No.
                  LIB3147-058-Q1-K1-B12
Seq. ID
                  BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   7.0e-11
E value
                   50
Match length
                   51
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   217064
Seq. No.
                   LIB3147-058-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4406787
                   398
BLAST score
                   8.0e-39
E value
                   102
Match length
% identity
NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]
                   217065
Seq. No.
                   LIB3147-058-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g4539405
NCBI GI
                   467
BLAST score
E value
                   6.0e-47
Match length
                   108
                   80
% identity
                   (ALO49524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
```

30412

217066

LIB3147-058-Q1-K1-B8

Seq. No.

Seq. ID



```
BLASTX
Method
                  g1173187
NCBI GI
BLAST score
                  549
                  2.0e-56
E value
                  109
Match length
                  94
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  217067
Seq. No.
                  LIB3147-058-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  g2826882
NCBI GI
                  425
BLAST score
                  6.0e-42
E value
                  89
Match length
                  92
% identity
                  (AJ223634) transcription factor IIA small subunit
NCBI Description
                   [Arabidopsis thaliana]
                  217068
Seq. No.
Seq. ID
                  LIB3147-058-Q1-K1-C11
                  BLASTX
Method
                  g4567286
NCBI GI
                  387
BLAST score
                  9.0e-46
E value
                  114
Match length
                  82
% identity
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                  thaliana]
                  217069
Seq. No.
Seq. ID
                  LIB3147-058-Q1-K1-C2
                  BLASTX
Method
                  q2497752
NCBI GI
BLAST score
                   289
                   6.0e-26
E value
Match length
                   90
                   60
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                   >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                   [Prunus dulcis]
Seq. No.
                   217070
                   LIB3147-058-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g224293
NCBI GI
BLAST score
                   407
E value
                   9.0e-40
Match length
                   82
                   99
% identity
```

Seq. No. 217071

Seq. ID LIB3147-058-Q1-K1-C6

NCBI Description histone H4 [Triticum aestivum]



```
BLASTX
Method
NCBI GI
                  g1199967
                  207
BLAST score
                  2.0e-16
E value
Match length
                  52
% identity
                  (X95689) histone H4 [Allium cepa]
NCBI Description
                  217072
Seq. No.
Seq. ID
                  LIB3147-058-Q1-K1-C7
                  BLASTX
Method
                  q4337175
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
                  54
Match length
                   67
% identity
                  (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb AA720210 come from this gene. [Arabidopsis thaliana]
                   217073
Seq. No.
Seq. ID
                   LIB3147-058-Q1-K1-C8
                   BLASTX
Method
                   g3202046
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
Match length
                   120
% identity
                   3
                  (AF069525) 190 kDa ankyrin isoform; AnkG190 [Rattus
NCBI Description
                   norvegicus]
Seq. No.
                   217074
Seq. ID
                   LIB3147-058-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g1542941
BLAST score
                   567
                   1.0e-58
E value
Match length
                 - 144
% identity
                   80
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                   217075
Seq. No.
                   LIB3147-058-Q1-K1-D3
Seq. ID
Method
                   BLASTX
                   g1653033
NCBI GI
                   270
BLAST score
                   9.0e-24
E value
                   66
Match length
                   76
% identity
NCBI Description (D90910) hypothetical protein [Synechocystis sp.]
                   217076
Seq. No.
                   LIB3147-058-Q1-K1-D4
Seq. ID
Method
                   BLASTX
```

30414

g113232

303

NCBI GI BLAST score

NCBI GI

BLAST score E value g417060 790

1.0e-84

```
1.0e-27
E value
                  58
Match length
                  100
% identity
NCBI Description ACTIN 2 >gi_100150_pir__S07003 actin 2 - carrot
                  217077
Seq. No.
                  LIB3147-058-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2914703
                  476
BLAST score
                  7.0e-48
E value
                  119
Match length
                  38
% identity
                  (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
                  217078
Seq. No.
                  LIB3147-058-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g2108252
NCBI GI
BLAST score
                   500
                  1.0e-50
E value
Match length
                  139
% identity
                   35
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi 2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   217079
Seq. No.
                   LIB3147-058-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g2146797
NCBI GI
                   504
BLAST score
                   4.0e-51
E value
                   153
Match length
                   40
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                   >gi_1134968 (U41385) protein disulphide isomerase PDI
                   [Ricinus communis] >gi 1587210 prf__2206331A protein
                   disulfide isomerase [Ricinus communis]
                   217080
Seq. No.
                   LIB3147-058-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   q3212116
NCBI GI
                   279
BLAST score
                   9.0e-25
E value
                   104
Match length
                   50
 % identity
NCBI Description (Y17393) prefoldin subunit 2 [Mus musculus]
                   217081
Seq. No.
Seq. ID
                   LIB3147-058-Q1-K1-E10
                   BLASTX
Method
```

Method

NCBI GI BLAST score BLASTX q531829



```
150
  Match length
                    92
  % identity
                    GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA
  NCBI Description
                    LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase
                    [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln
                    synthetase [Vigna aconitifolia]
                    217082
  Seq. No.
                    LIB3147-058-Q1-K1-E12
  Seq. ID
                    BLASTX
  Method
                    g3510256
  NCBI GI
                    149
  BLAST score
                    2.0e-09
  E value
                     64
  Match length
                     45
  % identity
                    (AC005310) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     217083
  Seq. No.
                     LIB3147-058-Q1-K1-E2
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g2454182
  BLAST score
                     648
                     5.0e-68
. E value
                     132
  Match length
                     92
  % identity
                     (U80185) pyruvate dehydrogenase E1 alpha subunit
  NCBI Description
                     [Arabidopsis thaliana]
                     217084
  Seq. No.
                     LIB3147-058-Q1-K1-E3
  Seq. ID
                     BLASTX
  Method
                     g2507421
  NCBI GI
                     396
  BLAST score
                     6.0e-39
  E value
                     94
  Match length
                     87
  % identity
  NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
                     (U81042) translation initiation factor [Arabidopsis
                     thaliana] >gi 4490709 emb_CAB38843.1_ (AL035680)
                     translation initiation factor [Arabidopsis thaliana]
                     217085
  Seq. No.
                     LIB3147-058-Q1-K1-E4
  Seq. ID
                     BLASTX
  Method
                     q418777
  NCBI GI
                     312
  BLAST score
                     1.0e-28
  E value
                     59
  Match length
                     95
   % identity
  NCBI Description phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic
                     chain (clone EP7) - Arabidopsis thaliana (fragment)
                     217086
   Seq. No.
   Seq. ID
                     LIB3147-058-Q1-K1-E5
```

BLAST score



```
1.0e-08
E value
                  79
Match length
                  43
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  217087
Seq. No.
                  LIB3147-058-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4204285
BLAST score
                  224
E value
                   6.0e-36
                   118
Match length
                   59
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   217088
Seq. No.
                   LIB3147-058-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g2811014
NCBI GI
BLAST score
                   146
E value
                   8.0e-10
                   59
Match length
                   53
% identity
                   DYNEIN LIGHT CHAIN LC6, FLAGELLAR OUTER ARM
NCBI Description
                   >qi 2208914 dbj BAA20525 (AB004830) outer arm dynein LC6
                   [Anthocidaris crassispina]
                   217089
Seq. No.
                   LIB3147-058-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q167367
BLAST score
                   585
E value
                   1.0e-60
                   127
Match length
                   87
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   217090
Seq. No.
                   LIB3147-058-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g1169839
NCBI GI
                   164
BLAST score
                   3.0e-11
E value
                   81
Match length
                   38
 % identity
NCBI Description GIBBERELLIN-REGULATED PROTEIN 1 PRECURSOR
                   >gi 2129588 pir S71441 GAST1 protein homolog (clone GASA1)
                   - Arabidopsīs thaliana >gi 887939 (U11766) GAST1 protein
                   homolog [Arabidopsis thaliana]
                   217091
 Seq. No.
 Seq. ID
                   LIB3147-058-Q1-K1-F12
                   BLASTX
 Method
 NCBI GI
                   q2809481
```



```
5.0e-22
E value
                   85
Match length
                   31
% identity
                  (AF042839) calmodulin [Oryza sativa]
NCBI Description
                   217092
Seq. No.
                   LIB3147-058-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3493172
                   772
BLAST score
                   1.0e-82
E value
                   150
Match length
                   52
% identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                   217093
                   LIB3147-058-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1694976
BLAST score
                   386
E value
                   3.0e-37
Match length
                   116
                   66
% identity
                   (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   217094
Seq. No.
                   LIB3147-058-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g129248
NCBI GI
BLAST score
                   169
                   7.0e-12
E value
                   107
Match length
                   38
% identity
NCBI Description ORGAN SPECIFIC PROTEIN S2 >gi 72318 pir KNPMS2 protein S2
                   - garden pea >gi_295831_emb_C\overline{A}A3594\overline{4}_ (\overline{X5}1595) S2 protein
                   [Pisum sativum]
                   217095
Seq. No.
Seq. ID
                   LIB3147-058-Q1-K1-G1
                   BLASTX
Method
NCBI GI
                   q3769472
                   299
BLAST score
                   2.0e-31
E value
                   92
Match length
                   67
% identity
NCBI Description (AF064732) putative phospholipase A2 [Dianthus
                   caryophyllus]
Seq. No.
                   217096
                   LIB3147-058-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2673868
BLAST score
                   433
                   8.0e-43
E value
Match length
                   100
```

Seq. ID



```
% identity
                  (Y14856) fimbriata-associated protein [Antirrhinum majus]
NCBI Description
                  217097
Seq. No.
Seq. ID
                  LIB3147-058-Q1-K1-G2
                  BLASTX
Method
                  q3493172
NCBI GI
BLAST score
                  768
                  4.0e-82
E value
                  154
Match length
                  56
% identity
                  (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
                  217098
Seq. No.
                  LIB3147-058-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                  g170753
NCBI GI
BLAST score
                   487
                   4.0e-49
E value
Match length
                  103
% identity
                  80
                  (M95819) initiation factor (iso) 4F p28 subunit [Triticum
NCBI Description
                  aestivum]
                   217099
Seq. No.
                  LIB3147-058-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g3242705
NCBI GI
                   698
BLAST score
                   7.0e-74
E value
Match length
                   152
                   84
% identity
                  (AC003040) putative nicotinate phosphoribosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   217100
Seq. No.
                   LIB3147-058-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   q2213626
NCBI GI
BLAST score
                   360
                   3.0e - 34
E value
Match length
                   148
                   47
% identity
NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]
Seq. No.
                   217101
Seq. ID
                   LIB3147-058-Q1-K1-G8
                   BLASTX
Method
NCBI GI
                   g1477428
BLAST score
                   670
                   1.0e-70
E value
Match length
                   129
                   94
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.
                   217102
```

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LIB3147-058-Q1-K1-H1



BLASTX Method NCBI GI g3176690 BLAST score 528 6.0e-54 E value 135 Match length 79 % identity (AC003671) Similar to ubiquitin ligase gb D63905 from S. NCBI Description cerevisiae. EST gb R65295 comes from this gene. [Arabidopsis thaliana] 217103 Seq. No. Seq. ID LIB3147-058-Q1-K1-H10 BLASTX Method g4490728 NCBI GI BLAST score 325 4.0e-30 E value 99 Match length 62 % identity NCBI Description (AL035709) putative protein [Arabidopsis thaliana] Seq. No. 217104 LIB3147-058-Q1-K1-H3 Seq. ID BLASTX Method q2529665 NCBI GI BLAST score 180 3.0e-13E value 50 Match length 70 % identity (AC002535) putative ribosomal protein L7A [Arabidopsis NCBI Description thaliana] 217105 Seq. No. LIB3147-058-Q1-K1-H5 Seq. ID Method BLASTX NCBI GI q3123264 BLAST score 424 7.0e-42E value 105 Match length % identity 76 NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279 (Z97337) hypothetical protein [Arabidopsis thaliana] Seq. No. 217106 LIB3147-058-Q1-K1-H7 Seq. ID BLASTX Method NCBI GI q2582351 BLAST score 233 E value 2.0e-19 Match length 107 % identity NCBI Description (AF018639) unknown [Dictyostelium discoideum]

Seq. No. 217107

Seq. ID LIB3147-058-Q1-K1-H8

Method BLASTX NCBI GI g434759 BLAST score 484

NCBI GI BLAST score

E value

515 1.0e-52



```
6.0e-49
E value
                  117
Match length
                  74
% identity
                  (D21163) similar to human elongation factor 2 mRNA (HSEF2).
NCBI Description
                  [Homo sapiens]
Seq. No.
                  217108
                  LIB3147-059-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4193382
BLAST score
                  386
                  2.0e-37
E value
                  86
Match length
                  83
% identity
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >qi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
                   217109
Seq. No.
                  LIB3147-059-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1694976
BLAST score
                   370
                   2.0e-35
E value
                   103
Match length
% identity
                  (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   217110
Seq. No.
                   LIB3147-059-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   q1076755
NCBI GI
                   318
BLAST score
                   2.0e-29
E value
                   100
Match length
                   62
% identity
NCBI Description protein kinase - rice >gi_450300 (L27821) protein kinase
                   [Oryza sativa]
                   217111
Seq. No.
                   LIB3147-059-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g456568
NCBI GI
BLAST score
                   652
                   2.0e-68
E value
                   132
Match length
 % identity
                   91
NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]
                   217112
 Seq. No.
                   LIB3147-059-Q1-K1-A6
 Seq. ID
                   BLASTX
 Method
                   g123620
```



```
120
Match length
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950
NCBI Description
                  heat shock cognate protein 70 - tomato
                  >gi 19258_emb_CAA37971_ (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
                  217113
Seq. No.
                  LIB3147-059-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617274
BLAST score
                  548
                  2.0e-56
E value
                  126
Match length
                  81
% identity
                 (Z72152) AMP-binding protein [Brassica napus]
NCBI Description
                  217114
Seq. No.
                  LIB3147-059-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g2706450
NCBI GI
BLAST score
                  371
                   1.0e-35
E value
                  82
Match length
                  84
% identity
                  (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                  pyrophosphatase [Solanum tuberosum]
                   217115
Seq. No.
                   LIB3147-059-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3337361
                   445
BLAST score
                   1.0e-44
E value
                   94
Match length
                   81
% identity
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
                   217116
Seq. No.
                   LIB3147-059-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g3341694
NCBI GI
                   278
BLAST score
                   3.0e-25
E value
                   76
Match length
% identity
NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]
                   217117
Seq. No.
                   LIB3147-059-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g464621
NCBI GI
                   160
BLAST score
                   7.0e-11
E value
                   61
Match length
                   56
 % identity
```

NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586



ribosomal protein ML16 - common ice plant

>gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 217118

Seq. ID LIB3147-059-Q1-K1-B5

Method BLASTX
NCBI GI 94539292
BLAST score 241
E value 6.0e-21
Match length 53

% identity 81

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

Seq. No. 217119

Seq. ID LIB3147-059-Q1-K1-B6

Method BLASTX
NCBI GI g2462825
BLAST score 244
E value 7.0e-21
Match length 79
% identity 59

NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding

region [Arabidopsis thaliana]

Seq. No. 217120

Seq. ID LIB3147-059-Q1-K1-B7

Method BLASTX
NCBI GI g1518540
BLAST score 607
E value 2.0e-63
Match length 123
% identity 94

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 217121

Seq. ID LIB3147-059-Q1-K1-B8

Method BLASTX
NCBI GI g3142301
BLAST score 314
E value 3.0e-29
Match length 89
% identity 63

NCBI Description (AC002411) Contains similarity to neural cell adhesion

molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,

gb_H3630

Seq. No. 217122

Seq. ID LIB3147-059-Q1-K1-C10

Method BLASTX
NCBI GI g3834310
BLAST score 624
E value 3.0e-65
Match length 131



```
% identity
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb D83004 from Homo sapiens. ESTs gb T88233, gb_Z24464,
                  gb_N37265, gb_H36151, gb_Z34711, gb_A\(\overline{A}\)040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
                  217123
Seq. No.
                  LIB3147-059-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g2765837
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
                  66
Match length
                  59
% identity
NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]
                  217124
Seq. No.
                  LIB3147-059-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g4127456
NCBI GI
BLAST score
                  285
                  1.0e-25
E value
                  106
Match length
% identity
                  40
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]
                  217125
Seq. No.
                  LIB3147-059-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g3892051
NCBI GI
BLAST score
                   377
                   3.0e-36
E value
                  8.5
Match length
                   80
% identity
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
                   217126
Seq. No.
                   LIB3147-059-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g464707
BLAST score
                   539
                   2.0e-55
E value
Match length
                   108
                   95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
                   protein S18.A - Arabidopsis thaliana
                   >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 434343_emb CAA82273_ (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >qi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi 434906_emb CAA82275_ (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >qi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
```

[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb T21121, gb Z17755, gb R64776 and

NCBI Description



gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]

```
217127
Seq. No.
                  LIB3147-059-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g542190
NCBI GI
                   295
BLAST score
                   8.0e-27
E value
Match length
                   99
                   38
% identity
                  hypothetical protein 1087 - maize >gi 459269 emb CAA54960
NCBI Description
                   (X78029) transcribed sequence 1087 [Zea mays]
                   217128
Seq. No.
                   LIB3147-059-Q1-K1-C6
Seq. ID
                   BLASTN
Method
                   g4512110
NCBI GI
                   43
BLAST score
E value
                   7.0e-15
                   79
Match length
                   89
% identity
                   Phalaenopsis sp. 'KCbutterfly' putative profilin mRNA,
NCBI Description
                   complete cds
                   217129
Seq. No.
                   LIB3147-059-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g3212869
NCBI GI
                   394
BLAST score
                   3.0e - 38
E value
                   98
Match length
                   73
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   217130
Seq. No.
                   LIB3147-059-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   g3023194
NCBI GI
                   478
BLAST score
                   2.0e-48
E value
Match length
                   98
                   97
% identity
NCBI Description 14-3-3-LIKE PROTEIN A (SGF14A) >gi_1575725 (U70533) SGF14A
                   [Glycine max]
                   217131
Seq. No.
Seq. ID
                   LIB3147-059-Q1-K1-D11
                   BLASTX
Method
NCBI GI
                   q3367534
BLAST score
                   187
                   3.0e-14
E value
Match length
                   77
 % identity
                   47
```

(AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis



thaliana]

```
217132
Seq. No.
Seq. ID
                  LIB3147-059-Q1-K1-D4
                  BLASTN
Method
NCBI GI
                  g1335861
                  67
BLAST score
                  3.0e-29
E value
                  135
Match length
% identity
                 Glycine max clathrin heavy chain mRNA, complete cds
NCBI Description
                  217133
Seq. No.
Seq. ID
                  LIB3147-059-Q1-K1-D5
                  BLASTX
Method
                  g549063
NCBI GI
                  316
BLAST score
                  3.0e-29
E value
                  81
Match length
                  74
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >qi 1072464 pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   217134
Seq. No.
Seq. ID
                  LIB3147-059-Q1-K1-E10
                   BLASTX
Method
                   g2493046
NCBI GI
BLAST score
                   251
                   1.0e-21
E value
                   77
Match length
                   62
% identity
                  ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                   3.6.1.34) delta' chain precursor - sweet potato
                   >gi 217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                   delta subunit [Ipomoea batatas]
Seq. No.
                   217135
                   LIB3147-059-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2262173
NCBI GI
BLAST score
                   616
                   3.0e-64
E value
Match length
                   135
% identity
                   89
                  (AC002329) NADPH thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   217136
Seq. No.
                   LIB3147-059-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   q4468817
NCBI GI
```

30426

648

131

4.0e-68

BLAST score

Match length

E value

NCBI GI



```
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                  217137
Seq. No.
                  LIB3147-059-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g2253442
NCBI GI
                  196
BLAST score
                  5.0e-15
E value
                   49
Match length
                   65
% identity
                  (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
                   217138
Seq. No.
                   LIB3147-059-Q1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3820614
BLAST score
                   270
                   7.0e-24
E value
                   111
Match length
                   53
% identity
NCBI Description (AF094516) E1-like protein [Homo sapiens]
                   217139
Seq. No.
                   LIB3147-059-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   q2911071
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   65
Match length
                   55
% identity
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   217140
                   LIB3147-059-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g1279222
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   87
Match length
 % identity
NCBI Description (X97455) specific tissue protein 2 [Cicer arietinum]
                   217141
 Seq. No.
                   LIB3147-059-Q1-K1-F6
 Seq. ID
                   BLASTX
 Method
                   q4337210
 NCBI GI
                   193
 BLAST score
                   1.0e-14
 E value
                   86
 Match length
                   45
 % identity
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
                   217142
 Seq. No.
 Seq. ID
                   LIB3147-059-Q1-K1-F7
                   BLASTX
 Method
```

30427

g1279206

```
K AND
```

```
576
 BLAST score
                    1.0e-59
 E value
                    127
 Match length
 % identity
                    87
                   (X97446) alpha-tubulin [Avena sativa]
 NCBI Description
                    217143
 Seq. No.
                    LIB3147-059-Q1-K1-F8
 Seq. ID
 Method
                    BLASTX
                    q2464852
 NCBI GI
                    171
 BLAST score
                    3.0e-12
 E value
                    101
 Match length
                    43
 % identity
                   (Z99707) putative protein [Arabidopsis thaliana]
 NCBI Description
                    217144
 Seq. No.
                    LIB3147-059-Q1-K1-G11
 Seq. ID
                    BLASTX
 Method
                    q2129771
 NCBI GI
 BLAST score
                    554
                    5.0e-57
 E value
                    141
 Match length
                    74
 % identity
                    xyloglucan endotransglycosylase-related protein XTR-6 -
NCBI Description
                    Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan
                    endotransglycosylase-related protein [Arabidopsis thaliana]
                    >gi 4539299 emb_CAB39602.1_ (AL049480) xyloglucan endo-1,
                    4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]
                    217145
 Seq. No.
                    LIB3147-059-Q1-K1-G12
 Seq. ID
                    BLASTX
 Method
                    g3367534
 NCBI GI
                    581
 BLAST score
                    4.0e-60
 E value
                    144
 Match length
                    81
  % identity
                    (AC004392) Strong similarity to coatamer alpha subunit
 NCBI Description
                    (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis
                    thaliana]
                    217146
  Seq. No.
 Seq. ID
                    LIB3147-059-Q1-K1-H1
                    BLASTX
  Method
  NCBI GI
                    q3236242
                    335
  BLAST score
                    3.0e - 31
  E value
                    87
 Match length
  % identity
                    (AC004684) putative ribosomal protein L36 [Arabidopsis
  NCBI Description
                    thaliana]
  Seq. No.
                    217147
                    LIB3147-059-Q1-K1-H10
  Seq. ID
```

30428

BLASTX

q3913791

Method NCBI GI



BLAST score 653 E value 1.0e-68 Match length 136 % identity 88

NCBI Description GLUTAMATE--CYSTEINE LIGASE PRECURSOR

(GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase

[Lycopersicon esculentum]

Seq. No. 217148

Seq. ID LIB3147-059-Q1-K1-H11

Method BLASTX
NCBI GI g3914442
BLAST score 390
E value 5.0e-38
Match length 93
% identity 80

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No. 217149

Seq. ID LIB3147-059-Q1-K1-H3

Method BLASTX
NCBI GI g2673908
BLAST score 288
E value 8.0e-26
Match length 106
% identity 53

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 217150

Seg. ID LIB3147-059-Q1-K1-H4

Method BLASTN
NCBI GI g2570118
BLAST score 55

E value 4.0e-22
Match length 83
% identity 92

NCBI Description S.latifolia mRNA, clone CCLS

Seq. No. 217151

Seq. ID LIB3147-059-Q1-K1-H5

Method BLASTX
NCBI GI g3269288
BLAST score 471
E value 3.0e-47
Match length 114
% identity 81

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 217152

Seq. ID LIB3147-059-Q1-K1-H7

Method BLASTX
NCBI GI g3158376
BLAST score 242
E value 1.0e-20

e.

Match length

125



```
90
Match length
                  54
% identity
                 (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217153
                  LIB3147-060-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914449
BLAST score
                  628
                  1.0e-65
E value
Match length
                  128
% identity
                  95
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                  7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                  persica]
                  217154
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-A2
                  BLASTX
Method
NCBI GI
                  g4467129
BLAST score
                  277
                  4.0e-25
E value
                  59
Match length
% identity
                  45
                  (AL035538) calcium-dependent protein kinase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  217155
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-A8
                  BLASTX
Method
NCBI GI
                  g231660
BLAST score
                  263
                  3.0e-23
E value
                  81
Match length
                  64
% identity
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
                  217156
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2961378
BLAST score
                  100
                  3.0e-11
E value
Match length
                  65
                  63
% identity
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]
                  217157
Seq. No.
                  LIB3147-060-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548774
BLAST score
                  327
                  3.0e-49
E value
```

% identity 82
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
protein L7a - rice >gi 303855 dbj BAA02156 (D12631)



Seq. No.

217158

ribosomal protein L7A [Oryza sativa]

```
LIB3147-060-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g135491
NCBI GI
                    376
BLAST score
                    4.0e-67
E value
                    147
Match length
                    85
% identity
                   TUBULIN BETA CHAIN >gi_320961_pir__A44949 tubulin beta
NCBI Description
                    chain - Plasmodium falciparum >gi 160732 (M28398)
                    beta-tubulin [Plasmodium falciparum]
                    217159
Seq. No.
                    LIB3147-060-Q1-K1-B2
Seq. ID
                    BLASTX
Method
                    g2911072
NCBI GI
                    235
BLAST score
                    1.0e-28
E value
                    92
Match length
                    74
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                    217160
Seq. No.
                    LIB3147-060-Q1-K1-B3
Seq. ID
                    BLASTX
Method
                    q3334320
NCBI GI
                    719
BLAST score
                    2.0e-76
E value
                    145
Match length
                    95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553)
                    ribosome-associated protein p40 [GTycine max]
                    217161
Seq. No.
                    LIB3147-060-Q1-K1-B7
Seq. ID
                    BLASTX
Method
NCBI GI
                    g122085
                     515
BLAST score
E value
                    2.0e-52
                    121
Match length
 % identity
NCBI Description HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis
                     thaliana >gi_8\overline{2}482_p\overline{i}r_\overline{S0}4099 histone H3 (variant H3R-21)
                     - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136)
                     [Oryza sativa] >gi_20253_emb_CAA31970 (X13680) histone H3
                     (AA 1-136) [Oryza \overline{s}ativa] > g\overline{i}_168493 (M36658) histone H3
                     (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]
                     >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506
                     (M35388) histone H3 [Zea mays] >gi_169655 (M7\overline{7}493) histone
                     H3 [Petroselinum crispum] >gi 1696\overline{5}7 (M77494) histone H3
                     [Petroselinum crispum] >gi 169659 (M77495) histone H3
                     [Petroselinum crispum] >gi_387565 (M17130) histone H3
                     [Arabidopsis thaliana] >gi 387567 (M17131) histone H3
                     [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377)
```



histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf_1303352A histone H3 [Helicoverpa zea] >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

217162 Seq. No. Seq. ID LIB3147-060-Q1-K1-B9 BLASTX Method g3451065 NCBI GI BLAST score 245 4.0e-27 E value Match length 66 % identity 95

NCBI Description (AL031326) water channel - like protein [Arabidopsis

thaliana]

Seq. No. 217163

Seq. ID LIB3147-060-Q1-K1-C10

Method BLASTX
NCBI GI g3219939
BLAST score 150
E value 1.0e-09
Match length 74
% identity 49

NCBI Description HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I

>gi 2094864 emb CAB08603 (Z95334) unknown

[Schizosaccharomyces pombe]

Seq. No. 217164

Seq. ID LIB3147-060-Q1-K1-C11

Method BLASTX
NCBI GI g1766048
BLAST score 456
E value 2.0e-45
Match length 131
% identity 73

NCBI Description (U81994) NAD+ dependent isocitrate dehydrogenase subunit 2

[Arabidopsis thaliana]

Seq. No. 217165

Seq. ID LIB3147-060-Q1-K1-C2

Method BLASTX
NCBI GI g1346172
BLAST score 399
E value 6.0e-39
Match length 104
% identity 76

NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)

>gi 170384 (L08830) glucose-regulated protein 78

[Lycopersicon esculentum]

Seq. No.

Seq. ID

217171

LIB3147-060-Q1-K1-D2



```
217166
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-C3
                  BLASTX
Method
                  g2811026
NCBI GI
BLAST score
                  252
                  2.0e-31
E value
                  79
Match length
                  86
% identity
                  TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi 1946375 (U93215)
NCBI Description
                  TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]
                  >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog
                  [Arabidopsis thaliana]
                  217167
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-C7
                  BLASTX
Method
                  g2055384
NCBI GI
BLAST score
                  157
                  2.0e-10
E value
                  99
Match length
                  45
% identity
                  (U69633) cold-stress inducible protein [Solanum tuberosum]
NCBI Description
                  217168
Seq. No.
                  LIB3147-060-Q1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2104681
BLAST score
                  243
                  2.0e-31
E value
Match length
                  134
                  57
% identity
                 (X97907) transcription factor [Vicia faba]
NCBI Description
                  217169
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-D1
Method
                  BLASTX
                  g2369714
NCBI GI
                  165
BLAST score
E value
                  1.0e-11
                  89
Match length
% identity
                  42
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                  217170
Seq. No.
                  LIB3147-060-Q1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1362093
BLAST score
                   343
                  2.0e-51
E value
Match length
                  132
                  76
% identity
NCBI Description
                  hypothetical protein (clone TPP15) - tomato (fragment)
                  >gi 924632 (U20595) unknown [Solanum lycopersicum]
```



```
BLASTX
Method
NCBI GI
                  g2982311
                  638
BLAST score
                  7.0e-67
E value
                  145
Match length
                  79
% identity
                  (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
NCBI Description
                  mariana]
                  217172
Seq. No.
                  LIB3147-060-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g4510383
NCBI GI
BLAST score
                  202
                  8.0e-16
E value
                  57
Match length
                  74
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                  217173
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-E11
                  BLASTX
Method
                  g4490705
NCBI GI
                  285
BLAST score
                  3.0e-47
E value
                  130
Match length
                  75
% identity
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  217174
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-E12
Method
                  BLASTX
                  q3953467
NCBI GI
BLAST score
                   314
                  1.0e-35
E value
                  90
Match length
                   49
% identity
                  (AC002328) F20N2.12 [Arabidopsis thaliana]
NCBI Description
                   217175
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-E3
                   BLASTX
Method
NCBI GI
                   q1173043
BLAST score
                   247
E value
                   5.0e-21
Match length
                   69
                   74
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi_479441_pir__S33899 ribosomal
NCBI Description
                   protein L38 - tomato (cv. Moneymaker)
                   >qi 313027 emb CAA49599 (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
```

Seq. No. 217176

Seq. ID LIB3147-060-Q1-K1-E6

Method BLASTX NCBI GI g4467108



```
BLAST score
                  210
E value
                  8.0e-17
Match length
                  58
                  72
% identity
                  (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217177
Seq. ID
                  LIB3147-060-Q1-K1-E7
                  BLASTX
Method
NCBI GI
                  g3080371
                  477
BLAST score
                  5.0e-48
E value
                  131
Match length
                  63
% identity
NCBI Description
                  (AL022580) putative pectinacetylesterase protein
                  [Arabidopsis thaliana]
                  217178
Seq. No.
Seq. ID
                  LIB3147-060-Q1-K1-E8
                  BLASTX
Method
NCBI GI
                  g3080415
BLAST score
                  514
                  3.0e-52
E value
                  130
Match length
                  78
% identity
                  (AL022604) cysteine proteinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  217179
Seq. ID
                  LIB3147-060-Q1-K1-E9
Method
                  BLASTX
                  g4580460
NCBI GI
BLAST score
                  678
E value
                  1.0e-71
Match length
                  138
% identity
                  97
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  217180
                  LIB3147-060-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  g1724102
NCBI GI
BLAST score
                  286
                  1.0e-25
E value
Match length
                  143
                  45
% identity
NCBI Description
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
Seq. No.
                  217181
                  LIB3147-060-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454468
BLAST score
                  372
```

1.0e-37

118

E value Match length



```
66
% identity
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  217182
Seq. No.
                  LIB3147-060-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  q136057
NCBI GI
BLAST score
                  264
                  5.0e-23
E value
Match length
                  63
                  79
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 99499_pir _A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi_556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
                   217183
Seq. No.
                  LIB3147-060-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4191796
BLAST score
                   139
                   5.0e-09
E value
                   62
Match length
                   42
% identity
                   (AC005917) putative senescence-associated protein 5
NCBI Description
                   [Arabidopsis thaliana]
                   217184
Seq. No.
                   LIB3147-060-Q1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g399940
                   268
BLAST score
                   2.0e-27
E value
                   112
Match length
                   63
% identity
                  MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
NCBI Description
                   >gi 100004 pir S25005 heat shock protein, 70K - kidney
                   bean >gi 22636 emb CAA47345 (X66874) 70 kDa heat shock
                   protein [Phaseolus vulgaris]
                   217185
Seq. No.
                   LIB3147-060-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g3687833
NCBI GI
                   236
BLAST score
                   1.0e-37
E value
                   130
Match length
                   29
 % identity
NCBI Description (AF069737) notchless [Xenopus laevis]
                   217186
```

Seq. ID LIB3147-060-Q1-K1-H4 BLASTX Method NCBI GI q1418127 233 BLAST score E value 2.0e-19

Seq. No.



71

34

Match length % identity

```
55
Match length
                   82
% identity
                  (D63166) CTP:phosphocholine cytidylyltransferase [Brassica
NCBI Description
                  napus]
                  217187
Seq. No.
                  LIB3147-060-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                   g4105772
NCBI GI
                   376
BLAST score
                   4.0e-36
E value
                   80
Match length
                   45
% identity
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
Seq. No.
                   217188
                   LIB3147-060-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g1076746
NCBI GI
                   305
BLAST score
E value
                   9.0e-44
                   120
Match length
                   82
% identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock p. tein 70
                   [Oryza sativa]
                   217189
Seq. No.
                   LIB3148-001-P1-K1-A10
Seq. ID
                   {\tt BLASTX}
Method
                   g122007
NCBI GI
                   172
BLAST score
                   2.0e-12
E value
                   65
Match length
                   58
% identity
                  HISTONE H2A >gi_100161 pir__S11498 histone H2A - parsley
NCBI Description
                   >gi_20448_emb_CAA37828_ (X\overline{53}831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
                   217190
Seq. No.
                   LIB3148-001-P1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2245091
BLAST score
                   168
                   9.0e-12
E value
                   50
Match length
                   68
% identity
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   217191
Seq. No.
Seq. ID
                   LIB3148-001-P1-K1-B4
                   BLASTX
Method
                   q4455250
NCBI GI
BLAST score
                   153
E value
                   1.0e-10
```

```
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                  217192
Seq. No.
                  LIB3148-001-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  g3264611
NCBI GI
BLAST score
                  361
                  2.0e-34
E value
                  81
Match length
                  81
% identity
                 (AF061511) seven in absentia homolog [Zea mays]
NCBI Description
                  217193
Seq. No.
Seq. ID
                  LIB3148-001-P1-K1-C10
                  BLASTX
Method
                  g1706326
NCBI GI
BLAST score
                  144
                  4.0e-09
E value
                  30
Match length
                  90
% identity
NCBI Description
                 PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
                  >gi 2146786_pir S65470 pyruvate decarboxylase (EC 4.1.1.1)
                  (clone PDC1) - Garden pea >gi 1177603 emb CAA91444
                  (Z66543) pyruvate decarboxylase [Pisum sativum]
                  217194
Seq. No.
                  LIB3148-001-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3785997
BLAST score
                  432
E value
                  1.0e-42
Match length
                  149
                  56
% identity
NCBI Description (AC005499) putative annexin [Arabidopsis thaliana]
Seq. No.
                  217195
                  LIB3148-001-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g1173049
NCBI GI
BLAST score
                  182
                  1.0e-13
E value
Match length
                  63
                  63
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32 (RP49) >gi 299925 bbs 130531
                  (S59382) ribosomal protein 49 [Drosophila pseudoobscura,
                  Peptide, 134 aa] [Drosophila pseudoobscura]
                  >gi 2950188 emb CAA70875 (Y09704) ribosomal protein 49
                  [Drosophila affinis] >gi 2950190 emb CAA70876 (Y09705)
                  ribosomal protein 49 [Drosophila azteca]
                  >gi_2950198_emb_CAA70880_ (Y09709) ribosomal protein 49
                  [Drosophila miranda] >gi 2950200 emb CAA70881 (Y09710)
                  ribosomal protein 49 [Drosophila persimilis]
```

Seq. No. 217196

Seq. ID LIB3148-001-P1-K1-C7

Method BLASTX NCBI GI q266463



309 BLAST score 1.0e-28 E value Match length 82 77 % identity 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM NCBI Description DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670 3-isopropylmalate dehydrogenase (EC $\overline{1.1.1.85}$) $\overline{\text{precursor}}$ potato >gi 22643 emb CAA47720 (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064 prf_ 1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum] Seq. No. 217197 LIB3148-001-P1-K1-D12 Seq. ID Method BLASTX NCBI GI q1084457 BLAST score 220 7.0e-18 E value 138 Match length 41 % identity NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ (D23674) elongation factor 1 beta [Oryza sativa] Seq. No. 217198 LIB3148-001-P1-K1-D9 Seq. ID Method BLASTX NCBI GI q4454468 BLAST score 542 E value 1.0e-55 Match length 149 68 % identity (AC006234) putative NADH dehydrogenase [Arabidopsis NCBI Description thaliana] 217199 Seq. No. Seq. ID LIB3148-001-P1-K1-E2 BLASTX Method q3851636 NCBI GI 185 BLAST score 2.0e-14 E value 51 Match length 71 % identity NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina] 217200 Seq. No. Seq. ID LIB3148-001-P1-K1-F12 BLASTX Method NCBI GI g2507421 493 BLAST score 7.0e-50 E value Match length 107 90 % identity

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]



```
217201
Seq. No.
Seq. ID
                  LIB3148-001-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g2511594
                  132
BLAST score
                  4.0e-11
E value
                  81
Match length
                  52
% identity
                  (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
                  precursor, beta subunit [Arabidopsis thaliana]
                  >qi 2827525 emb CAA16533 (AL021633) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                  [Arabidopsis thaliana] >gi 3421099 (AF043529) 20S
                  proteasome subunit PBA1 [Arabidopsis thaliana]
                  217202
Seq. No.
                  LIB3148-001-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g2754816
NCBI GI
BLAST score
                  193
E value
                  1.0e-14
Match length
                  140
% identity
                  34
                  (AF021346) non-race specific disease resistance protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  217203
                  LIB3148-001-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  g322678
NCBI GI
BLAST score
                  327
                  2.0e-30
E value
                  119
Match length
                  58
% identity
                  chalcone isomerase (EC 5.5.1.6) - apple tree (fragment)
NCBI Description
                  >gi 19585 emb_CAA48774 (X68978) chalcone isomerase [Malus
                  sp.]
                  217204
Seq. No.
Seq. ID
                  LIB3148-002-P1-K1-A1
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
E value
                   5.0e-11
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   217205
Seq. No.
                  LIB3148-002-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q421843
BLAST score
                   326
E value
                   3.0e-60
Match length
                   140
                   86
% identity
```

30440

NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana



>gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

217206 Seq. No. LIB3148-002-P1-K1-B12 Seq. ID BLASTX Method g3451474 NCBI GI BLAST score 167 1.0e-11 E value 70 Match length 49 % identity (AL031349) conserved hypothetical protein NCBI Description [Schizosaccharomyces pombe] 217207 Seq. No. LIB3148-002-P1-K1-B2 Seq. ID BLASTX Method g3953473 NCBI GI 220 BLAST score 5.0e-18 E value Match length 98 % identity 55 (AC002328) F2202.18 [Arabidopsis thaliana] NCBI Description 217208 Seq. No. LIB3148-002-P1-K1-B6 Seq. ID BLASTX Method g170354 NCBI GI 338 BLAST score 9.0e-32E value Match length 77 % identity 18 (M74156) pentameric polyubiquitin [Nicotiana sylvestris] NCBI Description 217209 Seq. No. Seq. ID LIB3148-002-P1-K1-C12 BLASTX Method q585963 NCBI GI 239 BLAST score 5.0e-20 E value 69 Match length 72 % identity NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT 217210 Seq. No. LIB3148-002-P1-K1-C4 Seq. ID BLASTX Method NCBI GI g170352 BLAST score 139 1.0e-08 E value Match length 45 13 % identity (M74101) hexameric polyubiquitin [Nicotiana sylvestris] NCBI Description

(L81140) ubiquitin [Pisum sativum]

>gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
>qi_4115333 (L81139) ubiquitin [Pisum sativum] >gi_4115335

Seq. No.

Seq. ID

217216

LIB3148-002-P1-K1-E4



```
217211
Seq. No.
                  LIB3148-002-P1-K1-C6
Seq. ID
                  BLASTX
Method
                  g226261
NCBI GI
BLAST score
                  323
                  6.0e-30
E value
Match length
                  64
                  97
% identity
NCBI Description alphal tubulin [Arabidopsis thaliana]
Seq. No.
                  217212
Seq. ID
                  LIB3148-002-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4191789
BLAST score
                  171
E value
                  4.0e-12
Match length
                  64
% identity
                  62
                  (AC005917) putative transmembrane transport protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  217213
                  LIB3148-002-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455258
BLAST score
                  311
                  2.0e-28
E value
Match length
                  113
% identity
                  48
                  (AL035523) acid phosphatase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  217214
Seq. No.
Seq. ID
                  LIB3148-002-P1-K1-D5
                  BLASTN
Method
                  g1418705
NCBI GI
BLAST score
                  72
                  2.0e-32
E value
                  201
Match length
                  89
% identity
NCBI Description G.hirsutum metallothionein-like gene
Seq. No.
                  217215
Seq. ID
                  LIB3148-002-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1345933
                  466
BLAST score
E value
                  1.0e-46
                  106
Match length
                  81
% identity
NCBI Description CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
                  >gi 1084323 pir S53007 citrate synthase - cucurbit
                  >qi 975633 dbj BAA07328 (D38132) glyoxysomal citrate
                   synthase [Cucurbita sp.]
```



```
Method
                  BLASTX
                  g3024431
NCBI GI
BLAST score
                  230
                  2.0e-19
E value
                  46
Match length
                  100
% identity
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 1) (TBP-1) >gi 2342675 (AC000106) Similar
                  to probable Mg-dependent ATPase (pir S56671). ESTs
                  gb T46782, gb AA04798 come from this gene. [Arabidopsis
                  thalianal
                  217217
Seq. No.
Seq. ID
                  LIB3148-002-P1-K1-F11
                  BLASTX
Method
                  g1644427
NCBI GI
BLAST score
                  662
                  1.0e-69
E value
                  150
Match length
                  81
% identity
                 (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217218
                  LIB3148-002-P1-K1-F3-
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832664
BLAST score
                  201
                  1.0e-15
E value
                  82
Match length
                  46
% identity
NCBI Description
                  (AL021710) pollen-specific protein - like [Arabidopsis
                  thaliana]
Seq. No.
                  217219
Seq. ID
                  LIB3148-002-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3023857
BLAST score
                  451
                  6.0e-45
E value
Match length
                  98
                  87
% identity
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN >gi 629591 pir S48839 guanine nucleotide
                  regulatory protein - rape >gi 563335 emb CAA83924 (Z33643)
                  guanine nucleotide regulatory protein [Brassica napus]
Seq. No.
                  217220
Seq. ID
                  LIB3148-002-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2146727
BLAST score
                  501
```

BLAST score 501 E value 8.0e-51 Match length 135 % identity 73

NCBI Description cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 - Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

% identity

46

```
217221
Seq. No.
Seq. ID
                  LIB3148-002-P1-K1-F9
                  BLASTX
Method
                  g629483
NCBI GI
BLAST score
                  279
                  1.0e-24
E value
Match length
                  102
                  54
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
                  217222
Seq. No.
Seq. ID
                  LIB3148-002-P1-K1-G3
                  BLASTX
Method
NCBI GI
                  g284351
BLAST score
                  413
E value
                  2.0e-40
Match length
                  143
% identity
                  55
                  phosphoglucomutase (EC 5.4.2.2) 1 - human >gi 189926
NCBI Description
                  (M83088) PGM1 [Homo sapiens]
                  >gi 4505765 ref NP 002624.1 pPGM1 phosphoglucomutase
                  217223
Seq. No.
                  LIB3148-002-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171978
BLAST score
                  479
E value
                  3.0e-48
                  128
Match length
                  20
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                  (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                  [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                  217224
Seq. No.
                  LIB3148-002-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g2982897
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
Match length
                  131
% identity
NCBI Description (AE000676) hypothetical protein [Aquifex aeolicus]
                  217225
Seq. No.
Seq. ID
                  LIB3148-002-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4204278
BLAST score
                  187
E value
                  4.0e-14
Match length
                  63
```



```
(AC004146) putative Cytochrome P450 protein [Arabidopsis
NCBI Description
                  thaliana]
                  217226
Seq. No.
Seq. ID
                  LIB3148-003-P1-K1-A4
                  BLASTX
Method
                  q3334261
NCBI GI
BLAST score
                  173
                  2.0e-12
E value
                  44
Match length
                  68
% identity
                 METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
NCBI Description
                  metallothionein-like protein [Malus domestica]
                  217227
Seq. No.
Seq. ID
                  LIB3148-003-P1-K1-A5
                  BLASTX
Method
NCBI GI
                  g1364059
BLAST score
                  230
E value
                  4.0e-19
                  108
Match length
                  43
% identity
                  dioscorin class A precursor - Dioscorea cayenensis
NCBI Description
                  >gi 433463 emb CAA53781 (X76187) storage protein
                  [Dioscorea cayenensis]
                  217228
Seq. No.
Seq. ID
                  LIB3148-003-P1-K1-B2
                  BLASTX
Method
NCBI GI
                  g3850571
BLAST score
                  168
                  5.0e-12
E value
                  60
Match length
                  60
% identity
                  (AC005278) Similar to gb U85207 snRNP core Sm protein
NCBI Description
                  homolog Sm-X5 from Mus musculus. EST gb AA612141 comes
                  from this gene. [Arabidopsis thaliana]
                  217229
Seq. No.
Seq. ID
                  LIB3148-003-P1-K1-B6
                  BLASTX
Method
NCBI GI
                  q465702
BLAST score
                  149
                  1.0e-09
E value
                  71
Match length
% identity
                  49
                  PROBABLE RIBOSOMAL PROTEIN B0303.15 IN CHROMOSOME III
NCBI Description
                  >qi 283555 pir S27795 ribosomal protein L11 homolog -
```

Caenorhabditis elegans >gi 156201 (M77697) ribosomal

protein L11 [Caenorhabditis elegans]

Seq. No. 217230

Seq. ID LIB3148-003-P1-K1-C2

Method BLASTX NCBI GI q417148 BLAST score 364 6.0e - 35E value



Match length 111 % identity 63

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)

 $(G2-4) > gi_99912_pir_A33654$ heat shock protein 26A - soybean $> gi_169981$ (M20363) Gmhsp26-A [Glycine max]

Seq. No. 217231

Seq. ID LIB3148-003-P1-K1-C3

Method BLASTX
NCBI GI g3980393
BLAST score 137
E value 1.0e-08
Match length 58
% identity 55

NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis

thaliana]

Seq. No. 217232

Seq. ID LIB3148-003-P1-K1-C4

Method BLASTX
NCBI GI g3063396
BLAST score 526
E value 8.0e-54
Match length 114
% identity 85

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 217233

Seq. ID LIB3148-003-P1-K1-C6

Method BLASTX
NCBI GI g4406807
BLAST score 409
E value 3.0e-40
Match length 107
% identity 75

NCBI Description (AC006201) putative elongation factor beta-1 [Arabidopsis

thaliana]

Seq. No. 217234

Seq. ID LIB3148-003-P1-K1-C7

Method BLASTX
NCBI GI g4249382
BLAST score 586
E value 9.0e-61
Match length 143
% identity 78

NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC

gb AC004481. [Arabidopsis thaliana]

Seq. No. 217235

Seq. ID LIB3148-003-P1-K1-D1

Method BLASTX
NCBI GI g1346172
BLAST score 185
E value 9.0e-14
Match length 37

Match length

% identity

73 90

NCBI Description (AB012110) ARG10 [Vigna radiata]



```
92
% identity
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)
NCBI Description
                  (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)
                  >gi 170384 (L08830) glucose-regulated protein 78
                  [Lycopersicon esculentum]
                  217236
Seq. No.
                  LIB3148-003-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  q3822223
NCBI GI
                  553
BLAST score
                  5.0e-57
E value
                  123
Match length
                  82
% identity
                  (AF077955) branched-chain alpha keto-acid dehydrogenase E1
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
                  217237
Seq. No.
                  LIB3148-003-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  g2435512
NCBI GI
                  397
BLAST score
                  9.0e-39
E value
                  117
Match length
                  70
% identity
NCBI Description (AF024504) No definition line found [Arabidopsis thaliana]
                   217238
Seq. No.
                   LIB3148-003-P1-K1-D5
Seq. ID
                  BLASTX
Method
                   g115525
NCBI GI
BLAST score
                   524
E value
                   2.0e-53
                   103
Match length
                   61
% identity
NCBI Description CALMODULIN >gi_71685_pir_MCSP calmodulin - spinach
                   217239
Seq. No.
Seq. ID
                  LIB3148-003-P1-K1-E12
                  BLASTX
Method
NCBI GI
                   q4406764
BLAST score
                   187
                   3.0e-14
E value
                   103
Match length
% identity
NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis
                   thaliana]
                   217240
Seq. No.
                   LIB3148-003-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2970051
BLAST score
                   359
                   3.0e-34
E value
```



```
217241
Seq. No.
                  LIB3148-003-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539452
                  377
BLAST score
                  2.0e-36
E value
                  130
Match length
                  53
% identity
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  217242
                  LIB3148-003-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4545261
BLAST score
                  108
                  8.0e-54
E value
                  136
Match length
                  95
% identity
                  Gossypium hirsutum metallothionein-like protein mRNA,
NCBI Description
                  complete cds
Seq. No.
                  217243
                  LIB3148-003-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4006895
BLAST score
                  285
                  2.0e-25
E value
Match length
                  91
                  65
% identity
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   217244
                  LIB3148-003-P1-K1-G4
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g1800281
                   696
BLAST score
                  1.0e-73
E value
                  144
Match length
                   21
% identity
NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]
                   217245
Seq. No.
                  LIB3148-003-P1-K1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g586339
BLAST score
                   146
                   3.0e-20
E value
                   94
Match length
                   52
% identity
NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi 626794 ir S46098
                   probable AMP-binding protein - yeast (Saccharomyces
```

Seq. No. 217246

[Saccharomyces cerevisiae]

cerevisiae) >gi 536615 emb CAA85185 (Z36091) ORF YBR222c



LIB3148-003-P1-K1-H9 Seq. ID Method BLASTN q1217627 NCBI GI BLAST score 100 5.0e-49 E value Match length 250 90 % identity G.hinsutum mRNA for stearoyl-acyl-carrier protein NCBI Description desaturase 217247 Seq. No. Seq. ID LIB3148-004-Q1-K1-A12 BLASTX Method NCBI GI q82035 357 BLAST score 6.0e-34 E value 136 Match length 35 % identity ricin E - castor bean (fragment) >gi 169715 (M17631) ricin NCBI Description E beta chain [Ricinus communis] >gi 225896 prf 1402359A ricin E [Ricinus communis] Seq. No. 217248 Seq. ID LIB3148-004-Q1-K1-A2 Method BLASTX NCBI GI g285286 236 BLAST score 9.0e-20 E value 76 Match length 55 % identity NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia 217249 Seq. No. LIB3148-004-Q1-K1-A5 Seq. ID Method BLASTX NCBI GI g4105097 BLAST score 157 2.0e-10 E value Match length 61 % identity 61 NCBI Description (AF043255) MADS box protein 26 [Cucumis sativus] 217250 Seq. No. LIB3148-004-Q1-K1-A9 Seq. ID Method BLASTX g2935294 NCBI GI 597 BLAST score 4.0e-62 E value 134 Match length % identity 87 NCBI Description (AF036948) phenylalanine ammonia-lyase; PAL1 [Prunus avium]

Seq. No. 217251

Seq. ID LIB3148-004-Q1-K1-B10

Method BLASTX NCBI GI g3986770 BLAST score 192



```
1.0e-14
E value
                   114
Match length
                   42
% identity
                  (AF109906) NG22 [Mus musculus]
NCBI Description
                   217252
Seq. No.
Seq. ID
                   LIB3148-004-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   q1173256
                   536
BLAST score
E value
                   6.0e-55
Match length
                   126
% identity
                   84
                   40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   217253
Seq. No.
                   LIB3148-004-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q549063
                   447
BLAST score
                   2.0e-44
E value
                   103
Match length
% identity
                   82
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   217254
                   LIB3148-004-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   q4321096
NCBI GI
BLAST score
                   334
E value
                   3.0e-31
                   136
Match length
                   47
% identity
NCBI Description (M84135) flavonol 3-sulfotransferase [Flaveria
                   chloraefolia]
                   217255
Seq. No.
Seq. ID
                   LIB3148-004-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   a1220453
BLAST score
                   379
                   2.0e-36
E value
                   124
Match length
% identity
                   56
```

NCBI Description (M79328) alpha-amylase [Solanum tuberosum]

Seq. ID LIB3148-004-Q1-K1-D1

217256

Method BLASTX NCBI GI g3850821 BLAST score 183

Seq. No.



```
9.0e-14
E value
                  44
Match length
                  70
% identity
                  (Y18350) U2 snRNP auxiliary factor, large subunit
NCBI Description
                  [Nicotiana plumbaginifolia]
                  217257
Seq. No.
                  LIB3148-004-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  q2829204
NCBI GI
BLAST score
                  308
                  3.0e-28
E value
Match length
                  85
% identity
                  65
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                  217258
Seq. No.
                  LIB3148-004-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220481
BLAST score
                  403
                  2.0e-39
E value
                  126
Match length
                  59
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  217259
Seq. No.
                  LIB3148-004-Q1-K1-D2
Seq. ID
                  BLASTN
Method
                  g1000085
NCBI GI
                  169
BLAST score
                   3.0e-90
E value
                  181
Match length
                   98
% identity
NCBI Description Gossypium hirsutum clone CKE6-4A E6 gene, complete cds
                   217260
Seq. No.
Seq. ID
                  LIB3148-004-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                   g4567225
BLAST score
                   296
E value
                   8.0e-27
                   98
Match length
                   60
% identity
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
                   217261
Seq. No.
Seq. ID
                   LIB3148-004-Q1-K1-E4
                   BLASTX
Method
NCBI GI
                   g1237250
BLAST score
                   152
                   6.0e-10
E value
Match length
                   111
% identity
```

NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]



```
217262
Seq. No.
                   LIB3148-004-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g4100433
NCBI GI
                   318
BLAST score
                   2.0e-29
E value
                   84
Match length
% identity
                   (AF000378) beta-glucosidase [Glycine max]
NCBI Description
                   217263
Seq. No.
                   LIB3148-004-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   q1705463
NCBI GI
                   143
BLAST score
                   5.0e-09
E value
Match length
                   39
                   69
% identity
                   BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi 2129547 pir S71201
NCBI Description
                   biotin sythase - Arabidopsis thaliana >\overline{gi}_10453\overline{1}6 (\overline{U2}4147)
                   biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806)
                   BIO2 protein [Arabidopsis thaliana] >gi_1\overline{7}69457 (L34413)
                   biotin synthase [Arabidopsis thaliana] >gi_2288983
                   (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                   >qi 1589016 prf 2209438A biotin synthase [Arabidopsis
                   thaliana]
                   217264
Seq. No.
                   LIB3148-004-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   33
                   5.0e-09
E value
Match length
                   33
                   58
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   217265
Seq. No.
                   LIB3148-004-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g585876
NCBI GI
                    339
BLAST score
                    8.0e-32
E value
                   125
Match length
                    58
 % identity
                   60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__$48026
NCBI Description
                    ribosomal protein L25 - common tobacco >gi 310935 (L18908)
                    60S ribosomal protein L25 [Nicotiana tabacum]
                    217266
 Seq. No.
                    LIB3148-004-Q1-K1-F4
 Seq. ID
                    BLASTX
Method
                    g1707955
NCBI GI
 BLAST score
                    537
                    5.0e-55
 E value
                    129
 Match length
```

77

% identity

NCBI Description



```
NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
                   (GLUTAMATE--AMMONIA LIGASE) >gi 1134896_emb CAA63981
                   (X94320) glutamine synthetase [Vitis vinifera]
                   217267
Seq. No.
                   LIB3148-004-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4512676
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
Match length
                   42
                   67
 % identity
                   (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                   217268
 Seq. No.
                   LIB3148-004-Q1-K1-F9
 Seq. ID
                   BLASTX
Method
                   q3955021
 NCBI GI
                   300
 BLAST score
                   3.0e-27
 E value
 Match length
                   117
 % identity
                   58
                   (AJ010811) HB2 homeodomain protein [Populus tremula x
 NCBI Description
                   Populus tremuloides]
                   217269
 Seq. No.
                   LIB3148-004-Q1-K1-G11
 Seq. ID
                   BLASTX
 Method
                    g2244898
 NCBI GI
                    312
 BLAST score
                    1.0e-28
 E value
                    103
 Match length
                    60
 % identity.
NCBI Description (Z97338) strong similarity to protein phosphatase 2A
                    regulatory chain, 74K [Arabidopsis thaliana]
                    217270
 Seq. No.
                    LIB3148-004-Q1-K1-G4
 Seq. ID
                    BLASTX
 Method
                    g560504
 NCBI GI
 BLAST score
                    162
                    4.0e-11
 E value
                    37
 Match length
                    84
 % identity
                    (Z29593) guanine nucleotide regulatory protein [Vicia faba]
 NCBI Description
                    >gi 1098296 prf 2115367D small GTP-binding protein [Vicia
                    faba]
                    217271
 Seq. No.
 Seq. ID
                    LIB3148-004-Q1-K1-G5
                    BLASTX
 Method
                    q4455365
 NCBI GI
                    374
 BLAST score
                    6.0e - 36
 E value
 Match length
                    74
 % identity
```

30453

(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

```
217272
Seq. No.
Seq. ID
                  LIB3148-004-Q1-K1-G6
Method
                  BLASTN
                  g3150006
NCBI GI
BLAST score
                  55
                  2.0e-22
E value
                  59
Match length
                  49
% identity
                  CIC5B11.1 check: 4870 from: 1 to: 167234, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
                  217273
Seq. No.
Seq. ID
                  LIB3148-004-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1206003
                  144
BLAST score
                  3.0e-09
E value
                  34
Match length
                  85
% identity
                  (U42399) putative MADS-box family transcription factor
NCBI Description
                  [Pinus radiata]
                  217274
Seq. No.
Seq. ID
                  LIB3148-004-Q1-K1-G8
                  BLASTX
Method
NCBI GI
                  g2894598
BLAST score
                  240
                  3.0e-20
E value
                  94
Match length
                  45
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                  217275
Seq. No.
Seq. ID
                  LIB3148-004-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2245125
BLAST score
                  172
                  3.0e-12
E value
Match length
                  45
% identity
                  64
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  217276
Seq. ID
                  LIB3148-004-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q3881234
BLAST score
                  182
                  2.0e-13
E value
Match length
                  60
% identity
                  55
NCBI Description
                  (AL032652) predicted using Genefinder; cDNA EST yk484f6.5
                  comes from this gene; cDNA EST yk484f6.3 comes from this
```

30454

gene [Caenorhabditis elegans]

LIB3148-004-Q1-K1-H11

217277



```
BLASTX
Method
                  g3242715
NCBI GI
                  188
BLAST score
                  4.0e-14
E value
                  42
Match length
                  86
% identity
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217278
                  LIB3148-004-Q1-K1-H2
Seq. ID
Method
                  BLASTN
                  g1922250
NCBI GI
                  166
BLAST score
                  1.0e-88
E value
                  173
Match length
                  99
% identity
NCBI Description G.arboreum mRNA for farnesyl pyrophosphate synthase
                  217279
Seq. No.
                  LIB3148-004-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827559
                  279
BLAST score
                  8.0e-25
E value
                  88
Match length
% identity
                  58
```

(AL021635) predicted protein [Arabidopsis thaliana] NCBI Description >gi_3292808_emb_CAA19798_ (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 217280

LIB3148-004-Q1-K1-H8 Seq. ID

Method BLASTX g3831441 NCBI GI BLAST score 169 7.0e-12 E value 58 Match length 74 % identity

NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No. 217281

Seq. ID LIB3148-005-Q1-K1-A10

Method BLASTX NCBI GI a2493694 292 BLAST score 2.0e-26 E value 106 Match length 54 % identity

NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII

6.1 KD PROTEIN) >gi 1076268 pir S53025 photosystem II protein - spinach >gi 728716 emb CAA59409 (X85038) protein

of photosystem II [Spinacia oleracea]

Seq. No. 217282

Seq. ID LIB3148-005-Q1-K1-A3

BLASTX Method NCBI GI g2506139



```
417
BLAST score
                  4.0e-41
E value
                  110
Match length
                  75
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
                  217283
Seq. No.
Seq. ID
                  LIB3148-005-Q1-K1-A4
Method
                  BLASTX
                  q3386565
NCBI GI
                  211
BLAST score
                  4.0e-17
E value
                  87
Match length
% identity
                  51
                  (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                   [Sorghum bicolor]
                  217284
Seq. No.
                  LIB3148-005-Q1-K1-A5
```

Seq. ID Method BLASTX q322525 NCBI GI BLAST score 573 2.0e-59 E value 122 Match length % identity 91

NCBI Description omnipotent suppressor protein SUP1 homolog (clone A18) -Arabidopsis thaliana (fragment) > gi 16512_emb_CAA49171_

(X69374) similar to yeast omnipotent suppressor protein

SUP1 (SUP45); ORF [Arabidopsis thaliana]

Seq. No. 217285

Seq. ID LIB3148-005-Q1-K1-A6

BLASTX Method g3377794 NCBI GI BLAST score 285 1.0e-25 E value 65 Match length 85 % identity

NCBI Description (AF034572) proteasome IOTA subunit [Glycine max]

217286 Seq. No.

LIB3148-005-Q1-K1-B12 Seq. ID

Method BLASTX NCBI GI q114682 BLAST score 303 1.0e-27 E value 104 Match length % identity 62

ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi 100471 pir A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi 168270 (J05397) F-1-ATPase delta subunit

precursor (EC 3.6.1.3) [Ipomoea batatas]

Method

NCBI GI BLAST score BLASTX q2275213

180



```
217287
Seq. No.
                  LIB3148-005-Q1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3819164
                  513
BLAST score
                  2.0e-52
E value
                  110
Match length
                  94
% identity
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  max]
                  217288
Seq. No.
Seq. ID
                   LIB3148-005-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                   g3107931
BLAST score
                   547
                   3.0e-56
E value
                   123
Match length
                   86
% identity
                  (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
Seq. No.
                   217289
                   LIB3148-005-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2935294
BLAST score
                   551
                   8.0e-57
E value
Match length
                   117
                   92
% identity
NCBI Description (AF036948) phenylalanine ammonia-lyase; PAL1 [Prunus avium]
Seq. No.
                   217290
                   LIB3148-005-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g2398829
NCBI GI
BLAST score
                   541
                   2.0e-55
E value
                   112
Match length
                   89
% identity
NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum
                   tuberosum]
                   217291
Seq. No.
                   LIB3148-005-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2204077
                   194
BLAST score
                   6.0e-15
E value
Match length
                   84
% identity
NCBI Description (D85623) extracellular insoluble cystatin [Daucus carota]
                   217292
Seq. No.
Seq. ID
                   LIB3148-005-Q1-K1-C3
```



3.0e-13E value 42 Match length 74 % identity (AC002337) hypothetical protein [Arabidopsis thaliana] NCBI Description 217293 Seq. No. LIB3148-005-Q1-K1-C7 Seq. ID BLASTX Method q584711 NCBI GI BLAST score 548 2.0e-56 E value 115 Match length 92 % identity 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) NCBI Description (ETHYLENE-FORMING ENZYME) (EFE) >gi_629707_pir__S42561 1-aminocyclopropane-1-carboxylate oxidase - garden petunia >qi 347417 (L21978) 1-aminocyclopropane-1-carboxylate oxidase [Petunia hybrida] 217294 Seq. No. Seq. ID LIB3148-005-Q1-K1-C8 Method BLASTX q3928090 NCBI GI 318 BLAST score 2.0e-29 E value 140 Match length % identity 41 NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana] 217295 Seq. No. Seq. ID LIB3148-005-Q1-K1-D11 Method BLASTX q4558665 NCBI GI 180 BLAST score 2.0e-13 E value 38 Match length 79 % identity NCBI Description (AC007063) putative white protein [Arabidopsis thaliana] 217296 ' Seq. No. Seq. ID LIB3148-005-Q1-K1-D3 BLASTN Method NCBI GI q2921331 BLAST score 112 E value 2.0e-56 143 Match length 93 % identity NCBI Description Gossypium hirsutum MYB-like DNA-binding domain protein (Cmy-D) mRNA, complete cds

Seq. No. 217297

LIB3148-005-Q1-K1-D4 Seq. ID BLASTX Method

NCBI GI q541978 BLAST score 141 3.0e-09 E value .Match length 67



```
% identity
                  guanine nucleotide regulatory protein - fava bean
NCBI Description
                  >gi_303734_dbj_BAA02118_ (D12550) GTP-binding protein
                  [Pisum sativum] >gi_452359_emb_CAA82707_ (Z29590) guanine
                  nucleotide regulatory protein [Vicia faba]
                  >gi_738942_prf__2001457K GTP-binding protein [Pisum _
                  sativum] >gi 1098293 prf 2115367A small GTP-binding
                  protein [Vicia faba]
                  217298
Seq. No.
                  LIB3148-005-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  q3024386
NCBI GI
                  520
BLAST score
                  4.0e-53
E value
Match length
                  135
                  72
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                  >qi 2129500 pir S52006 polygalacturonase - upland cotton
                  >qi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  217299
                  LIB3148-005-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g548852
NCBI GI
                  232
BLAST score
                  2.0e-19
E value
                  54
Match length
                  80
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi 303839_dbj_BAA02158_ (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
                  217300
Seq. No.
                  LIB3148-005-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                  g1172635
NCBI GI
BLAST score
                  539
                  3.0e-55
E value
                  122
Match length
                  89
% identity
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615 (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
                  217301
Seq. No.
                  LIB3148-005-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  q4126473
NCBI GI
BLAST score
                  261
E value
                  1.0e-22
```

49 Match length 98 % identity

(AB014884) adenylyl cyclase associated protein [Gossypium NCBI Description

hirsutum]

Seq. No. 217302



LIB3148-005-Q1-K1-F4 Seq. ID BLASTX Method NCBI GI g548852 BLAST score 361 2.0e-34 E value 82 Match length 80 % identity 40S RIBOSOMAL PROTEIN S21 >qi 481227 pir S38357 ribosomal NCBI Description protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S subunit ribosomal protein [Oryza sativa] 217303 Seq. No. Seq. ID LIB3148-005-Q1-K1-F5 BLASTX Method NCBI GI g3821793 BLAST score 692 3.0e-73 E value 132 Match length 95 % identity NCBI Description (Y11526) casein kinase II alpha subunit [Zea mays] 217304 Seq. No. LIB3148-005-Q1-K1-G12 Seq. ID Method BLASTX NCBI GI q4263712 BLAST score 251 E value 1.0e-21 63 Match length 68 % identity (AC006223) putative ribosomal protein S12 [Arabidopsis NCBI Description thaliana] Seq. No. 217305 LIB3148-005-Q1-K1-G7 Seq. ID Method BLASTX NCBI GI q3341687 BLAST score 154 4.0e-10 E value 58 Match length % identity (AC003672) putative ras protein [Arabidopsis thaliana] NCBI Description 217306 Seq. No. LIB3148-005-Q1-K1-G8 Seq. ID Method BLASTX NCBI GI g1079720 BLAST score 479 3.0e-48E value Match length 122 78 % identity

NCBI Description (U39764) eukaryotic release factor 3 [Ricinus communis]

Seq. No. 217307

Seq. ID LIB3148-005-Q1-K1-G9

Method BLASTX NCBI GI g267070 BLAST score 388



7.0e-38 E value 76 Match length 97 % identity TUBULIN ALPHA-6 CHAIN >gi_282852 pir JQ1597 tubulin NCBI Description alpha-6 chain - Arabidopsīs thalīana >gi 166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana] 217308 Seq. No. LIB3148-005-Q1-K1-H12 Seq. ID BLASTX Method q3126969 NCBI GI BLAST score 180 3.0e-13 E value 90 Match length 48 % identity (AF061808) chalcone isomerase [Elaeagnus umbellata] NCBI Description 217309 Seq. No. LIB3148-005-Q1-K1-H3 Seq. ID Method BLASTX q3821793 NCBI GI 612 BLAST score 4.0e-66 E value 127 Match length 87 % identity (Y11526) casein kinase II alpha subunit [Zea mays] NCBI Description 217310 Seq. No. LIB3148-005-Q1-K1-H4 Seq. ID BLASTX Method g3098571 NCBI GI BLAST score 188 3.0e-14E value Match length 64 55 % identity NCBI Description (AF049028) BURP domain containing protein [Brassica napus] 217311 Seq. No. Seq. ID LIB3148-005-Q1-K1-H8 BLASTX Method q2642158 NCBI GI 565 BLAST score 2.0e-58 E value 127 Match length 79 % identity NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana] 217312 Seq. No. Seq. ID LIB3148-006-Q1-K1-A11 BLASTX Method

Method BLASTX
NCBI GI g401322
BLAST score 575
E value 1.0e-59
Match length 111
% identity 100

Match length

% identity

48

94



```
VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                  subunit [Gossypium hirsutum]
Seq. No.
                  217313
                  LIB3148-006-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                  q2765366
NCBI GI
BLAST score
                  247
                  5.0e-21
E value
Match length
                  118
% identity
                  45
NCBI Description (Y14038) putative Ole e 1 protein [Betula pendula]
                  217314
Seq. No.
                  LIB3148-006-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351271
BLAST score
                  624
                  3.0e-65
E value
Match length
                  130
% identity
                  91
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >qi 1084309 pir S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi_806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
                  217315
Seq. No.
                  LIB3148-006-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2911052
BLAST score
                  269
                  3.0e-24
E value
                  57
Match length
                  81
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  217316
Seq. No.
                  LIB3148-006-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  q790687
NCBI GI
BLAST score
                  222
E value
                   4.0e-18
                  86
Match length
                   56
% identity
NCBI Description (L39651) zinc finger protein [Arabidopsis thaliana]
                  217317
Seq. No.
Seq. ID
                  LIB3148-006-Q1-K1-C5
                  BLASTN
Method
                  q2760165
NCBI GI
BLAST score
                  36
E value
                  8.0e-11
```

30462

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Seq. No.

217323



MAC9, complete sequence [Arabidopsis thaliana]

```
217318
Seq. No.
                  LIB3148-006-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080439
                  197
BLAST score
                  5.0e-31
E value
                  105
Match length
% identity
                  69
                 (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                  217319
Seq. No.
Seq. ID
                  LIB3148-006-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g100196
BLAST score
                  627
                  1.0e-65
E value
Match length
                  126
% identity
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.
                  217320
                  LIB3148-006-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3142294
BLAST score
                  192
E value
                  8.0e-15
Match length
                  46
                  78
% identity
                  (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                  gb_N37529 come from this gene. [Arabidopsis thaliana]
                  217321
Seq. No.
                  LIB3148-006-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g3901014
NCBI GI
                  234
BLAST score
                  2.0e-19
E value
Match length
                  55
                  76
% identity
                 (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
                  217322
Seq. No.
                  LIB3148-006-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g2961349
NCBI GI
                  172
BLAST score
                  1.0e-12
E value
Match length
                  71
% identity
NCBI Description (AL022140) LTR retrotransposon like protein [Arabidopsis
                  thaliana]
```

30463



LIB3148-006-Q1-K1-F5 Seq. ID BLASTX Method g3821280 NCBI GI 562 BLAST score 6.0e-58 E value 136 Match length 79 % identity (AJ009952) asparagine synthetase type II [Phaseolus NCBI Description vulgaris] 217324 Seq. No. LIB3148-006-Q1-K1-F7 Seq. ID BLASTX Method g296502 NCBI GI 371 BLAST score 4.0e-36 E value 74 Match length 95 % identity NCBI Description (X69187) beta tubulin 3 [Anemia phyllitidis] 217325 Seq. No. LIB3148-006-Q1-K1-G1 Seq. ID Method BLASTX q4417291 NCBI GI 140 BLAST score 1.0e-08 E value 39 Match length % identity 69 NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana] 217326 Seq. No. LIB3148-006-Q1-K1-G5 Seq. ID BLASTX Method g1750404 NCBI GI 177 BLAST score 6.0e-13 E value 52 Match length 54 % identity (U80953) Similar to 40S ribosomal protein S29; coded for by NCBI Description C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk107e8.5; coded for by C. elegans cDNA CEESF55F; coded for by C. elegans cDNA yk107e8.3; 217327 Seq. No. Seq. ID LIB3148-006-01-K1-G6 Method BLASTN g3687405 NCBI GI

Method BLASTN
NCBI GI g3687405
BLAST score 40
E value 3.0e-13
Match length 63
% identity 92

NCBI Description Lycopersicon esculentum mRNA for hypothetical protein

Seq. No. 217328

Seq. ID LIB3148-006-Q1-K1-H2

Method BLASTN

```
g969118
NCBI GI
                  94
BLAST score
                  7.0e-46
E value
Match length
                  102
                  98
% identity
                  Gossypium herbaceum 5S ribosomal RNA gene and
NCBI Description
                  non-transcribed spacer, clone
                  217329
Seq. No.
                  LIB3148-006-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q4104931
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
Match length
                  103
                  62
% identity
                  (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
                  217330
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-B8
Method
                  BLASTN
                  g3821780
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  217331
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-C11
Method
                  BLASTX
                  g3913067
NCBI GI
                  445
BLAST score
                  2.0e-44
E value
Match length
                  96
% identity
                  86
NCBI Description ALTERNATIVE OXIDASE 2 PRECURSOR >gi 1946336 (U87906)
                  alternative oxidase [Glycine max]
Seq. No.
                  217332
                  LIB3148-007-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244898
BLAST score
                  128
E value
                  5.0e-09
Match length
                  64
% identity
                   59
                  (Z97338) strong similarity to protein phosphatase 2A
NCBI Description
                   regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.
                   217333
                  LIB3148-007-Q1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3821780
BLAST score
                   33
```

30465

6.0e-09

65

E value

Match length

Match length

NCBI Description

% identity

86

91



```
72
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  217334
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-C6
                  BLASTN
Method
                  g296442
NCBI GI
BLAST score
                  33
                  5.0e-09
E value
                  65
Match length
                  88
% identity
NCBI Description G.max ADR11 mRNA
                  217335
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-C8
                  BLASTX
Method
                  g1220196
NCBI GI
BLAST score
                  223
                  1.0e-18
E value
Match length
                  45
% identity
                  98
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  217336
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-D10
                  BLASTX
Method
                  g1173234
NCBI GI
                  324
BLAST score
                  3.0e-30
E value
Match length
                  72
% identity
                  88
NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi 481909 pir S40089 ribosomal
                  protein S25 - tomato >gi 435679 emb CAA54132 (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                  >gi 1584836 prf 2123431A ribosomal protein S25
                  [Lycopersicon esculentum]
                  217337
Seq. No.
                  LIB3148-007-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  q4567232
NCBI GI
BLAST score
                  287
                  2.0e-26
E value
                  99
Match length
                  67
% identity
NCBI Description
                  (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
                  thaliana]
Seq. No.
                  217338
Seq. ID
                  LIB3148-007-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4455293
BLAST score
                  370
                  2.0e-35
E value
```

30466

(AL035528) putative protein [Arabidopsis thaliana]

Seq. ID

```
217339
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-E10
                  BLASTX
Method
                  g2346972
NCBI GI
                  186
BLAST score
                  5.0e-14
E value
                  82
Match length
                  49
% identity
                  (AB006598) ZPT2-11 [Petunia x hybrida]
NCBI Description
                  217340
Seq. No.
                  LIB3148-007-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  g2804280
NCBI GI
                  595
BLAST score
                   6.0e-62
E value
                  127
Match length
                  79
% identity
                   (AB003687) 6-4 photolyase [Arabidopsis thaliana]
NCBI Description
                  >gi 3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase
                   [Arabidopsis thaliana]
                   217341
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-F5
                  BLASTX
Method
                   g169211
NCBI GI
BLAST score
                   145
                   1.0e-09
E value
                   36
Match length
                   81
% identity
                  (M90294) ethylene-forming enzyme [Petunia hybrida]
NCBI Description
                   >qi 445591 prf 1909343A ethylene-forming enzyme [Petunia x
                   hybrida]
                   217342
Seq. No.
                   LIB3148-007-Q1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4139266
BLAST score
                   211
E value
                   4.0e-27
                   103
Match length
                   63
% identity
NCBI Description (AF112444) L-asparaginase [Lupinus luteus]
                   217343
Seq. No.
Seq. ID
                   LIB3148-007-Q1-K1-H12
Method
                   BLASTX
                   q4508073
NCBI GI
BLAST score
                   422
E value
                   1.0e-41
                   144
Match length
% identity
                   58
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
                   217344
Seq. No.
```

30467

LIB3148-007-Q1-K1-H5



```
BLASTX
Method
NCBI GI
                  g3025188
BLAST score
                  293
                  1.0e-26
E value
                  85
Match length
                  61
% identity
                  HYPOTHETICAL 11.9 KD PROTEIN SLR1846
NCBI Description
                  >gi_1652154_dbj_BAA17078_ (D90903) hypothetical protein
                  [Synechocystis sp.]
                  217345
Seq. No.
                  LIB3148-007-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g3914359
NCBI GI
                  396
BLAST score
                  8.0e-39
E value
                  84
Match length
% identity
                  86
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1928979 (U92656) phospholipase D [Vigna unguiculata]
                  217346
Seq. No.
Seq. ID
                  LIB3148-007-Q1-K1-H9
                  BLASTN
Method
                  q3299824
NCBI GI
BLAST score
                  36
                  6.0e-11
E value
                  48
Match length
                  94
% identity
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                  near 17 cM, complete sequence [Arabidopsis thaliana]
                  217347
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-A1
Method
                  BLASTX
                  g1705840
NCBI GI
                  194
BLAST score
                   4.0e-15
É value
Match length
                   42
% identity
                   90
NCBI Description
                  CHALCONE SYNTHASE 1A (NARINGENIN-CHALCONE SYNTHASE 1A)
                  >gi 1076535 pir S49202 naringenin-chalcone synthase (EC
                   2.3.1.74) - garden pea >gi 510543 emb CAA56316 (X80007)
                   naringenin-chalcone synthase [Pisum sativum]
                   217348
Seq. No.
                  LIB3148-008-Q1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2746826
BLAST score
                   144
```

(AF040646) No definition line found [Caenorhabditis

5.0e-09

elegans]

89

E value Match length

% identity

NCBI Description



```
217349
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-A5
                  BLASTX
Method
NCBI GI
                  g4102727
BLAST score
                  159
                  1.0e-10
E value
Match length
                  100
                  40
% identity
                  (AF015782) blight-associated protein p12 precursor [Citrus
NCBI Description
                  jambhiri]
                  217350
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1945611
BLAST score
                  309
                  2.0e-28
E value
                  136
Match length
                  46
% identity
                  (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                  >gi 4506221 ref NP 002807.1 pPSMD12 proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
                  217351
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-B1
                  BLASTX
Method
NCBI GI
                  g1864017
BLAST score
                  647
                  5.0e-68
E value
                  124
Match length
                  99
% identity
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
                  217352
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4056469
BLAST score
                  335
                  1.0e-31
E value
Match length
                  67
                  100
% identity
                 (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                  factor from Arabidopsis thaliana. ESTs gb Z25826,
                  gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                  gb_AA712956, gb T46403, gb T46050, gb AI100391 and
                  gb Z25043 come from t
Seq. No.
                  217353
```

Seq. ID LIB3148-008-Q1-K1-B8

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. ID

Method



```
217354
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-B9
Method
                  BLASTX
                  g531829
NCBI GI
BLAST score
                  152
                  6.0e-10
E value
Match length
                   69
                   46
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  217355
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  g1743354
                   333
BLAST score
                   3.0e-31
E value
                  73
Match length
                  82
% identity
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
NCBI Description
Seq. No.
                   217356
Seq. ID
                  LIB3148-008-Q1-K1-C12
Method
                  BLASTX
                   g3114901
NCBI GI
BLAST score
                   446
                   2.0e-44
E value
                   112
Match length
                   78
% identity
                  (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   >gi 3114905 emb CAA06709 (AJ005806) pceberh [Populus
                   balsamifera subsp. trichocarpa]
                   217357
Seq. No.
                   LIB3148-008-Q1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3184282
BLAST score
                   238
                   5.0e-20
E value
Match length
                   74
% identity
                   62
NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]
                   217358
Seq. No.
                   LIB3148-008-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829204
BLAST score
                   450
                   7.0e-45
E value
Match length
                   120
% identity
                   68
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   217359
```

30470

LIB3148-008-Q1-K1-C6

BLASTX



```
NCBI GI
                    g3643608
 BLAST score
                    203
 E value
                    2.0e-16
                    51
 Match length
                    75
 % identity
 NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   217360
 Seq. ID
                   LIB3148-008-Q1-K1-D10
 Method
                   BLASTX
 NCBI GI
                   g2495365
 BLAST score
                    296
                   8.0e-27
 E value
                   92
 Match length
                    71
 % identity
 NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B
                   heat shock protein HSP81-2 [Arabidopsis thaliana]
                    217361
 Seq. No.
 Seq. ID
                    LIB3148-008-Q1-K1-D2
 Method
                    BLASTX
 NCBI GI
                   g2911053
 BLAST score
                    400
                    4.0e-39
 E value
                   89
 Match length
 % identity
                   82
 NCBI Description (AL021961) hypothetical protein [Arabidopsis thaliana]
                    217362
 Seq. No.
 Seq. ID
                    LIB3148-008-Q1-K1-D4
                   BLASTX
 Method
 NCBI GI
                    q730583
 BLAST score
                    245
 E value
                    8.0e-21
                    114
 Match length
                    47
 % identity
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
                    (X78213) 60s acidic ribosomal protein P2 [Parthenium
                    argentatum]
                    217363
 Seq. No.
 Seq. ID
                    LIB3148-008-Q1-K1-D6
 Method
                    BLASTX
 NCBI GI
                    a2501578
 BLAST score
                    543
 E value
                    9.0e-56
                    141
 Match length
 % identity
                    77
 NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047
                    ethylene-responsive protein 1 - Para rubber tree
                    >gi_1209317 (M88254) ethylene-inducible protein [Hevea
```

brasiliensis]

Seq. No. 217364

Seq. ID LIB3148-008-Q1-K1-D7

Method BLASTX NCBI GI g3913919

BLAST score

E value Match length 295 1.0e-26

116



```
331
BLAST score
                  6.0e-31
E value
                  87
Match length
                  69
% identity
                  ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
NCBI Description
                  SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                  (VACUOLAR INVERTASE) >gi_2351827 (U92438) soluble acid
                  invertase [Phaseolus vulgaris]
                  217365
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-D9
Method
                  BLASTN
                  q2275090
NCBI GI
BLAST score
                  64
                  7.0e-28
E value
Match length
                  72
                  97
% identity
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
                  217366
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g4572668
BLAST score
                  243
                  1.0e-20
E value
Match length
                  100
                  47
% identity
                  (AC006954) putative retrotransposon polyprotein
NCBI Description
                   [Arabidopsis thaliana]
                   217367
Seq. No.
                  LIB3148-008-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2980770
NCBI GI
                  243
BLAST score
                  7.0e-21
E value
                  59
Match length
                  76
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                   217368
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-E5
                  BLASTX
Method
                   g533692
NCBI GI
                   210
BLAST score
                   1.0e-16
E value
                   72
Match length
                   62
% identity
NCBI Description (U12150) protease inhibitor [Glycine max]
                   217369
Seq. No.
                  LIB3148-008-Q1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3395424
```

30472



```
% identity
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3786024 (AC005499) hypothetical protein [Arabidopsis
                  thaliana]
                  217370
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q3687251
BLAST score
                  447
E value
                  1.0e-44
Match length
                  128
% identity
                  68
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217371
                  LIB3148-008-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g2253442
NCBI GI
BLAST score
                  206
E value
                  3.0e-16
Match length
                  56
% identity
                  62
                  (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
                  217372
Seq. No.
                  LIB3148-008-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  g1843527
NCBI GI
BLAST score
                  407
                  8.0e-40
E value
Match length
                  81
                  53
% identity
                 (U73747) annexin [Gossypium hirsutum]
NCBI Description
                   217373
Seq. No.
Seq. ID
                  LIB3148-008-Q1-K1-F4
                  BLASTN
Method
NCBI GI
                   g1843526
BLAST score
                   37
E value
                   2.0e-11
                   81
Match length
                   86
% identity
NCBI Description Gossypium hirsutum annexin (AnnGh2) mRNA, partial cds
                   217374
Seq. No.
                   LIB3148-008-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g2435519
NCBI GI
BLAST score
                   330
E value
                   6.0e-31
```

Match length 66 % identity 92

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110)

[Arabidopsis thaliana]



```
217375
Seq. No.
                    LIB3148-008-Q1-K1-G1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g122106
BLAST score
                    406
                    1.0e-39
E value
Match length
                    81
                    100
% identity
                    HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
NCBI Description
                    >qi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                    >gi_2119028_pir__S60475 histone H4 - garden pea
                    >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                    aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_168742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
                    >gi 168501 (M\overline{1}3370) histone H4 [Zea mays] >gi_168503
                    (M1\overline{3}377) histone H4 [Zea mays] >gi_498898 (U1\overline{0}042) histone
                    H4 homolog [Pisum sativum] >gi 1806285 emb_CAB01914_
                    (Z79638) histone H4 homologue [Sesbania rostrata]
                    >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                    >gi 4580385_gb AAD24364.1 AC007184_4 (AC007184) histone H4
                    [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4
                    [Arabidopsis thaliana]
                    217376
Seq. No.
Seq. ID
                    LIB3148-008-Q1-K1-G11
Method
                    BLASTN
                    g2687434
NCBI GI
                    292
BLAST score
                    1.0e-163
E value
                    340
Match length
% identity
                    96
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                    partial sequence
                    217377
Seq. No.
Seq. ID
                    LIB3148-008-Q1-K1-G3
                    BLASTX
Method
                    q2982303
NCBI GI
BLAST score
                    578
                    6.0e-60
E value
                    124
Match length
                    87
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
                    217378
Seq. No.
Seq. ID
                    LIB3148-008-Q1-K1-G6
Method
                    BLASTX
                    g4102703
NCBI GI
BLAST score
                    496
E value
                    3.0e-50
Match length
                    133
% identity
                    79
NCBI Description (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
```

30474

thaliana]

217379

Seq. No.

Method

NCBI GI

BLAST score

BLASTX

329

q4204315



```
LIB3148-008-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g4204315
NCBI GI
                  499
BLAST score
                  1.0e-50
E value
                  135
Match length
                  67
% identity
                 (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  217380
Seq. No.
                  LIB3148-008-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  q2811025
NCBI GI
                  539
BLAST score
                  3.0e-55
E value
Match length
                  135
                  70
% identity
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
                  (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  217381
                  LIB3148-008-Q1-K1-H6
Seq. ID
Method
                  BLASTX
                  q2811025
NCBI GI
                  473
BLAST score
                  1.0e-47
E value
Match length
                  120
                  70
% identity
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
                  (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  217382
                  LIB3148-009-Q1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3242753
BLAST score
                  165
E value
                  1.0e-11
                  120
Match length
                  31
% identity
NCBI Description (AC005162) probable carboxypeptidase precursor; 64% similar
                  to P42660 (PID:g1718107) [Homo sapiens]
Seq. No.
                  217383
Seq. ID
                  LIB3148-009-Q1-K1-A2
                  BLASTX
Method
                  q3860323
NCBI GI
                  378
BLAST score
                  2.0e-36
E value
                  78
Match length
% identity
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  217384
Seq. ID
                  LIB3148-009-Q1-K1-A4
```

30475



```
8.0e-31
E value
                  106
Match length
                  58
% identity
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
                  217385
Seq. No.
                  LIB3148-009-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885334
                   524
BLAST score
E value
                  2.0e-53
Match length
                  110
                  89
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                   217386
Seq. No.
                  LIB3148-009-Q1-K1-B1
Seq. ID
Method
                  BLASTX
                   q3420052
NCBI GI
BLAST score
                   314
E value
                   5.0e-29
                   69
Match length
                   81
% identity
                   (AC004680) putative ubiqinone reductase [Arabidopsis
NCBI Description
                   thaliana]
                   217387
Seq. No.
                   LIB3148-009-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g1091678
NCBI GI
                   169
BLAST score
                   6.0e-12
E value
                   71
Match length
                   45
% identity
NCBI Description activator-like transposable element [Pennisetum glaucum]
                   217388
Seq. No.
                   LIB3148-009-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1041704
BLAST score
                   399
E value
                   6.0e-39
                   87
Match length
                   84
% identity
NCBI Description (U30478) expansin At-EXP5 [Arabidopsis thaliana]
                   217389
Seq. No.
Seq. ID
                   LIB3148-009-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   q3377797
BLAST score
                   429
                   1.0e-42
E value
Match length
                   95
% identity
                   87
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
```

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA



H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

 Seq. No.
 217390

 Seq. ID
 LIB3148-009-Q1-K1-C10

 Method
 BLASTX

NCBI GI g2190553
BLAST score 363
E value 8.0e-35
Match length 109
% identity 63

NCBI Description (AC001229) Strong similarity to Arabidopsis

zeta-crystallin-like protein (gb_Z49268). [Arabidopsis

thaliana]

Seq. No. 217391

Seq. ID LIB3148-009-Q1-K1-C11

Method BLASTX
NCBI GI g3885343
BLAST score 225
E value 2.0e-18
Match length 110
% identity 41

NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 217392

Seq. ID LIB3148-009-Q1-K1-C4

Method BLASTX
NCBI GI g3646340
BLAST score 271
E value 1.0e-40
Match length 109
% identity 82

NCBI Description (AJ000763) MADS-box protein [Malus domestica]

Seq. No. 217393

Seq. ID LIB3148-009-Q1-K1-C6

Method BLASTX
NCBI GI g4567229
BLAST score 343
E value 2.0e-32
Match length 105
% identity 52

NCBI Description (AC007119) putative pectin methylesterase [Arabidopsis

thaliana]

Seq. No. 217394

Seq. ID LIB3148-009-Q1-K1-D8

Method BLASTX
NCBI GI g3549652
BLAST score 149
E value 1.0e-09
Match length 33
% identity 91

NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis

thaliana]

Seq. No.

Seq. ID

Method

NCBI GI

```
217395
Seq. No.
                   LIB3148-009-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g2388689
NCBI GI
BLAST score
                   608
                   2.0e-63
E value
                   129
Match length
                   88
% identity
NCBI Description (AF016633) GH1 protein [Glycine max]
Seq. No.
                   217396
                   LIB3148-009-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   q4262225
NCBI GI
                   506
BLAST score
                   2.0e-51
E value
Match length
                   117
                   76
% identity
NCBI Description (AC006200) putative phosphatidic acid phosphatase
                   [Arabidopsis thaliana]
                   217397
Seq. No.
                   LIB3148-009-Q1-K1-E5
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
                   36
BLAST score
                   4.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                   217398
                   LIB3148-009-Q1-K1-E8
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   q224293
 BLAST score
                   410
                   3.0e-40
 E value
Match length
                   82
                   100
 % identity
 NCBI Description histone H4 [Triticum aestivum]
 Seq. No.
                   217399
                   LIB3148-009-Q1-K1-E9
 Seq. ID
 Method
                   BLASTX
                   g4455288
 NCBI GI
 BLAST score
                   188
                   4.0e-14
 E value
                   71
 Match length
                   55
 % identity
                   (AL035527) putative protein (fragment) [Arabidopsis
 NCBI Description
                   thaliana]
                   217400
```

30478

LIB3148-009-Q1-K1-F10

BLASTX

g1619300

```
BLAST score
                  595
                  6.0e-62
E value
Match length
                  124
                  92
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                  217401
Seq. No.
                  LIB3148-009-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114734
BLAST score
                  166
E value
                  1.0e-11
                  34
Match length
                  85
% identity
                  AUXIN-INDUCED PROTEIN AUX28 >gi_81759_pir_A285 3 aux28
NCBI Description
                  protein - soybean >gi_169921 (JO3919) auxin-regulated
                  protein (Aux28) [Glycine max]
                  217402
Seq. No.
                  LIB3148-009-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3287688
BLAST score
                  478
                  4.0e-48
E value
                  116
Match length
                  80
% identity
                  (AC003979) Contains similarity to ycf37 gene product
NCBI Description
                  gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs
                  gb T43026, gb R64902, gb Z18169 and gb N37374 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  217403
                  LIB3148-009-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q417360
NCBI GI
                   308
BLAST score
                   3.0e-28
E value
Match length
                  112
                   49
% identity
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                   >gi_2131280_pir__S67767 high mobility group-like protein
                   NHP2 - yeas\overline{t} (Saccharomyces cerevisiae)
                   >gi_666101_emb_CAA40885_ (X57714) high mobility group-like
                   nuclear protein 2 [Saccharomyces cerevisiae]
                   >gi 1429348_emb CAA67483 (X99000) high-mobility-group-like
                   protein [Saccharomyces cerevisiae]
                   >qi 1431346 emb CAA98786 (Z74256) ORF YDL208w
                   [Saccharomyces cerevisiae]
                   217404
Seq. No.
Seq. ID
                   LIB3148-009-Q1-K1-G1
```

 Seq. No.
 217404

 Seq. ID
 LIB3148-009-Q1-K1-G1

 Method
 BLASTX

 NCBI GI
 g2961389

 BLAST score
 230

 E value
 4.0e-19

 Match length
 71

 % identity
 54



(AL022141) purple acid phosphatase like protein NCBI Description [Arabidopsis thaliana] >gi 4006925 emb CAB16853 (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana] Seq. No. 217405 LIB3148-009-Q1-K1-G11 Seq. ID Method BLASTN NCBI GI g169712 BLAST score 43 5.0e-15 E value Match length 134 % identity 87 NCBI Description Ricinus communis metallothionein (RCMIT) mRNA, complete cds Seq. No. 217406 Seq. ID LIB3148-009-Q1-K1-G2 Method BLASTX NCBI GI g2583118 BLAST score 218 4.0e-18 E value Match length 52 % identity 81 NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana] 217407 Seq. No. LIB3148-009-Q1-K1-G3 Seq. ID Method BLASTN g1418705 NCBI GI 209 BLAST score 1.0e-114 E value 289 Match length % identity 93 NCBI Description G.hirsutum metallothionein-like gene 217408 Seq. No. Seq. ID LIB3148-009-Q1-K1-G4 BLASTX Method g3250675 NCBI GI BLAST score 212 3.0e-17 E value Match length 92 57 % identity NCBI Description (AL024486) putative protein [Arabidopsis thaliana] Seq. No. 217409 Seq. ID LIB3148-009-Q1-K1-G5 Method BLASTN q169712 NCBI GI BLAST score 41 7.0e-14 E value Match length 73 % identity 89 NCBI Description Ricinus communis metallothionein (RCMIT) mRNA, complete cds

Seq. No. 217410

Seq. ID LIB3148-009-Q1-K1-G8

Method BLASTX



```
NCBI GI
                  q4468813
BLAST score
                  308
E value
                  3.0e-28
                  99
Match length
% identity
                  56
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  217411
Seq. ID
                  LIB3148-009-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g114330
BLAST score
                  148
                  1.0e-13
E value
Match length
                  78
% identity
                  58
NCBI Description
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                  >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                  type 1, plasma membrane - Arabidopsis thaliana >gi_166746
                   (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                  thaliana]
Seq. No.
                  217412
Seq. ID
                  LIB3148-009-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2213871
BLAST score
                  295
E value
                  1.0e-26
                  90
Match length
                  72
% identity
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  217413
Seq. ID
                  LIB3148-009-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q531829
BLAST score
                  172
E value
                  3.0e-12
                  79
Match length
                  49
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                  217414
Seq. ID
                  LIB3148-009-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4567225
BLAST score .
                  269
E value
                  9.0e-24
Match length
                  71
% identity
                  72
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.
                  217415
Seq. ID
                  LIB3148-009-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q231503
```



```
BLAST score
                  591
E value
                  2.0e-61
Match length
                  119
                  96
% identity
NCBI Description ACTIN 97 >gi 100417_pir__S20098 actin - potato
                  >gi 21544 emb CAA39280 (X55751) actin [Solanum tuberosum]
                  217416
Seq. No.
                  LIB3148-010-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2497539
BLAST score
                  662
                  1.0e-69
E value
                  139
Match length
                  91
% identity
NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703
                  (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
                  217417
Seq. No.
                  LIB3148-010-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617270
BLAST score
                  179
                  4.0e-13
E value
                  36
Match length
                  92
% identity
NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]
                  217418
Seq. No.
                  LIB3148-010-Q1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18777
BLAST score
                  52
                  8.0e-21
E value
Match length
                  52
                  100
% identity
NCBI Description Soybean gene for Ula small nuclear RNA
                  217419
Seq. No.
                  LIB3148-010-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3805956
                  188
BLAST score
                  4.0e-14
E value
                  52
Match length
                  94
% identity
NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]
                  217420
Seq. No.
                  LIB3148-010-Q1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1345965
```

Method BLASTX
NCBI GI g1345965
BLAST score 448
E value 1.0e-44
Match length 125
% identity 75

NCBI Description FLORAL HOMEOTIC PROTEIN FBP2 (FLORAL BINDING PROTEIN 2)



217421 Seq. No. LIB3148-010-Q1-K1-B11 Seq. ID Method BLASTX g2760326 NCBI GI BLAST score 280 6.0e-25 E value 126 Match length % identity 46 NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana] 217422 Seq. No. LIB3148-010-Q1-K1-B7 Seq. ID BLASTX Method NCBI GI g2245131 146 BLAST score 3.0e-09 E value Match length 81 40 % identity NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana] 217423 Seq. No. LIB3148-010-Q1-K1-B9 Seq. ID BLASTX Method q1256436 NCBI GI 159 BLAST score 9.0e-11 E value 76 Match length 46 % identity NCBI Description (U51204) APC-binding protein EB2 [Mus musculus] 217424 Seq. No. LIB3148-010-Q1-K1-C1 Seq. ID BLASTX Method q4262140 NCBI GI 219 BLAST score 8.0e-18 E value 80 Match length 61 % identity (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana] NCBI Description Seq. No. 217425 LIB3148-010-Q1-K1-C10 Seq. ID BLASTX Method g1707939 NCBI GI 718 BLAST score 3.0e-76E value 137 Match length % identity GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT NCBI Description PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_1076256_pir__S51943 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small

>gi 1181186 (M91666) transcription factor [Petunia hybrida]

>gi_556622_emb_CAA55515_ (X78899) glucose-1-phosphate

chain B1 precursor - beet (fragment)

217431



adenylyltransferase [Beta vulgaris]

```
217426
Seq. No.
                  LIB3148-010-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231688
BLAST score
                  722
                  9.0e-77
E value
Match length
                  136
                  98
% identity
                  CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC
NCBI Description
                  1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_
                  subunit 2 of cotton catalase [Gossypium hirsutum]
                  217427
Seq. No.
                  LIB3148-010-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262140
BLAST score
                  260
                  1.0e-22
E value
Match length
                  102
% identity
                  57
                  (ACO05275) putative C-type U1 snRNP [Arabidopsis thaliana]
NCBI Description
                   217428
Seq. No.
                  LIB3148-010-Q1-K1-C8
Seq. ID
Method
                  BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
                   3.0e-11
E value
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   217429
Seq. No.
                   LIB3148-010-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   q505482
NCBI GI
                   664
BLAST score
                   6.0e-70
E value
                   135
Match length
                   93
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                   photosystem II [Nicotiana tabacum]
                   217430
Seq. No.
                   LIB3148-010-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   q140185
NCBI GI
                   298
BLAST score
                   5.0e-27
E value
                   135
Match length
                   44
% identity
NCBI Description PROBABLE GYP7 PROTEIN >gi 173243 (M17741) unidentified
                   peptide [Yarrowia lipolytica]
```



```
LIB3148-010-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  g3386611
NCBI GI
BLAST score
                  564
                  3.0e-58
E value
                  139
Match length
                  66
% identity
                 (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                  217432
Seq. No.
                  LIB3148-010-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128225
BLAST score
                  440
E value
                  1.0e-43
Match length
                  135
% identity
                  68
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
                  217433
Seq. No.
Seq. ID
                  LIB3148-010-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g169211
BLAST score
                  192
                  8.0e-15
E value
Match length
                  44
                  89
% identity
                  (M90294) ethylene-forming enzyme [Petunia hybrila]
NCBI Description
                  >gi 445591 prf 1909343A ethylene-forming enzyme [Petunia x
                  hybrida]
Seq. No.
                  217434
                  LIB3148-010-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                  q4455177
NCBI GI
BLAST score
                  265
E value
                  4.0e-23
                  102
Match length
                  52
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                  217435
Seq. ID
                  LIB3148-010-Q1-K1-E2
                  BLASTX
Method
                  g1351856
NCBI GI
                  370
BLAST score
                  2.0e-35
E value
                  89
Match length
                  81
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi 868003 dbj BAA06108 (D29629) aconitase
                   [Cucurbita sp.]
                  217436
```

Seq. ID LIB3148-010-Q1-K1-E4

Method BLASTX NCBI GI q3738331

E value

Match length

NCBI Description

% identity

6.0e-44

thaliana]

104

82



```
251
BLAST score
                  2.0e-21
E value
Match length
                  55
                  76
% identity
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                  217437
Seq. No.
Seq. ID
                  LIB3148-010-Q1-K1-E5
                  BLASTX
Method
                  q1839022
NCBI GI
                  200
BLAST score
                  7.0e-16
E value
                  91
Match length
                  52
% identity
NCBI Description (Y11121) amino acid carrier [Ricinus communis]
                  217438
Seq. No.
                  LIB3148-010-Q1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2970051
BLAST score
                  549
                  2.0e-56
E value
Match length
                  121
                  87
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
                  217439
Seq. No.
Seq. ID
                  LIB3148-010-Q1-K1-F3
                  BLASTX
Method
NCBI GI
                  g3158476
BLAST score
                  661
E value
                  1.0e-69
                  134
Match length
                  96
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                  217440
Seq. No.
                  LIB3148-010-Q1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204257
BLAST score
                  548
E value
                  2.0e-56
                  140
Match length
% identity
                  69
NCBI Description (AC005223) 5493 [Arabidopsis thaliana]
                  217441
Seq. No.
                  LIB3148-010-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497486
BLAST score
                  442
```

30486

URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis

Seq. ID

217447

LIB3148-010-Q1-K1-H10

```
217442
Seq. No.
Seq. ID
                  LIB3148-010-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g4455210
BLAST score
                  526
                  9.0e-54
E value
                  126
Match length
% identity
                  79
                  (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  217443
Seq. ID
                  LIB3148-010-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                  111
E value
                  6.0e-11
Match length
                  46
                  80
% identity
NCBI Description
                 (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  217444
Seq. ID
                  LIB3148-010-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                  q2463663
BLAST score
                  70
E value
                  4.0e-31
Match length
                  77
% identity
                  99
NCBI Description Gossypium hirsutum adenine nucleotide translocator 1
                  (CANT1) mRNA, complete cds
Seq. No.
                  217445
Seq. ID
                  LIB3148-010-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1362009
BLAST score
                  452
                  3.0e-45
E value
                  109
Match length
                  51
% identity
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
                  217446
Seq. No.
Seq. ID
                  LIB3148-010-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1077539
BLAST score
                  138
E value
                  8.0e-09
                  36
Match length
                  72
% identity
                  hypothetical protein YDR190c - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_755784_emb_CAA88704_ (Z48784) unknown
                  [Saccharomyces cerevisiae]
```

```
Method BLASTX
NCBI GI g3128175
BLAST score 185
E value 8.0e-14
Match length 108
% identity 38
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
```

 Seq. No.
 217448

 Seq. ID
 LIB3148-010-Q1-K1-H5

 Method
 BLASTX

 NCBI GI
 g533256

 A17

NCBI GI g533256
BLAST score 417
E value 6.0e-41
Match length 136
% identity 58

NCBI Description (L27101) pectinesterase [Petunia inflata]

 Seq. No.
 217449

 Seq. ID
 LIB3148-010-Q1-K1-H7

 Method
 BLASTX

 NCBI GI
 g417103

 BLAST score
 586

BLAST score 586
E value 8.0e-61
Match length 120
% identity 97

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911 emb CAA56153 (X79714) histone H3 [Lolium_temulentum] >gi 1435157_emb_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa]

>gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 217450

Seq. ID LIB3148-010-Q1-K1-H8

Method BLASTX
NCBI GI g4455292
BLAST score 152
E value 6.0e-10
Match length 120
% identity 35

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 217451



```
LIB3148-011-Q1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2581785
BLAST score
                  225
                  1.0e-18
E value
                  60
Match length
                  70
% identity
                  (U94999) class 2 non-symbiotic hemoglobin [Arabidopsis
NCBI Description
                  thaliana]
                  217452
Seq. No.
                  LIB3148-011-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g4097547
NCBI GI
BLAST score
                  245
                  7.0e-21
E value
Match length
                  75
                  30
% identity
                  (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217453
                  LIB3148-011-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                   q4539352
NCBI GI
BLAST score
                  298
                   4.0e-27
E value
                   112
Match length
                   55
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   217454
Seq. No.
                   LIB3148-011-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   g1705826
NCBI GI
                   184
BLAST score
                   8.0e-14
E value
                   38
Match length
                   89
% identity
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                   >gi 437708 (M91193) chalcone synthase [Trifolium
                   subterraneum] >gi_741008_prf__2006270A chalcone synthase
                   [Trifolium subterraneum]
                   217455
Seq. No.
                   LIB3148-011-Q1-K1-A5
 Seq. ID
                   BLASTX
Method
                   g3738294
NCBI GI
                   163
BLAST score
                   3.0e-11
 E value
                   116
Match length
 % identity
                   39
 NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]
                   217456
 Seq. No.
                   LIB3148-011-Q1-K1-A7
 Seq. ID
```

30489

BLASTX

q1840425

Method

NCBI GI



```
BLAST score
                   186
E value
                   6.0e-14
Match length
                   50
% identity
                   68
                  (U36586) alcohol dehydrogenase [Vitis vinifera]
NCBI Description
                   217457
Seq. No.
                   LIB3148-011-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122572
BLAST score
                   569
E value
                   8.0e-59
                   137
Match length
% identity
                   77
                  NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                   >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
                   217458
Seq. No.
                   LIB3148-011-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4376815
BLAST score
                   280
                   6.0e-25
E value
Match length
                   125
% identity
                   43
NCBI Description (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia
                   pneumoniae]
Seq. No.
                   217459
Seq. ID
                   LIB3148-011-Q1-K1-C3
Method
                   BLASTN
NCBI GI
                   q1658196
BLAST score
                  . 33
E value
                   5.0e-09
Match length
                   72
% identity
                   87
NCBI Description Ricinus communis calreticulin mRNA, complete cds
Seq. No.
                   217460
Seq. ID
                   LIB3148-011-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   q466334
BLAST score
                   264
E value
                   5.0e-23
Match length
                   78
% identity
                   72
```

NCBI Description

(L29151) 14-3-3 protein homologue [Solanum lycopersicum] >gi 1090846 prf 2019487A 14-3-3 protein [Lycopersicon

esculentum]

217461 Seq. No.

Seq. ID LIB3148-011-Q1-K1-D5

Method BLASTN



```
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  2.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  217462
Seq. No.
Seq. ID
                  LIB3148-011-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  203
E value
                  5.0e-16
Match length
                  74
% identity
                  58
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
                  217463
Seq. No.
Seq. ID
                  LIB3148-011-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q2924512
BLAST score
                  301
E value
                  2.0e-27
Match length
                  119
% identity
                  50
NCBI Description
                 (AL022023) beta-galactosidase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  217464
Seq. ID
                  LIB3148-011-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  174
E value
                  4.0e-13
Match length
                  39
% identity
                  85
NCBI Description
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                  >gi_2129500_pir__S52006 polygalacturonase - upland cotton
                  >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  217465
Seq. ID
                  LIB3148-011-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2129752
BLAST score
                  338
E value
                  1.0e-31
Match length
                  112
% identity
                  53
NCBI Description thioredoxin - Arabidopsis thaliana >gi 992964 emb CAA84612
                  (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.
                  217466
Seq. ID
                  LIB3148-011-Q1-K1-E9
Method
                  BLASTX
NCBI GI
```

g2454182

8.0e-38

390

BLAST score

E value



```
Match length
                   101
% identity
                   76
NCBI Description
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                   217467
Seq. ID
                   LIB3148-011-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   q4006913
BLAST score
                   385
E value
                   3.0e - 37
Match length
                   83
% identity
                   84
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   217468
Seq. ID
                  LIB3148-011-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   q169211
BLAST score
                   347
E value
                   9.0e-33
                   73
Match length
% identity
                   92
                  (M90294) ethylene-forming enzyme [Petunia hybrida]
NCBI Description
                   >gi 445591 prf 1909343A ethylene-forming enzyme [Petunia x
                  hybrida]
Seq. No.
                   217469
Seq. ID
                   LIB3148-011-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                   g1429226
BLAST score
                   149
E value
                   1.0e-09
Match length
                  29
% identity
                   90
NCBI Description (X98861) TFIIA [Arabidopsis thaliana]
Seq. No.
                   217470
Seq. ID
                  LIB3148-011-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                   g3850778
BLAST score
                   403
E value
                   2.0e-39
                  99
Match length
% identity
                   75
NCBI Description (Y18346) gluaredoxin [Lycopersicon esculentum]
Seq. No.
                  217471
Seq. ID
                  LIB3148-011-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2253579
BLAST score
                  168
E value
                   8.0e-12
Match length
                   60
% identity
```

30492

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]



```
217472
Seq. No.
Seq. ID
                  LIB3148-011-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2500376
BLAST score
                  466
                  9.0e-47
E value
                  95
Match length
% identity
                  93
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
                  (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.
                  217473
                  LIB3148-011-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3659907
BLAST score
                  431
E value
                  1.0e-42
Match length
                  108
% identity
                  80
NCBI Description
                  (AF091857) protein translation factor SUI1 homolog
                  [Pimpinella brachycarpa]
Seq. No.
                  217474
Seq. ID
                  LIB3148-011-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q2924512
BLAST score
                  273
E value
                  4.0e-24
Match length
                  125
% identity
                  49
NCBI Description (AL022023) beta-galactosidase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  217475
Seq. ID
                  LIB3148-011-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1335862
BLAST score
                  628
E value
                  9.0e-66
Match length
                  132
                  92
% identity
NCBI Description (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                  217476
Seq. ID
                  LIB3148-012-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4510387
BLAST score
                  310
E value
                  2.0e-28
Match length
                  98
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3148-012-Q1-K1-A7

Method BLASTX NCBI GI g1730843



BLAST score E value 5.0e-10 Match length 116 % identity 13

HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC NCBI Description REGION >gi_2131945_pir__S63228 hypothetical protein YNL255c
- yeast (Saccharomyces cerevisiae)

>gi_1255963_emb_CAA65489_ (X96722) ORF N0852 [Saccharomyces cerevisiae] >gi_1302303_emb_CAA96162_ (Z71531) ORF YNL255c

[Saccharomyces cerevisiae]

217478 Seq. No.

LIB3148-012-Q1-K1-B11 Seq. ID

Method BLASTX NCBI GI a2632105 262 BLAST score 6.0e-23 E value Match length 100 59 % identity

NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

>gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

217479 Seq. No.

LIB3148-012-Q1-K1-B12 Seq. ID

Method BLASTX NCBI GI q4544380 BLAST score 149 1.0e-09 E value Match length 106 % identity 30

NCBI Description (AC006920) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 217480

Seq. ID LIB3148-012-Q1-K1-B2

Method BLASTX NCBI GI q2497753 325 BLAST score E value 3.0e-30 97 Match length 57 % identity

NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) NCBI Description

>gi 1321915 emb_CAA65477_ (X96716) lipid transfer protein

[Prunus dulcis]

Seq. No. 217481

Seq. ID LIB3148-012-Q1-K1-B7

Method BLASTX NCBI GI q544129 597 BLAST score E value 4.0e-62 131 Match length 82 % identity

VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE PROTEINASE NCBI Description

EP-C1) >gi_20994_emb_CAA44816_ (X63102) endopeptidase

[Phaseolus vulgaris]

```
217482
LIB3148-0
```

```
Seq. No.
Seq. ID
                  LIB3148-012-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1076746
                  530
BLAST score
                  3.0e-54
E value
                  128
Match length
% identity
                  84
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                  217483
Seq. ID
                  LIB3148-012-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q2828291
                  404
BLAST score
                  2.0e-39
E value
Match length
                  129
% identity
                   64
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                  217484
Seq. No.
                  LIB3148-012-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2952433
BLAST score
                  190
E value
                  1.0e-14
Match length
                  95
% identity
                   44
NCBI Description
                   (AF051135) putative ubiquitin activating enzyme E1
                   [Arabidopsis thaliana]
Seq. No.
                   217485
Seq. ID
                  LIB3148-012-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2952433
BLAST score
                  383
E value
                  3.0e-37
Match length
                  103
% identity
                   69
                  (AF051135) putative ubiquitin activating enzyme E1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   217486
Seq. ID
                  LIB3148-012-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1079720
BLAST score
                  314
E value
                   4.0e-29
                  80
Match length
% identity
```

NCBI Description (U39764) eukaryotic release factor 3 [Ricinus communis]

Seq. No. 217487

Seq. ID LIB3148-012-Q1-K1-E2



```
Method
                  BLASTX
                  g135497
NCBI GI
BLAST score
                  248
                  3.0e-21
E value
Match length
                  48
                  98
% identity
                  TUBULIN BETA CHAIN (BETA-1 AND BETA-2)
NCBI Description
                  >gi_84375_pir__S00683 tubulin beta-1 chain - Stylonychia
                  lemnae (SGC5) >gi_10159_emb_CAA29853_ (X06653) beta-1
                  tubulin (AA 1 - 442) [Stylonychia lemnae]
                  >gi_578493_emb_CAA29995_ (X06874) beta-2 tubulin (AA 1 -
                  442) [Stylonychia lemnae]
                  217488
Seq. No.
                  LIB3148-012-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g125887
NCBI GI
BLAST score
                  217
E value
                  1.0e-17
                  81
Match length
                  53
% identity
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                  >gi_82092_pir__S04765 LAT52 protein precursor - tomato
                  ≥gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                  esculentum]
Seq. No.
                  217489
                  LIB3148-012-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3492806
BLAST score
                  541
E value
                  2.0e-55
Match length
                  137
% identity
                  75
                  (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
                  domestical
                  217490
Seq. No.
Seq. ID
                  LIB3148-012-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2935294
BLAST score
                  615
E value
                  3.0e-64
Match length
                  130
% identity
                  93
NCBI Description (AF036948) phenylalanine ammonia-lyase; PAL1 [Prunus avium]
Seq. No.
                  217491
```

Seq. ID LIB3148-012-Q1-K1-G10

Method BLASTX
NCBI GI g2160160
BLAST score 403
E value 2.0e-39
Match length 101
% identity 75

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]



Seq. ID LIB3148-012-Q1-K1-G3

Method BLASTX
NCBI GI g3892714
BLAST score 298
E value 5.0e-27
Match length 80
% identity 72

NCBI Description (AL033545) trehalose-6-phosphate phosphatase - like protein

[Arabidopsis thaliana]

Seq. No. 217493

Seq. ID LIB3148-012-Q1-K1-G4

Method BLASTX
NCBI GI g730526
BLAST score 240
E value 3.0e-20
Match length 63
% identity 73

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 217494

Seq. ID LIB3148-012-Q1-K1-G5

Method BLASTX
NCBI GI 982263
BLAST score 181
E value 2.0e-13
Match length 55
% identity 65

NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome

c1 precursor (clone pC(1)3II) - potato

Seq. No. 217495

Seq. ID LIB3148-012-Q1-K1-H1

Method BLASTX
NCBI GI g3046815
BLAST score 378
E value 1.0e-36
Match length 103
% identity 69

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 217496

Seq. ID LIB3148-012-Q1-K1-H10

Method BLASTX
NCBI GI g3860263
BLAST score 417
E value 5.0e-41
Match length 138
% identity 64

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis

thaliana]

Seq. No. 217497

Sea. ID

Method



```
Seq. ID
                  LIB3148-012-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1710587
BLAST score
                  200
E value
                  2.0e-15
                  79
Match length
% identity
                  52
NCBI Description
                 60S ACIDIC RIBOSOMAL PROTEIN PO >gi_1196897 (L46848) acidic
                  ribosomal protein PO [Glycine max]
Seq. No.
                  217498
Seq. ID
                  LIB3148-012-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  629
E value
                  7.0e-66
Match length
                  121
                  97
% identity
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  217499
Seq. ID
                  LIB3148-012-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  a4580523
BLAST score
                  474
E value
                  1.0e-47
Match length
                  126
% identity
                  73
NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
Seq. No.
                  217500
Seq. ID
                  LIB3148-013-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  q4454468
BLAST score
                  460
E value
                  4.0e-46
Match length
                  129
% identity
                  65
NCBI Description
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  217501
Seq. ID
                  LIB3148-013-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  200
E value
                  7.0e-16
                  46
Match length
                  80
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  217502
```

LIB3148-013-Q1-K1-A9

BLASTX



```
q1091678
NCBI GI
BLAST score
                  145
E value
                  3.0e-09
Match length
                  46
% identity
                  59
NCBI Description activator-like transposable element [Pennisetum glaucum]
                  217503
Seq. No.
Seq. ID
                  LIB3148-013-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q4325369
BLAST score
                  181
E value
                  2.0e-13
Match length
                  104
% identity
                  39
NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
                  217504
Seq. No.
Seq. ID
                  LIB3148-013-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1771780
BLAST score
                  198
E value
                  2.0e-15
Match length
                  38
                  100
% identity
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
Seq. No.
                  217505
Seq. ID
                  LIB3148-013-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3334659
BLAST score
                  497
E value
                  2.0e-50
Match length
                  136
% identity
                  64
NCBI Description
                  (Y10489) putative cytochrome P450 [Glycine max]
                  217506
Seq. No.
Seq. ID
                  LIB3148-013-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1169534
BLAST score
                  583
E value
                  2.0e-60
Match length
                  125
% identity
                  91
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__$39203
                  phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
```

>gi 433609 emb CAA82232 (Z28386) enolase [Ricinus

communis

Seq. No. 217507

Seq. ID LIB3148-013-Q1-K1-C12

Method BLASTX NCBI GI q2465434 BLAST score 576 E value 1.0e-59

Seq. ID

217512

LIB3148-013-Q1-K1-D10





```
Match length
                    127
% identity
NCBI Description
                   (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
                    217508
Seq. No.
                   LIB3148-013-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                    g3219766
BLAST score
                    689
                    6.0e-73
E value
Match length
                    131
% identity
                    99
NCBI Description ACTIN 82 >gi 1498370 (U60483) actin [Solanum tuberosum]
Seq. No.
                    217509
                   LIB3148-013-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                    g729504
BLAST score
                    276
E value
                    2.0e-24
Match length
                    67
                    76
% identity
                   NARINGENIN, 2-OXOGLUTARATE 3-DIOXYGENASE
NCBI Description
                    (FLAVONONE-3-HYDROXYLASE) (FHT) >gi_322408_pir__S32149
                    naringenin 3-dioxygenase (EC 1.14.11.9) - clove pink
                    >gi_322409_pir__S31921 naringenin 3-dioxygenase (EC
                    1.14.11.9) - clove pink >gi_481215_pir__$38337 naringenin 3-dioxygenase (EC 1.14.11.9) - clove pink
                    >gi_22675_emb_CAA49839 (X70378) naringenin 3-dioxygenase
[Dianthus caryophyllus] >gi_288078_emb_CAA51190 (X72592)
                    naringenin, 2-oxoglutarate 3-dioxygenase [Dianthus
                    caryophyllus]
                    217510
Seq. No.
Seq. ID
                   LIB3148-013-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                    g1871196
BLAST score
                    160
E value
                    7.0e-11
Match length
                    39
% identity
                    82
NCBI Description
                    (U90439) GMP kinase isolog [Arabidopsis thaliana]
                    >gi 2335091 (AC002339) putative GMP kinase [Arabidopsis
                    thaliana]
Seq. No.
                    217511
Seq. ID
                    LIB3148-013-Q1-K1-C8
Method
                   BLASTN
NCBI GI
                    g3821780
BLAST score
                   36
E value
                    2.0e-11
                   36
Match length
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

```
Method
                   BLASTX
                   g4544443
NCBI GI
BLAST score
                   479
E value
                   2.0e-48
Match length
                   136
                   35
% identity
                  (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   217513
                  LIB3148-013-Q1-K1-D11
Seq. ID
Method
                   BLASTX
                   g3184098
NCBI GI
BLAST score
                   398
                   6.0e-39
E value
                   135
Match length
% identity
                   54
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
                   pombe]
                   217514
Seq. No.
                   LIB3148-013-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1781348
BLAST score
                   330
E value
                   9.0e-32
Match length
                   83
                   88
% identity
NCBI Description
                  (Y10380) homologous to plastidic aldolases [Solanum
                   tuberosum]
Seq. No.
                   217515
                  LIB3148-013-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245030
BLAST score
                   290
E value
                   4.0e-26
Match length
                   65
% identity
                   78
NCBI Description
                  (Z97341) apetala2 domain TINY homolog [Arabidopsis
                   thaliana]
Seq. No.
                   217516
Seq. ID
                   LIB3148-013-Q1-K1-D9
Method
                   BLASTN
NCBI GI
                   g467324
BLAST score
                   35
E value
                   3.0e-10
                   87
Match length
                   85
% identity
NCBI Description Nicotiana tabacum (clone 6.2.1) mRNA, complete cds
```

Seq. ID LIB3148-013-Q1-K1-E10

Method BLASTX NCBI GI g2431769 BLAST score 263



```
E value 5.0e-23
Match length 112
% identity 53
```

NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]

Seq. No. 217518

Seq. ID LIB3148-013-Q1-K1-E12

Method BLASTX
NCBI GI g231509
BLAST score 153
E value 1.0e-10
Match length 36
% identity 81

NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935

actin-depolymerizing factor - trumpet lily

>gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing

factor [Lilium longiflorum]

Seq. No. 217519

Seq. ID LIB3148-013-Q1-K1-E2

Method BLASTX
NCBI GI g3552003
BLAST score 589
E value 3.0e-61
Match length 110
% identity 99

NCBI Description (AF085083) alcohol dehydrogenase A [Gossypium hirsutum]

>gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A

[Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium

hirsutum]

Šeg. No. 217520

Seq. ID LIB3148-013-Q1-K1-E4

Method BLASTX
NCBI GI g3914386
BLAST score 182
E value 1.0e-13
Match length 77
% identity 48

NCBI Description ALLERGEN MF1 >gi 3445490 dbj BAA32435 (AB011804) MF1

[Malassezia furfur]

Seq. No. 217521

Seq. ID LIB3148-013-Q1-K1-E9

Method BLASTX
NCBI GI g1871196
BLAST score 169
E value 6.0e-12
Match length 43
% identity 79

NCBI Description (U90439) GMP kinase isolog [Arabidopsis thaliana]

>gi 2335091 (AC002339) putative GMP kinase [Arabidopsis



thaliana]

217522 Seq. No. Seq. ID LIB3148-013-Q1-K1-F12 Method BLASTX NCBI GI g2887288 BLAST score 256 E value 4.0e-22 Match length 108 % identity 44 NCBI Description (AJ001810) mRNA cleavage factor I 25 kDa subunit [Homo sapiens] 217523 Seq. No. Seq. ID LIB3148-013-Q1-K1-F2 Method BLASTX NCBI GI g3258569 BLAST score 352 E value 2.0e-33 Match length 111 % identity 69 NCBI Description (U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana] Seq. No. 217524 Seq. ID LIB3148-013-Q1-K1-F7 Method BLASTX NCBI GI g1620982 BLAST score 465 E value 1.0e-46 Match length 97 % identity 98 NCBI Description (Y08860) 40S ribosomal protein S5 [Nicotiana plumbaginifolia] Seq. No. 217525 Seq. ID LIB3148-013-Q1-K1-F9 Method BLASTX NCBI GI g2789466 BLAST score 149 E value 1.0e-09 Match length 105 % identity 31 NCBI Description (AB008798) nuclear pore complex glycoprotein p62 [Oncorhynchus mykiss] 217526 Seq. No. LIB3148-013-Q1-K1-G9 Seq. ID Method BLASTX NCBI GI g3790359 BLAST score 164 E value 2.0e-11 . Match length 53 % identity

Seq. No. 217527

NCBI Description (AB013359) DPM2 [Rattus norvegicus]

Seq. ID

Method

217532

BLASTX

LIB3148-014-Q1-K1-A6



```
Seq. ID
                  LIB3148-013-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3924609
BLAST score
                  153
E value
                   5.0e-10
Match length
                  63
% identity
                   48
NCBI Description (AF069442) putative polyprotein of LTR transposon
                   [Arabidopsis thaliana]
Seq. No.
                  217528
Seq. ID
                  LIB3148-013-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  512
E value
                  4.0e-52
Match length
                  99
% identity
                  100
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  217529
Seq. ID
                  LIB3148-014-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2791806
BLAST score
                  210
E value
                  1.0e-16
Match length
                  59
% identity
                  66
NCBI Description (AF041433) bet3 [Mus musculus]
Seq. No.
                  217530
Seq. ID
                  LIB3148-014-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g547684
BLAST score
                  351
E value
                  2.0e-33
Match length
                  105
% identity
                  70
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100336_pir S18865 heat shock
                  protein 82 - common tobacco (fragment)
                  >gi 19880_emb_CAA44877_ (X63195) heat shock protein 82
                  [Nicotiana tabacum]
Seq. No.
                  217531
Seq. ID
                  LIB3148-014-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1370166
BLAST score
                  277
                  4.0e-25
E value
Match length
                  59
% identity
                  92
NCBI Description (Z73932) RAB1C [Lotus japonicus]
```

```
NCBI GI
                  q542050
BLAST score
                  363
E value
                  1.0e-34
Match length
                  101
% identity
                  64
                  catechol O-methyltransferase (EC 2.1.1.6) III - common
NCBI Description
                  tobacco >gi_429114_emb_CAA50561_ (X71430) catechol
                  O-methyltransferase [Nicotiana tabacum]
Seq. No.
                  217533
Seq. ID
                  LIB3148-014-Q1-K1-A8
Method
                  BLASTX
```

217534

NCBI GI q2104558 BLAST score 146 E value 2.0e-09 Match length 69 % identity 38

NCBI Description (AB000216) CCA3 [Rattus norvegicus]

Seq. No. LIB3148-014-Q1-K1-A9 Seq. ID Method BLASTX NCBI GI g3860249 BLAST score 391 E value 6.0e-38

Match length 137 % identity 61

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 217535

Seq. ID LIB3148-014-Q1-K1-B12

Method BLASTX NCBI GI q3334261 BLAST score 166 E value 1.0e-11 Match length 37 % identity 70

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 > gi 1655851 (U61973)

metallothionein-like protein [Malus domestica]

Seq. No. 217536

Seq. ID LIB3148-014-Q1-K1-B4

Method BLASTX NCBI GI g2492515 BLAST score 210 E value 1.0e-35 Match length 85 % identity 98

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi_2129924_pir__S58298 ATPase - pepper (fragment)
>gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]

Seq. No. 217537

Seq. ID LIB3148-014-Q1-K1-B9

Method BLASTX NCBI GI g4322940 BLAST score 358



E value 5.0e - 34Match length 131 % identity 39 (AF096299) DNA-binding protein 2 [Nicotiana tabacum] NCBI Description 217538 Seq. No. Seq. ID LIB3148-014-Q1-K1-C10 Method BLASTX NCBI GI q3599491 BLAST score 526 E value 9.0e-54 Match length 135 70 % identity NCBI Description (AF085149) putative aminotransferase [Capsicum chinense] 217539 Seq. No. LIB3148-014-Q1-K1-C7 Seq. ID Method BLASTN q19602 NCBI GI BLAST score 38 6.0e-12 E value 58 Match length % identity 91 NCBI Description Malus sp. mRNA for naringenin, 2-oxoglutarate, 3-dioxygenase 217540 Seq. No. LIB3148-014-Q1-K1-C8 Seq. ID Method BLASTN NCBI GI q167346 BLAST score 40 E value 4.0e-13 Match length 195 83 % identity NCBI Description Gossypium hirsutum Lea5-A late embryogenesis-abundant protein (Lea5-A) gene, complete cds Seq. No. 217541 LIB3148-014-Q1-K1-C9 Seq. ID Method BLASTX NCBI GI q4567210 BLAST score 473 E value 1.0e-47103 Match length % identity 85 NCBI Description (AC007168) unknown protein [Arabidopsis thaliana] Seq. No. 217542 Seq. ID LIB3148-014-Q1-K1-E1

Method BLASTX NCBI GI g2982303 279 BLAST score E value 8.0e-25 84 Match length 57 % identity

NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 217543

```
Seq. ID
                  LIB3148-014-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4490728
BLAST score
                  136
E value
                   1.0e-08
Match length
                  31
% identity
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
                  217544
Seq. No.
Seq. ID
                  LIB3148-014-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q2760836
BLAST score
                  394
E value
                   3.0e-38
Match length
                  94
                  72
% identity
NCBI Description
                  (AC003105) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  217545
Seq. ID
                  LIB3148-014-Q1-K1-F4
Method
                  BLASTN
                  g3510339
NCBI GI
BLAST Score
                  33
E value
                  4.0e-09
Match length
                  49
                  92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   217546
                  LIB3148-014-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1296816
BLAST score
                  455
E value
                  2.0e-45
Match length
                  96
                  92
% identity
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]
Seq. No.
                  217547
Seq. ID
                  LIB3148-014-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1705826
BLAST score
                  191
E value
                  1.0e-14
Match length
                  42
% identity
                  86
NCBI Description
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
                  >gi 437708 (M91193) chalcone synthase [Trifolium
                  subterraneum] >gi_741008_prf__2006270A chalcone synthase
                  [Trifolium subterraneum]
```

Seq. ID LIB3148-014-Q1-K1-G10

Method BLASTX



NCBI GI q131194 BLAST score 481 2.0e-48 E value Match length 116 80 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR NCBI Description (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 72686 pir F1SP5 photosystem I chain V precursor - spinach >gi_21299_emb_CAA31524_ (X13134) PSI subunit V preprotein (AA -69 to 98) [Spinacia oleracea] >gi_226167_prf__1413236B photosystem I reaction center V [Spinacia oleracea] Seq. No. 217549 Seq. ID LIB3148-014-Q1-K1-G2 Method BLASTX NCBI GI q3128228 BLAST score 543 7.0e-56 E value Match length 111 91 % identity NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana] Seq. No. 217550 Seq. ID LIB3148-014-Q1-K1-G6 Method BLASTX NCBI GI q1362162 BLAST score 296 E value 9.0e-27 Match length 143 43 % identity NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656 (L41869) beta-glucosidase [Hordeum vulgare] Seq. No. 217551 LIB3148-014-Q1-K1-H4 Seq. ID Method BLASTX NCBI GI g3219951 BLAST score 141 E value 1.0e-08 Match length 42 % identity 62 NCBI Description HYPOTHETICAL 11.7 KD PROTEIN C6B12.13 IN CHROMOSOME I >gi 2330843 emb CAB11073 (Z98531) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 217552

Seq. ID LIB3148-014-Q1-K1-H6

Method BLASTX
NCBI GI g2497543
BLAST score 253
E value 2.0e-22
Match length 57
% identity 93

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_

NCBI GI

BLAST score



(Z29492) pyruvate kinase [Nicotiana tabacum]

```
217553
Seq. No.
Seq. ID
                   LIB3148-014-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   g2253442
BLAST score
                   206
                   3.0e-16
E value
Match length
                   56
% identity
                   62
NCBI Description
                  (AF007784) LTCOR11 [Lavatera thuringiaca]
Seq. No.
                   217554
                   LIB3148-015-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3329366
BLAST score
                   154
E value
                   3.0e-10
                   47
Match length
                   66
% identity
                  (AF031243) nodule-specific protein Nlj70 [Lotus japonicus]
NCBI Description
                   217555
Seq. No.
Seq. ID
                   LIB3148-015-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   g3721926
BLAST score
                   333
E value
                   2.0e-31
Match length
                   74
                   91
% identity
NCBI Description
                  (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
                   217556
Seq. No.
Seq. ID
                   LIB3148-015-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g3402684
BLAST score
                   498
E value
                   2.0e-50
Match length
                   134
% identity
                   69
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   217557
Seq. ID
                   LIB3148-015-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   g3237190
BLAST score
                   202
E value
                   7.0e-16
                   82
Match length
% identity
NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]
Seq. No.
                   217558
Seq. ID
                   LIB3148-015-Q1-K1-C10
                   BLASTX
Method
```

30509

g2440044

```
E value
                   5.0e-21
Match length
                   45
% identity
                   96
NCBI Description
                  (AJ001293) major intrinsic protein PIPB [Craterostigma
                  plantagineum]
Seq. No.
                  217559
Seq. ID
                  LIB3148-015-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2500376
BLAST score
                  389
E value
                  1.0e-37
```

% identity 95 NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177 gb AAD14494 (AC005508) 23552 [Arabidopsis thaliana]

Seq. No. 217560 Seq. ID LIB3148-015-Q1-K1-C3 Method BLASTX NCBI GI q119354 BLAST score 181 E value 2.0e-13 Match length 38 % identity 92

79

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185

phosphopyruvate hydratase (EC 4.2.1.11) - tomato

>gi_19281 emb CAA41115 (X58108) enolase [Lycopersicon

esculentum]

Seq. No. 217561

Match length

Seq. ID LIB3148-015-Q1-K1-C5

Method BLASTX NCBI GI g1345975 BLAST score 170 E value 4.0e-12Match length 41 % identity 78

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM NCBI Description >gi_1084421_pir__JC2555 omega-3 fatty acid desaturase Common tobacco (cv. SR1) >gi_599592_dbj_BAA05515_ (D26509)
microsomal omega-3 acid desaturase [Nicotiana tabacum]

Seq. No. 217562

Seq. ID LIB3148-015-Q1-K1-C6

Method BLASTX NCBI GI q122087 BLAST score 449 E value 9.0e-45 Match length 107 % identity 84

NCBI Description

HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat .
>gi_19607_emb_CAA31964_(X13673) histone H3 (AA 1-136)
[Medicago sativa] >gi_19609_emb_CAA31965_(X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_



217563

(X00937) H3 histone [Triticum aestivum] $>gi_488565$ (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No. Seq. ID LIB3148-015-Q1-K1-C7 Method BLASTX NCBI GI q4490705 BLAST score 508

E value 1.0e-51 Match length 113 % identity 89

(AL035680) ribosomal protein L14-like protein [Arabidopsis NCBI Description

thaliana]

217564 Seq. No.

LIB3148-015-Q1-K1-C8 Seq. ID

Method BLASTX NCBI GI q4406763 BLAST score 159 E value 9.0e-11Match length 131 % identity 34

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

217565 Seq. No.

Seq. ID LIB3148-015-Q1-K1-D11

Method BLASTX NCBI GI q2832681 BLAST score 497 E value 2.0e-50 Match length 97

91 % identity

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 217566

Seq. ID LIB3148-015-Q1-K1-D2

Method BLASTX NCBI GI q99809 BLAST score 467 E value 6.0e-47Match length 118 % identity 69

NCBI Description gene Bp10 protein - rape >gi 17795 emb CAA47177 (X66608)

Bplo [Brassica napus]

Seq. No. 217567

Seq. ID LIB3148-015-Q1-K1-D8

Method BLASTX NCBI GI q3292830 BLAST score 148 E value 1.0e-09 36 Match length % identity

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 217568

```
LIB3148-015-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1854386
BLAST score
                   189
E value
                   3.0e-14
Match length
                   44
% identity
                   80
NCBI Description
                   (AB001375) similar to soluble NSF attachment protein [Vitis
                   vinifera]
Seq. No.
                   217569
Seq. ID
                   LIB3148-015-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q4091804
BLAST score
                   359
E value
                   3.0e - 34
Match length
                   98
% identity
                   74
NCBI Description (AF052584) CONSTANS-like protein 1 [Malus domestica]
Seq. No.
                   217570
Seq. ID
                   LIB3148-015-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   q130600
BLAST score
                   204
E value
                   2.0e-26
Match length
                   98
% identity
                   60
NCBI Description
                   ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE;
                   ENDONUCLEASE; REVERSE TRANSCRIPTASE ] >gi 76782 pir S01283
                   hypothetical protein 5 - figwort mosaic virus >gi_58813_emb_CAA29527_ (X06166) ORF V (AA 1-666) [Figwort
                   mosaic virus]
Seq. No.
                   217571
Seq. ID
                   LIB3148-015-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   311
E value
                   1.0e-28
Match length
                   61
% identity
                   98
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   217572
Seq. ID
                   LIB3148-015-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g3928090
BLAST score
                   254
E value
                   6.0e-22
```

98 Match length % identity 28

NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No. 217573

Seq. ID LIB3148-015-Q1-K1-F6

Method BLASTX

Match length

```
NCBI GI
                   q3212879
BLAST score
                   245
E value
                   6.0e-21
Match length
                   59
                   76
% identity
NCBI Description
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
                   thaliana]
Seq. No.
                   217574
Seq. ID
                   LIB3148-015-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g533256
BLAST score
                   319
                   2.0e-29
E value
Match length
                   125
% identity
NCBI Description (L27101) pectinesterase [Petunia inflata]
Seq. No.
                   217575
Seq. ID
                   LIB3148-015-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                   q4105772
BLAST score
                   358
E value
                   4.0e-34
Match length
                  86
% identity
                   40
NCBI Description (AF049917) PGP9B [Petunia x hybrida]
                   217576
Seq. No.
Seq. ID
                  LIB3148-015-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                   q3522943
BLAST score
                   247
E value
                   4.0e-21
Match length
                   71
% identity
NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
Seq. No.
                   217577
Seq. ID
                  LIB3148-015-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                   g4220529
BLAST score
                  237
E value
                   4.0e-20
Match length
                  70
% identity
                   70
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   217578
Seq. ID
                  LIB3148-015-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3915096
BLAST score
                  530
E value
                  3.0e-55
```

% identity NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

128



4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi_1574976 (U47293) trans-cinnamate 4-hydroxylase [Populus tremuloides]

Seq. No. 217579

Seq. ID LIB3148-015-Q1-K1-H6

Method BLASTX
NCBI GI g2980795
BLAST score 274
E value 2.0e-24
Match length 59
% identity 86

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 217580

Seq. ID LIB3148-015-Q1-K1-H7

Method BLASTN
NCBI GI g1217627
BLAST score 123
E value 9.0e-63
Match length 296
% identity 94

NCBI Description G.hinsutum mRNA for stearoyl-acyl-carrier protein

desaturase

Seq. No. 217581

Seq. ID LIB3148-015-Q1-K1-H9

Method BLASTX
NCBI GI g2739000
BLAST score 201
E value 7.0e-16
Match length 59
% identity 66

NCBI Description (AF022459) CYP71D10p [Glycine max]

Seq. No. 217582

Seq. ID LIB3148-016-Q1-K1-A8

Method BLASTN
NCBI GI g2244733
BLAST score 57
E value 3.0e-23
Match length 112
% identity 91

NCBI Description Cotton mRNA for actin, clone CF456, partial cds

Seq. No. 217583

Seq. ID LIB3148-016-Q1-K1-A9

Method BLASTX
NCBI GI 94193388
BLAST score 494
E value 5.0e-50
Match length 105
% identity 90

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 217584



```
Seq. ID
                   LIB3148-016-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   726
E value
                   3.0e-77
Match length
                   136
                   99
% identity
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                   217585
Seq. ID
                  LIB3148-016-Q1-K1-B4
Method
                  BLASTN
NCBI GI
                  q18058
BLAST score
                  72
E value
                  1.0e-32
Match length
                  104
                   92
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
Seq. No.
                   217586
Seq. ID
                  LIB3148-016-Q1-K1-B6
Method
                  BLASTN
NCBI GI
                  q2687442
BLAST score
                   38
E value
                   4.0e-12
Match length
                   38
                  100
% identity
NCBI Description Mitella pentandra large subunit 26S ribosomal RNA gene,
                  partial sequence
Seq. No.
                  217587
Seq. ID
                  LIB3148-016-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2244979
BLAST score
                  203
E value
                   6.0e-16
Match length
                   66
% identity
                   62
NCBI Description
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
                  thaliana]
Seq. No.
                  217588
Seq. ID
                  LIB3148-016-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  7.0e-11
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Seq. ID LIB3148-016-Q1-K1-C5

Method BLASTN
NCBI GI g3821780
BLAST score 36



E value 8.0e-11 Match length 38 61 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

217590 Seq. No.

LIB3148-016-Q1-K1-C6 Seq. ID

Method BLASTX NCBI GI q320585 BLAST score 451 E value 5.0e-45Match length 89 89 % identity

polygalacturonase (EC 3.2.1.15) 1 beta chain precursor -NCBI Description

tomato >gi_170480 (M98466) polygalacturonase isoenzyme 1 beta subunīt [Lycopersicon esculentum] >gi_1762586 (U63374) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon

esculentum]

Seq. No. 217591

LIB3148-016-Q1-K1-C7 Seq. ID

Method BLASTX NCBI GI q3914442 BLAST score 292 E value 2.0e-26 Match length 60 92 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR NCBI Description

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No. 217592

Seq. ID LIB3148-016-Q1-K1-C8

Method BLASTX NCBI GI q3264769 BLAST score 532 E value 1.0e-54

Match length 121 % identity

(AF071894) late embryogenesis-like protein [Prunus NCBI Description

armeniaca]

Seq. No. 217593

Seq. ID LIB3148-016-Q1-K1-C9

Method BLASTX NCBI GI q585963 BLAST score 246 E value 6.0e-2169 Match length 75 % identity

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 217594

Seq. ID LIB3148-016-Q1-K1-D6

Method BLASTX NCBI GI g4512679 BLAST score 352



E value 2.0e-33 Match length 88 % identity 77

(AC006931) putative 60S ribosomal protein L11B [Arabidopsis NCBI Description

thaliana]

Seq. No.

217595

Seq. ID LIB3148-016-Q1-K1-D8

Method BLASTX NCBI GI q464987 BLAST score 559 E value 9.0e-58 Match length 107 96 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 217596

Seq. ID LIB3148-016-Q1-K1-D9

Method BLASTX NCBI GI g2565275 BLAST score 193 E value 1.0e-14 Match length 55 % identity 78

NCBI Description (AF023611) Dimlp homolog [Homo sapiens]

Seq. No. 217597

Seq. ID LIB3148-016-Q1-K1-E11

Method BLASTX NCBI GI g1619602 BLAST score 310 E value 1.0e-28

Match length 98 % identity 62

NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 217598

Seq. ID LIB3148-016-Q1-K1-E4

Method BLASTX NCBI GI g2829275 BLAST score 499 E value 1.0e-50 Match length 103 % identity 86

NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis

thaliana] >gi 3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

```
217599
Seq. No.
Seq. ID
                   LIB3148-016-Q1-K1-E6
Method
                   BLASTN
NCBI GI
                   g12474
BLAST score
                   67
E value
                   3.0e-29
Match length
                   95
% identity
                   93
NCBI Description Zea mays chloroplast tV-UAC gene for transfer RNA-Val (UAC)
Seq. No.
                   217600
                   LIB3148-016-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q465820
BLAST score
                   373
E value
                   5.0e-36
Match length
                   106
% identity
                   63
NCBI Description
                   HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
                   >gi_280536_pir__S28301 hypothetical protein C40H1.6 -
                   Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)
                   C40H1.6 [Caenorhabditis elegans]
Seq. No.
                   217601
Seq. ID
                   LIB3148-016-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   q3123745
BLAST score
                   329
E value
                   9.0e-31
Match length
                   119
% identity
                   50
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                   217602
Seq. ID
                   LIB3148-016-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q136452
BLAST score
                   146
E value
                   2.0e-09
Match length
                   51
                   47
% identity
NCBI Description STEM-SPECIFIC PROTEIN TSJT1 >gi 100383 pir S13551
                   stem-specific protein - common tobacco
>gi_20037_emb_CAA36525_ (X52283) stem specific, weakly
                   expressed in other organs [Nicotiana tabacum]
```

Seq. No. 217603

Seq. ID LIB3148-016-Q1-K1-F9

Method BLASTX
NCBI GI g3688123
BLAST score 430
E value 1.0e-42
Match length 102
% identity 78

NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum

majus]



```
Seq. No.
                   217604
Seq. ID
                  LIB3148-016-Q1-K1-G1
Method
                  BLASTX
                  g3786001
NCBI GI
BLAST score
                   378
E value
                   2.0e-36
Match length
                  96
                   75
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                  217605
Seq. ID
                  LIB3148-016-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2129834
BLAST score
                  150
E value
                   3.0e-10
Match length
                   43
                   63
% identity
                  low molecular weight heat shock protein precursor (clone
NCBI Description
                  Hsp22.3) - soybean >gi_710434 (U21723) Hsp22.3 [Glycine
                  max]
Seq. No.
                   217606
Seq. ID
                  LIB3148-016-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3056601
BLAST score
                   493
E value
                   6.0e - 50
Match length
                  112
% identity
NCBI Description (AC004255) T1F9.22 [Arabidopsis thaliana]
Seq. No.
                  217607
Seq. ID
                  LIB3148-016-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4539350
BLAST score
                  198
E value
                  2.0e-15
Match length
                  46
% identity
                  76
NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                  217608
Seq. ID
                  LIB3148-016-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3879734
BLAST score
                  165
E value
                  2.0e-11
Match length
                  126
```

35 % identity

(Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 NCBI Description

comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST

EMBL:D74229 comes from this gene; cDNA EST EMBL:D727

Seq. No. 217609

Seq. ID LIB3148-016-Q1-K1-G8



Method BLASTX
NCBI GI g3986119
BLAST score 582
E value 2.0e-60
Match length 127
% identity 84

NCBI Description (AB013101) 1-aminocyclopropane-1-carboxylate oxidase

[Lycopersicon esculentum]

Seq. No. 217610

Seq. ID LIB3148-016-Q1-K1-G9

Method BLASTX
NCBI GI g3377797
BLAST score 261
E value 1.0e-22
Match length 55
% identity 98

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 217611

Seq. ID LIB3148-016-Q1-K1-H10

Method BLASTX
NCBI GI g2118222
BLAST score 242
E value 1.0e-20
Match length 70
% identity 73

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 217612

Seq. ID LIB3148-016-Q1-K1-H12

Method BLASTX
NCBI GI g2924781
BLAST score 434
E value 5.0e-43
Match length 122
% identity 70

NCBI Description (AC002334) putative cellulose synthase [Arabidopsis

thaliana]

Seq. No. 217613

Seq. ID LIB3148-016-Q1-K1-H3

Method BLASTX
NCBI GI g2829204
BLAST score 355
E value 9.0e-34
Match length 120
% identity 55

NCBI Description (AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

```
217614
Seq. No.
Seq. ID
                  LIB3148-016-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4580389
BLAST score
                  200
E value
                  1.0e-15
Match length
                  107
% identity
                  42
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  217615
Seq. ID
                  LIB3148-017-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g4455192
BLAST score
                  250
E value
                  2.0e-21
                  132
Match length
% identity
                  48
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  217616
Seq. ID
                  LIB3148-017-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2583130
                  95
BLAST score
E value
                  8.0e-09
Match length
                  88
% identity
                  41
NCBI Description (AC002387) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  217617
Seq. ID
                  LIB3148-017-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2765240
BLAST score
                  209
E value
                  1.0e-16
Match length
                  119
% identity
                  39
NCBI Description (Y12805) invertase inhibitor [Nicotiana tabacum]
Seq. No.
                  217618
Seq. ID
                  LIB3148-017-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2160322
BLAST score
                  395
E value
                  2.0e-38
Match length
                  96
% identity
                  78
NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana
                  sylvestris]
Seq. No.
                  217619
Seq. ID
                  LIB3148-017-Q1-K1-A7
Method
                  BLASTN
NCBI GI
```

30521

g3821780

```
BLAST score
E value
                   2.0e-09
Match length
                   37
% identity
                   97
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   217620
Seq. ID
                   LIB3148-017-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g1800147
BLAST score
                   290
E value
                   4.0e-26
Match length
                   85
% identity
                   68
NCBI Description (U83655) membrane associated protein [Arabidopsis thaliana]
Seq. No.
                   217621
Seq. ID
                  LIB3148-017-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4127456
BLAST score
                   160
E value
                   6.0e-11
Match length
                  34
% identity
                   91
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                   217622
Seq. ID
                  LIB3148-017-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  159
E value
                  9.0e-11
Match length
                  44
% identity
                  64
NCBI Description (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
Seq. No.
                  217623
Seq. ID
                  LIB3148-017-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                  502
E value
                  6.0e-51
Match length
                  105
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  217624
Seq. ID
                  LIB3148-017-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  391
E value
                  5.0e-38
Match length
```

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

108

% identity

```
Seq. No.
                   217625
Seq. ID
                   LIB3148-017-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2062169
BLAST score
                   204
E value
                   2.0e-16
                   75
Match length
% identity
                   45
NCBI Description
                  (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
                   thaliana]
Seq. No.
                   217626
Seq. ID
                   LIB3148-017-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                   q3879792
BLAST score
                   178
E value
                   6.0e-13
Match length
                   83
% identity
                   49
NCBI Description
                   (Z81120) similar to Ank repeat; cDNA EST yk400c12.5 comes
                   from this gene; cDNA EST EMBL: D75223 comes from this gene;
                   cDNA EST yk400c12.3 comes from this gene [Caenorhabditis
                   elegans]
Seq. No.
                   217627
Seq. ID
                  LIB3148-017-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                   q4539301
BLAST score
                   407
E value
                   8.0e-40
Match length
                  136
% identity
                   61
NCBI Description
                  (AL049480) putative mitochondrial protein [Arabidopsis
                  thaliana]
Seq. No.
                  217628
Seq. ID
                  LIB3148-017-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q3860321
BLAST score
                  359
E value
                  6.0e-42
Match length
                  134
% identity
                   63
NCBI Description
                 (AJ012687) beta-galactosidase [Cicer arietinum]
Seq. No.
                  217629
Seq. ID
                  LIB3148-017-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2583130
BLAST score
                  144
E value
                  6.0e-09
Match length
                  125
```

Seq. No. 217630

30

thaliana]

% identity

NCBI Description

(AC002387) putative reverse transcriptase [Arabidopsis

```
LIB3148-017-Q1-K1-D10
Seq. ID
Method
                  BLASTN
                  q606651
NCBI GI
BLAST score
                   139
E value
                   1.0e-72
                  179
Match length
                   95
% identity
                 Gossypium barbadense polygalacturonase gene, complete cds
NCBI Description
                  217631
Seq. No.
                  LIB3148-017-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  g2245107
NCBI GI
                  257
BLAST score
                   3.0e-22
E value
Match length
                  120
                  23
% identity
                 (Z97343) thioesterase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  217632
                  LIB3148-017-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4027897
                   534
BLAST score
                   1.0e-54
E value
Match length
                   134
% identity
                   75
                 (AF049353) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                   217633
Seq. No.
                  LIB3148-017-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076809
                   539
BLAST score
E value
                   2.0e-55
Match length
                   126
% identity
                   83
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
Seq. No.
                   217634
Seq. ID
                   LIB3148-017-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4102861
BLAST score
                   650
E value
                   3.0e-68
Match length
                   134
% identity
NCBI Description
                   (AF016893) copper/zinc-superoxide dismutase [Populus
                   tremuloides]
```

Seq. No. 217635

Seq. ID LIB3148-017-Q1-K1-E6 Method BLASTX NCBI GI q3668118

BLAST score 345



E value 1.0e-53 Match length 136 % identity 78

NCBI Description (AJ224078) hypothetical protein [Brassica napus]

Seq. No. 217636

Seq. ID LIB3148-017-Q1-K1-E7

Method BLASTX
NCBI GI g4539004
BLAST score 153
E value 4.0e-10
Match length 49
% identity 55

NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana]

Seq. No. 217637

Seq. ID LIB3148-017-Q1-K1-E8

Method BLASTN
NCBI GI g4519193
BLAST score 34
E value 2.0e-09
Match length 62

% identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 217638

Seq. ID LIB3148-017-Q1-K1-F2

Method BLASTX
NCBI GI g2760606
BLAST score 611
E value 1.0e-63
Match length 129
% identity 86

NCBI Description (AB001568) phospholipid hydroperoxide glutathione

peroxidase-like protein [Arabidopsis thaliana] >gi_3004869

(AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase

[Arabidopsis thaliana]

Seq. No. 217639

Seq. ID LIB3148-017-Q1-K1-F6

Method BLASTX
NCBI GI g2194136
BLAST score 152
E value 4.0e-13
Match length 99
% identity 48

NCBI Description (AC002062) Strong similarity to Zea mays retrotransposon

Hopscotch polyprotein (gb_U12626). [Arabidopsis thaliana]

Seq. No. 217640

Seq. ID LIB3148-017-Q1-K1-F7

Method BLASTX NCBI GI g4455207 BLAST score 435



```
E value 4.0e-43
Match length 91
% identity 91
```

NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 217641

Seq. ID LIB3148-017-Q1-K1-F8

Method BLASTN
NCBI GI g2558943
BLAST score 144
E value 2.0e-75
Match length 171
% identity 97

NCBI Description Gossypium hirsutum histone 3 mRNA, complete cds

Seq. No. 217642

Seq. ID LIB3148-017-Q1-K1-G1

Method BLASTX
NCBI GI g2832406
BLAST score 145
E value 4.0e-09
Match length 67
% identity 57

NCBI Description (Y14208) R2R3-MYB transcription factor [Arabidopsis

thaliana]

Seq. No. 217643

Seq. ID LIB3148-017-Q1-K1-G10

Method BLASTX
NCBI GI g3122357
BLAST score 221
E value 5.0e-18
Match length 57
% identity 70

NCBI Description PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS

PROTEIN B) >gi_2494127 (AC002376) Contains similarity to

Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis

thaliana]

Seq. No. 217644

Seq. ID LIB3148-017-Q1-K1-G7

Method BLASTX
NCBI GI g3885328
BLAST score 207
E value 1.0e-16
Match length 57
% identity 60

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 217645

Seq. ID LIB3148-017-Q1-K1-G9

Method BLASTX
NCBI GI g3941512
BLAST score 168
E value 3.0e-12
Match length 31

30526



% identity NCBI Description (AF062910) putative transcription factor [Arabidopsis thaliana] Seq. No. 217646 Seq. ID LIB3148-017-Q1-K1-H12

Method BLASTX NCBI GI g1702983 BLAST score 254 E value 5.0e-22 Match length 95 53 % identity

NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850

hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 217647 Seq. ID LIB3148-017-Q1-K1-H8 Method BLASTX

NCBI GI g2493694 BLAST score 214 E value 3.0e-17Match length 101 % identity 47

NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII

6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein

of photosystem II [Spinacia oleracea]

Seq. No. 217648

Seq. ID LIB3148-018-Q1-K1-A2

Method BLASTX NCBI GI g2213610 BLAST score 142 E value 1.0e-08 Match length 120 % identity 22

NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No. 217649

Seq. ID LIB3148-018-Q1-K1-A3

Method BLASTX NCBI GI g4090884 BLAST score 410 E value 9.0e-53 132 Match length % identity 74

NCBI Description (AF025333) vesicle-associated membrane protein 7B;

synaptobrevin 7B [Arabidopsis thaliana]

Seq. No. 217650

Seq. ID LIB3148-018-Q1-K1-A8

Method BLASTX NCBI GI g4154352 BLAST score 238



```
6.0e-20
E value
Match length
                  130
% identity
                  42
NCBI Description
                  (AF110333) PrMC3 [Pinus radiata]
                  217651
Seq. No.
Seq. ID
                  LIB3148-018-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3924613
BLAST score
                  101
E value
                  2.0e-10
Match length
                  74
                  45
% identity
                  (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein
                  [Arabidopsis thaliana]
                  217652
Seq. No.
                  LIB3148-018-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1903034
BLAST score
                  339
E value
                  8.0e-32
Match length
                  97
                  66
% identity
NCBI Description (X94625) amp-binding protein [Brassica napus]
Seq. No.
                  217653
Seq. ID
                  LIB3148-018-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3914359
BLAST score
                  411
E value
                  3.0e-40
Match length
                  87
% identity
                  86
NCBI Description
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1928979 (U92656) phospholipase D [Vigna unguiculata]
Seq. No.
                  217654
Seq. ID
                  LIB3148-018-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4510363
BLAST score
                  682
E value
                  5.0e-72
```

144 Match length % identity

NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 217655

Seq. ID LIB3148-018-Q1-K1-C10

Method BLASTX NCBI GI q1710530 BLAST score 402 E value 2.0e-39 79 Match length



% identity 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 NCBI Description ribosomal protein L27a - Arabidopsis thaliana >gi 1107487 emb CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] 217656 Seq. No. LIB3148-018-Q1-K1-C11 Seq. ID Method BLASTX NCBI GI g4193950 BLAST score 389 E value 1.0e-37 Match length 115 62 % identity (AF110519) ethylene-inducible CTR1-like protein kinase; NCBI Description ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v [Lycopersicon esculentum] 217657 Seq. No. LIB3148-018-Q1-K1-C6 Seq. ID Method BLASTX g4432821 NCBI GI 176 BLAST score 1.0e-12 E value Match length 122 36 % identity NCBI Description (AC006593) putative transmembrane protein [Arabidopsis thaliana] 217658 Seq. No. Seq. ID LIB3148-018-Q1-K1-C7 Method BLASTX NCBI GI q1710530 BLAST score 666 4.0e-70 E value Match length 134 % identity 89 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 NCBI Description ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] Seq. No. 217659 LIB3148-018-Q1-K1-D12 Seq. ID Method BLASTX NCBI GI g3065835 BLAST score 351 E value 3.0e-33Match length 97 % identity (AF058800) putative methyltransferase [Arabidopsis NCBI Description

thaliana]

Seq. No.

Seq. ID LIB3148-018-Q1-K1-D7

217660

Method BLASTX NCBI GI 93355474



```
BLAST score
E value
                  1.0e-63
                  125
Match length
                  91
% identity
                 (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                  217661
Seq. No.
                  LIB3148-018-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  390
E value
                  7.0e-38
                  131
Match length
                  35
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  217662
                  LIB3148-018-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738287
BLAST score
                  209
                  1.0e-16
E value
Match length
                  65
% identity
                   60
                  (AC005309) glutathione s-transferase, GST6 [Arabidopsis
NCBI Description
                  thaliana]
                  217663
Seq. No.
                  LIB3148-018-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1705826
BLAST score
                   199
E value
                   1.0e-15
Match length
                   41
% identity
                   90
NCBI Description
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
                  >gi 437708 (M91193) chalcone synthase [Trifolium
                   subterraneum] >gi_741008_prf__2006270A chalcone synthase
                   [Trifolium subterraneum]
                  217664
Seq. No.
Seq. ID
                  LIB3148-018-Q1-K1-F10
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                  37
E value
                   5.0e-12
Match length
                   49
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   217665
Seq. ID
                  LIB3148-018-Q1-K1-F3
Method
```

Method BLASTX
NCBI GI g1076511
BLAST score 454
E value 3.0e-45
Match length 112



79 % identity H+-transporting ATPase (EC 3.6.1.35) - kidney bean NCBI Description >gi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase [Phaseolus vulgaris] 217666 Seq. No. LIB3148-018-Q1-K1-F5 Seq. ID BLASTX Method g3192881 NCBI GI BLAST score 225 E value 1.0e-18 48 Match length 88 % identity (AF068834) starch synthase [Ipomoea batatas] NCBI Description 217667 Seq. No. LIB3148-018-Q1-K1-F7 Seq. ID BLASTX Method NCBI GI q1911765 400 BLAST score E value 5.0e-39 135 Match length 53 % identity (\$83359) iEP4=42.6-kda elicitor-induced glycoprotein/EP4 NCBI Description homolog/ENOD8 homolog [carrots, Peptide, 391 aa] [Daucus carota] >gi 4204870 (U56392) iEP4 [Daucus carota] Seq. No. 217668 LIB3148-018-Q1-K1-G12 Seq. ID Method BLASTX g400992 NCBI GI BLAST score 371 1.0e-35 E value Match length 117 64 % identity NCBI Description 50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR (CL28) >gi_279656_pir__R5NT28 ribosomal protein L28 precursor, chloroplast - tobacco >gi_20016_emb_CAA48211_ (X68078) ribosomal protein CL28 [Nicotiana tabacum] Seq. No. 217669 LIB3148-018-Q1-K1-G9 Seq. ID Method BLASTX NCBI GI g1617270 BLAST score 204 E value 3.0e-16 Match length 44 % identity NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

Seq. No. 217670

Seq. ID LIB3148-018-Q1-K1-H4

Method BLASTX NCBI GI g4097915 BLAST score 157 E value 2.0e-10 Match length 116

```
% identity
                   33
NCBI Description (U72147) unknown [Anabaena sp. CA]
                   217671
Seq. No.
                   LIB3148-018-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g1076715
NCBI GI
                   275
BLAST score
                   2.0e-24
E value
Match length
                   88
                   53
% identity
                  abscisic acid-induced protein HVA22 - barley >gi_404589
NCBI Description
                   (L19119) A22 [Hordeum vulgare]
                   217672
Seq. No.
                   LIB3148-018-Q1-K1-H6
Seq. ID
Method
                   BLASTN
                   q2924257
NCBI GI
                   85
BLAST score
                   1.0e-40
E value
Match length
                   97
                   48
% identity
NCBI Description Tobacco chloroplast genome DNA
                   217673
Seq. No.
                   LIB3148-018-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   q4090533
NCBI GI
                   609
BLAST score
                   2.0e-63
E value
Match length
                   128
% identity
                   88
NCBI Description (U68215) ACC oxidase [Carica papaya]
                   217674
Seq. No.
Seq. ID
                   LIB3148-019-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q1730621
BLAST score
                   271
                    4.0e-24
E value
Match length
                   92
% identity
                    58
                   HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION
NCBI Description
                   >gi_630106_pir__S48817 hypothetical protein YML079w - yeast
                    (Saccharomyces cerevisiae) >gi_587531_emb_CAA86498_
(Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa
                    overlap with S36201 S36201 hypothetical protein 1 -
                    Rhizobium leguminosarum [Saccharomyces cerevisiae]
Seq. No.
                    217675
                   LIB3148-019-Q1-K1-A11
Seq. ID
Method
                   BLASTX
                   g3832512
NCBI GI
                   296
BLAST score
```

30532

8.0e-27

67 85

E value Match length

% identity



104

56

Match length

% identity



```
(AF097922) granule-bound glycogen (starch) synthase
NCBI Description
                  [Astragalus membranaceus]
                  217676
Seq. No.
                  LIB3148-019-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  q3128194
NCBI GI
BLAST score
                  145
E value
                  2.0e-09
                  88
Match length
                  45
% identity
                  (AC004521) putative heme A: farnesyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  217677
Seq. No.
                  LIB3148-019-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g2924784
NCBI GI
                  155
BLAST score
                  2.0e-10
E value
                  68
Match length
                   41
% identity
                  (AC002334) similar to jasmonate inducible protein
NCBI Description
                   [Arabidopsis thaliana]
                   217678
Seq. No.
                  LIB3148-019-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                   g1705678
NCBI GI
                   230
BLAST score
E value
                   4.0e-19
Match length
                   51
                   90
% identity
NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
                   217679
Seq. No.
                   LIB3148-019-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g3885884
NCBI GI
                   286
BLAST score
                   8.0e-26
E value
                   59
Match length
                   92
% identity
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                   217680
Seq. No.
                   LIB3148-019-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g4432846
NCBI GI
                   281
BLAST score
                   5.0e-25
E value
```

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]



```
217681
Seq. No.
                  LIB3148-019-Q1-K1-B7
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g2213558
BLAST score
                   217
                  1.0e-17
E value
                  94
Match length
                   46
% identity
                  (Z97052) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  217682
                  LIB3148-019-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99752
BLAST score
                   267
                   5.0e-35
E value
Match length
                  117
                   76
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
NCBI Description
                  Arabidopsis thaliana
Seq. No.
                   217683
                  LIB3148-019-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2760362
BLAST score
                   153
E value
                   1.0e-10
                   51
Match length
                   65
% identity
                  (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
                   217684
Seq. No.
                  LIB3148-019-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3757521
BLAST score
                   167
E value
                   1.0e-11
Match length
                   97
% identity
                   36
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                   217685
Seq. No.
Seq. ID
                   LIB3148-019-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q3334299
BLAST score
                   571
E value
                   4.0e-59
Match length
                   117
                   92
% identity
```

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >qi 2315211 emb CAA74725 (Y14339)

proteasome alpha subunit [Lycopersicon esculentum]

Seq. No. 217686

Seq. ID LIB3148-019-Q1-K1-C9

Method BLASTX



```
NCBI GI
                  g4249409
                  250
BLAST score
                  2.0e-21
E value
Match length
                  119
                  45
% identity
                  (AC006072) putative sugar transporter [Arabidopsis
NCBI Description
                  thaliana]
                  217687
Seq. No.
                  LIB3148-019-Q1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131754
                  183
BLAST score
                  1.0e-13
E value
Match length
                  87
% identity
                  41
                  PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein
NCBI Description
                   (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_
                   (X51767) put. pPLZ2 product (AA 1-164) [Lupinus
                  polyphyllus]
                  217688
Seq. No.
                  LIB3148-019-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g4510389
NCBI GI
                   372
BLAST score
                   9.0e-36
E value
Match length
                  132
                   62
% identity
                  (AC007017) putative solute carrier protein [Arabidopsis
NCBI Description
                   thaliana]
                   217689
Seq. No.
                   LIB3148-019-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2275196
                   193
BLAST score
E value
                   2.0e-15
                   52
Match length
                   83
% identity
                  (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   217690
Seq. No.
                   LIB3148-019-Q1-K1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4490737
BLAST score
                   234
E value
                   1.0e-19
Match length
                   68
                   74
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                   217691
Seq. No.
                   LIB3148-019-Q1-K1-E10
Seq. ID
```

30535

BLASTN

g3821780

Method NCBI GI

Method

BLASTX



```
BLAST score
                  36
                  5.0e-11
E value
                  36
Match length
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  217692
Seq. No.
                  LIB3148-019-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  g1362086
NCBI GI
                  219
BLAST score
                  2.0e-18
E value
                  60
Match length
                  77
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >qi 886471 emb CAA58474 (X83499) methionine synthase
                   [Catharanthus roseus]
                  217693
Seq. No.
                  LIB3148-019-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g4538965
NCBI GI
BLAST score
                  251
                   1.0e-21
E value
Match length
                   64
                   64
% identity
NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]
                   217694
Seq. No.
                   LIB3148-019-Q1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2262100
BLAST score
                   405
                   1.0e-39
E value
                   93
Match length
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                   217695
Seq. No.
                   LIB3148-019-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q100335
NCBI GI
BLAST score
                   542
E value
                   1.0e-55
Match length
                   133
                   77
% identity
                   heat shock protein 70 - common tobacco (fragment)
NCBI Description
                   >qi 19878 emb CAA44820 (X63106) heat shock protein 70
                   [Nicotiana tabacum]
                   217696
Seq. No.
                   LIB3148-019-Q1-K1-F11
Seq. ID
```

30536

```
g4417289
NCBI GI
                   289
BLAST score
                   4.0e-26
E value
Match length
                  81
                   65
% identity
                  (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                  217697
Seq. No.
                  LIB3148-019-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                   g2388689
NCBI GI
BLAST score
                   394
                   3.0e-38
E value
Match length
                   97
                   77
% identity
                  (AF016633) GH1 protein [Glycine max]
NCBI Description
```

217698 Seq. No. LIB3148-019-Q1-K1-G9 Seq. ID BLASTX Method q2662415 NCBI GI BLAST score 147 2.0e-09 E value 53 Match length

% identity (U97494) metallothionein-like protein [Prunus armeniaca] NCBI Description

Seq. No. 217699 LIB3148-019-Q1-K1-H1 Seq. ID BLASTX Method g3334157 NCBI GI 406 BLAST score 1.0e-39 E value 82 Match length 95 % identity

49

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 1220142 emb CAA59468_ (X85185) cyclophilin

[Catharanthus roseus]

217700 Seq. No.

LIB3148-019-Q1-K1-H12 Seq. ID

Method BLASTX q3885515 NCBI GI 240 BLAST score 1.0e-20 E value Match length 46 % identity 96

(AF084202) similar to ribosomal protein S26 [Medicago NCBI Description

sativa]

217701 Seq. No.

Seq. ID LIB3148-019-Q1-K1-H2

BLASTX Method NCBI GI g2765244 BLAST score 348 E value 7.0e-33

% identity

51

NCBI Description (Y09541) pectate lyase [Zinnia elegans]



```
129
Match length
% identity
                  51
                  (Y12807) invertase inhibitor homolog [Arabidopsis thaliana]
NCBI Description
                  217702
Seq. No.
                  LIB3148-019-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345785
                  697
BLAST score
                  8.0e-74
E value
                  137
Match length
                  98
% identity
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                  >gi 567935 dbj BAA05640 (D26593) chalcone synthase
                   [Camellia sinensis]
                  217703
Seq. No.
                  LIB3148-019-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3319882
BLAST score
                  458
                  5.0e-46
E value
                  99
Match length
                  89
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                  arietinum]
                  217704
Seq. No.
                  LIB3148-020-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g3492803
NCBI GI
BLAST score
                   258
                   6.0e-23
E value
                   69
Match length
                   70
% identity
NCBI Description (AJ002479) ENBP1 [Medicago truncatula]
Seq. No.
                   217705
                  LIB3148-020-Q1-K1-A2
Seq. ID
Method
                  BLASTN
                   q3821780
NCBI GI
BLAST score
                   33
                   2.0e-09
E value
Match length
                   33
                   58
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   217706
Seq. ID
                   LIB3148-020-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                   q2463509
BLAST score
                   216
E value
                   2.0e-17
Match length
                   87
```



```
217707
Seq. No.
                  LIB3148-020-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129772
                  368
BLAST score
                  1.0e-35
E value
                  82
Match length
                  83
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR-7 -
                  Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  217708
Seq. No.
                  LIB3148-020-Q1-K1-B1
Seq. ID
Method
                  BLASTN
                  q3449312
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
                   40
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K16L22, complete sequence [Arabidopsis thaliana]
                   217709
Seq. No.
                  LIB3148-020-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                   g286001
NCBI GI
                   169
BLAST score
E value
                   5.0e-12
Match length
                  118
                   32
% identity
NCBI Description (D13630) KIAA0005 [Homo sapiens]
                   217710
Seq. No.
                   LIB3148-020-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3702339
                   238
BLAST score
                   3.0e-20
E value
Match length
                   101
                   49
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                   217711
Seq. No.
                   LIB3148-020-Q1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3859609
BLAST score
                   453
E value
                   2.0e-45
```

Match length 114 75 % identity

NCBI Description (AF104919) Arabidopsis thaliana ABC1 protein (GB:AJ001158)

[Arabidopsis thaliana]

217712 Seq. No.

LIB3148-020-Q1-K1-B8 Seq. ID

Method BLASTX



```
g114093
NCBI GI
                  347
BLAST score
                  2.0e-33
E value
Match length
                  69
                  94
% identity
                  RAS-RELATED PROTEIN ARA-5 >gi_217841_dbj_BAA00832_ (D01027)
NCBI Description
                  small GTP-binding protein [Arabidopsis thaliana]
                  217713
Seq. No.
                  LIB3148-020-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2369766
BLAST score
                  267
                   2.0e-23
E value
                   52
Match length
                   96
% identity
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   217714
Seq. No.
                  LIB3148-020-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3128168
                   451
BLAST score
                   5.0e-45
E value
                   111
Match length
% identity
                   68
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
                   217715
Seq. No.
                   LIB3148-020-Q1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244847
BLAST score
                   249
                   2.0e-21
E value
Match length
                   124
% identity
                   51
                  (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   217716
Seq. No.
                   LIB3148-020-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4559334
BLAST score
                   219
                   8.0e-18
E value
Match length
                   102
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                   217717
Seq. ID
                   LIB3148-020-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g1771778
```

409

84

2.0e-40

BLAST score

E value Match length



```
% identity
                  (X99320) 23 kDa oxygen evolving protein of photosystem II
NCBI Description
                  [Solanum tuberosum]
                  217718
Seq. No.
                  LIB3148-020-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g485742
NCBI GI
BLAST score
                  269
                  4.0e-24
E value
                  61
Match length
                  87
% identity
                  (L32791) pyrophosphatase [Beta vulgaris]
NCBI Description
                  217719
Seq. No.
                  LIB3148-020-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  q2245066
NCBI GI
                  307
BLAST score
                  4.0e-28
E value
                  131
Match length
                  44
% identity
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
                  217720
Seq. No.
                  LIB3148-020-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g4102727
NCBI GI
                   144
BLAST score
                   4.0e-09
E value
                   75
Match length
                   43
% identity
                  (AF015782) blight-associated protein p12 precursor [Citrus
NCBI Description
                   jambhiri]
                   217721
Seq. No.
                   LIB3148-020-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   q2244993
NCBI GI
BLAST score
                   262
                   8.0e-23
E value
Match length
                   103
% identity
                   52
                  (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                   [Arabidopsis thaliana]
                   217722
Seq. No.
                   LIB3148-020-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   g2288981
NCBI GI
BLAST score
                   345
                   1.0e-32
E value
Match length
                   116
                   40
% identity
                   (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
```

30541

protein [Arabidopsis thaliana]

thaliana] >gi_3763938 (AC004450) putative calcium binding



```
217723
Seq. No.
                  LIB3148-020-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g1117821
NCBI GI
                  232
BLAST score
E value
                  2.0e-19
                  99
Match length
                  49
% identity
NCBI Description (U31454) MNG10 [Manduca sexta]
                  217724
Seq. No.
                  LIB3148-020-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g629602
NCBI GI
                  347
BLAST score
                  7.0e-33
E value
                  115
Match length
                   60
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi_488787_emb_CAA55893_ (X79330) putative imbibition
                  protein [Brassica oleracea]
                  217725
Seq. No.
                  LIB3148-020-Q1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4093157
BLAST score
                   136
                   1.0e-08
E value
                   62
Match length
% identity
                   48
                  (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   217726
Seq. No.
                   LIB3148-020-Q1-K1-E9
Seq. ID
Method
                   BLASTN
                   q3600062
NCBI GI
BLAST score
                   34
E value
                   1.0e-09
                   172
Match length
% identity
NCBI Description Arabidopsis thaliana BAC T25C13
                   217727
Seq. No.
                   LIB3148-020-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1363492
BLAST score
                   206
                   3.0e-16
E value
Match length
                   43
                   88
% identity
                   outer envelope membrane protein OEP75 precursor - garden
NCBI Description
```

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

% identity

NCBI Description



```
217728
Seq. No.
Seq. ID
                  LIB3148-020-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4090884
                  197
BLAST score
                  3.0e-15
E value
                  63
Match length
                  63
% identity
                  (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                  synaptobrevin 7B [Arabidopsis thaliana]
                  217729
Seq. No.
                  LIB3148-020-Q1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q102290
BLAST score
                  186
                   4.0e-14
E value
                  36
Match length
                  100
% identity
                  histone H4.2 - slime mold (Physarum polycephalum)
NCBI Description
                  >gi_1183935_emb_CAA33239 (X15141) histone H42 [Physarum
                  polycephalum]
                  217730
Seq. No.
                  LIB3148-020-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g322750
                   535
BLAST score
                   6.0e - 55
E value
                   105
Match length
                   100
% identity
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
                   >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
                   217731
Seq. No.
Seq. ID
                   LIB3148-020-Q1-K1-G3
                   BLASTX
Method
NCBI GI
                   g1173187
BLAST score
                   497
E value
                   2.0e-50
Match length
                   101
                   94
% identity
                   40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi_643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
Seq. No.
                   217732
                   LIB3148-020-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g441457
                   237
BLAST score
                   2.0e-20
E value
                   47
Match length
```

(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon



esculentum]

```
217733
Seq. No.
                    LIB3148-020-Q1-K1-G5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2739383
                    270
BLAST score
                    8.0e-24
E value
                    71
Match length
                    79
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                    217734
Seq. No.
                    LIB3148-020-Q1-K1-G8
Seq. ID
                    BLASTX
Method
                    g3914535
NCBI GI
                    356
BLAST score
                    7.0e - 34
E value
                    80
Match length
                    81
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_
                    (AJ223363) ribosomal protein L13a [Lupinus luteus]
                    217735
Seq. No.
                    LIB3148-020-Q1-K1-H1
Seq. ID
                    BLASTX
Method
                    g4510395
NCBI GI
BLAST score
                    358
                    5.0e - 34
E value
                    105
Match length
                    66
% identity
NCBI Description (AC006587) putative beta-galactosidase precursor
                    [Arabidopsis thaliana]
                    217736
Seq. No.
                    LIB3148-020-Q1-K1-H11
Seq. ID
Method
                    BLASTX
                    q1702983
NCBI GI
                     356
BLAST score
                    7.0e-34
E value
                    111
Match length
% identity
                     59
                    AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855 pir _S11850
NCBI Description
                    hypothetical protein - garden strawberry

>gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria

x ananassa] >gi_927034 (L44142) auxin-repressed protein
                     [Fragaria ananassa]
Seq. No.
                     217737
                    LIB3148-020-Q1-K1-H6
Seq. ID
Method
                     BLASTX
NCBI GI
                     g3298547
                     290
BLAST score
                     3.0e-26
E value
                    70
Match length
% identity
                    (AC004681) putative condensin protein [Arabidopsis
NCBI Description
```

Method

BLASTX



thaliana]

```
217738
Seq. No.
                  LIB3148-020-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g1370276
NCBI GI
                  253
BLAST score
                  4.0e-22
E value
                  72
Match length
                  65
% identity
                  (X96428) MADS-box protein [Nicotiana tabacum]
NCBI Description
                  217739
Seq. No.
                  LIB3148-021-Q1-K1-A5
Seq. ID
                  BLASTN
Method
                  q4545261
NCBI GI
                  36
BLAST score
                  6.0e-11
E value
                  56
Match length
                  91
% identity
                  Gossypium hirsutum metallothionein-like protein mRNA,
NCBI Description
                  complete cds
                  217740
Seq. No.
                  LIB3148-021-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                   g3759184
NCBI GI
BLAST score
                   304
                   1.0e-27
E value
                  82
Match length
                   67
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   217741
Seq. No.
                   LIB3148-021-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g3746069
NCBI GI
                   149
BLAST score
                   2.0e-09
E value
                   97
Match length
                   35
% identity
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   217742
Seq. No.
                   LIB3148-021-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4027893
BLAST score
                   326
                   2.0e-30
E value
                   83
Match length
% identity
NCBI Description (AF049351) alpha-expansin precursor [Nicotiana tabacum]
                   217743
Seq. No.
                   LIB3148-021-Q1-K1-C3
Seq. ID
```



g2829204 NCBI GI 363 BLAST score 1.0e-34 E value 96 Match length 66 % identity (AF044204) lipid transfer protein precursor [Gossypium NCBI Description hirsutum] 217744 Seq. No. LIB3148-021-Q1-K1-D10 Seq. ID BLASTX Method g2642443 NCBI GI 193 BLAST score 5.0e-15 E value Match length 94 47 % identity (AC002391) putative cytochrome P450 [Arabidopsis thaliana] NCBI Description 217745 Seq. No. LIB3148-021-Q1-K1-D3 Seq. ID BLASTX Method g3882081 NCBI GI BLAST score 351 3.0e-33 E value Match length 72 33 % identity (AJ012552) polyubiquitin [Vicia faba] NCBI Description 217746 Seq. No. LIB3148-021-Q1-K1-D6 Seq. ID BLASTX Method g2739046 NCBI GI 553 BLAST score 7.0e-57 E value 150 Match length 66 % identity (AF024652) polyphosphoinositide binding protein Ssh2p NCBI Description [Glycine max] 217747 Seq. No. LIB3148-021-Q1-K1-D9 Seq. ID BLASTX Method q3659907 NCBI GI 329 BLAST score 7.0e - 31E value 83 Match length 78 % identity (AF091857) protein translation factor SUI1 homolog NCBI Description [Pimpinella brachycarpa] Seq. No. 217748 LIB3148-021-Q1-K1-E1 Seq. ID Method BLASTX NCBI GI g3785998

30546

455

120

2.0e-45

BLAST score

E value Match length

Seq. No.

217754



```
% identity
                    (AC005499) unknown protein [Arabidopsis thaliana]
  NCBI Description
                    217749
  Seq. No.
                    LIB3148-021-Q1-K1-E12
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    q2262135
  BLAST score
                    41
                    1.0e-13
  E value
  Match length
                    77
                    88
  % identity
                    Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
  NCBI Description
                    cM, complete sequence
                    217750
  Seq. No.
                    LIB3148-021-Q1-K1-E2
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q4432841
                    148
  BLAST score
                    2.0e-09
  E value
  Match length
                    43
                     65
  % identity
  NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]
                     217751
 -Seq. No.
                    LIB3148-021-Q1-K1-E4
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     q231503
                     693
  BLAST score
                     3.0e-73
  E value
  Match length
                     138
                     94
  % identity
                    ACTIN 97 >gi_100417_pir__S20098 actin - potato
  NCBI Description
                     >gi 21544 emb CAA39280 (X55751) actin [Solanum tuberosum]
  Seq. No.
                     217752
  Seq. ID
                     LIB3148-021-Q1-K1-E6
                     BLASTX
  Method
  NCBI GI
                     q1524121
  BLAST score
                     149
  E value
                     2.0e-09
  Match length
                     39
  % identity
                     69
                    (X96539) malate dehydrogenase [Mesembryanthemum
  NCBI Description
                     crystallinum]
  Seq. No.
                     217753
                     LIB3148-021-Q1-K1-E8
  Seq. ID
                     BLASTX
  Method
                     g2914701
  NCBI GI
  BLAST score
                     241
                     3.0e-20
  E value
                     101
. Match length
                     49
  % identity
  NCBI Description (AC003974) putative cytochrome b5 [Arabidopsis thaliana]
```

30547



```
LIB3148-021-Q1-K1-F4
Seq. ID
                  BLASTN
Method
                  q2143322
NCBI GI
                  46
BLAST score
                  5.0e-17
E value
                  66
Match length
                  92
% identity
NCBI Description P.deltoides chloroplast DNA for psbB operon
                  217755
Seq. No.
                  LIB3148-021-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g2443886
NCBI GI
                  370
BLAST score
                  2.0e-35
E value
                  91
Match length
                  80
% identity
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  217756
Seq. No.
                  LIB3148-021-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  g2649565
NCBI GI
                   142
BLAST score
                   1.0e-08
E value
Match length
                   83
% identity
                   36
                  (AE001032) long-chain-fatty-acid--CoA ligase (fadD-5)
NCBI Description
                   [Archaeoglobus fulgidus]
                   217757
Seq. No.
                   LIB3148-021-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q322596
                   653
BLAST score
E value
                   1.0e-68
Match length
                   138
                   90
% identity
                   serine/threonine protein kinase (EC 2.7.-.-) AK21 -
NCBI Description
                   Arabidopsis thaliana >gi 166600 (M93023) SNF1-related
                   protein kinase [Arabidopsis thaliana]
                   >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase
                   [Arabidopsis thaliana]
                   217758
Seq. No.
Seq. ID
                   LIB3148-021-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   g4049341
BLAST score
                   162
                   4.0e-11
E value
                   135
Match length
% identity
                   34
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
```

Seq. No. 217759

Seq. ID LIB3148-021-Q1-K1-H2

Method BLASTX



```
g2191187
NCBI GI
BLAST score
                   143
E value
                   7.0e-09
Match length
                   84
                   45
% identity
                  (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   217760
                   LIB3148-021-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   q3660469
NCBI GI
BLAST score
                   425
E value
                   6.0e-42
                   92
Match length
                   95
% identity
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.
                   217761
Seq. ID
                   LIB3148-021-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   g3033397
BLAST score
                   313
                   7.0e-29
E value
Match length
                   62
% identity
                   92
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]
                   217762
Seq. No.
Seq. ID
                   LIB3148-022-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2388999
BLAST score
                   143
                   5.0e-09
E value
                   94
Match length
                   32
% identity
NCBI Description (Z98981) hypothetical protein [Schizosaccharomyces pombe]
                   217763
Seq. No.
Seq. ID
                   LIB3148-022-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g232031
BLAST score
                   247
E value
                   4.0e-24
                   116
Match length
                   57
% identity
NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224
                   translation elongation factor eEF-1 beta chain - rice
                   >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   217764
Seq. No.
```

Seq. ID LIB3148-022-Q1-K1-A4

Method BLASTX NCBI GI g4191780

30549



```
BLAST score
                  245
                   7.0e-21
E value
                  93
Match length
                  49
% identity
NCBI Description
                  (AC005917) putative cytokinin oxidase [Arabidopsis
                  thaliana]
                  217765
Seq. No.
                  LIB3148-022-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3121825
                  303
BLAST score
                  1.0e-27
E value
                  105
Match length
                   67
% identity
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi 1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
                   217766
Seq. No.
                  LIB3148-022-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g294845
BLAST score
                   159
                   7.0e-14
E value
Match length
                   53
% identity
                   68
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
Seq. No.
                   217767
                   LIB3148-022-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   g2306917
NCBI GI
                   288
BLAST score
E value
                   4.0e-26
Match length
                   67
                   87
% identity
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   217768
                   LIB3148-022-Q1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2341034
BLAST score
                   511
E value
                   5.0e-52
Match length
                   105
% identity
                   96
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                   217769
                   LIB3148-022-Q1-K1-B2
Seq. ID
```

BLASTX Method g531829 NCBI GI BLAST score 144 4.0e-09 E value

```
79
Match length
% identity
NCBI Description
                   (U12390) beta-galactosidase alpha peptide [cloning vector
                   pSport1]
Seq. No.
                   217770
Seq. ID
                   LIB3148-022-Q1-K1-B6
Method
                   BLASTN
NCBI GI
                   q790507
BLAST score
                   49
E value
                   1.0e-18
Match length
                   88
% identity
                   90
NCBI Description Z.mays mRNA for 60S acidic ribosomal protein
Seq. No.
                   217771
Seq. ID
                   LIB3148-022-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1652892
BLAST score
                   317
E value
                   2.0e-36
Match length
                   128
% identity
                   33
NCBI Description (D90909) ABC transporter [Synechocystis sp.]
Seq. No.
                   217772
Seq. ID
                  LIB3148-022-Q1-K1-C3
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   38
E value
                   6.0e-12
Match length
                   50
% identity
                   40
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   217773
Seq. ID
                   LIB3148-022-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                   q1432058
BLAST score
                   178
E value
                   2.0e-18
Match length
                  127
                   53
% identity
NCBI Description (U58540) WRKY2 [Petroselinum crispum]
Seq. No.
                   217774
Seq. ID
                  LIB3148-022-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1781299
BLAST score
                  179
E value
                  3.0e-13
Match length
                  88
% identity
                   45
```

Seq. No. 217775

tabacum]

NCBI Description

(Y09506) transformer-SR ribonucleoprotein [Nicotiana

Seq. ID

Method

NCBI GI

E value

BLAST score

```
Seq. ID
                   LIB3148-022-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   g3132696
BLAST score
                   404
E value
                   3.0e-53
Match length
                   119
% identity
                   88
NCBI Description (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
Seq. No.
                   217776
Seq. ID
                   LIB3148-022-Q1-K1-E3
Method
                  BLASTN
NCBI GI
                   g2342673
BLAST score
                   44
E value
                   1.0e-15
Match length
                   64
% identity
                   92
                  Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   217777
Seq. ID
                   LIB3148-022-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                   q3169180
BLAST score
                   171
E value
                   1.0e-15
Match length
                   59
% identity
                   68
                  (AC004401) putative casein kinase II catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   217778
Seq. ID
                  LIB3148-022-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                   q3935169
BLAST score
                   313
E value
                   8.0e-29
Match length
                  68
% identity
                  88
NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]
Seq. No.
                  217779
Seq. ID
                  LIB3148-022-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  147
E value
                  2.0e-10
Match length
                  41
% identity
                  71
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  217780
```

30552

LIB3148-022-Q1-K1-F5

BLASTX

139

g3142289

3.0e-13

Seq. No.

Seq. ID

217786

LIB3148-022-Q1-K1-H9

```
Match length
                   51
% identity
                   71
NCBI Description
                   (AC002411) Strong similarity to beta-keto-Coa synthase
                   gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                   217781
Seq. ID
                   LIB3148-022-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   q2253442
BLAST score
                   137
E value
                   2.0e-15
Match length
                   61
% identity
                   62
NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]
Seq. No.
                  217782
Seq. ID
                  LIB3148-022-Q1-K1-G8
Method
                  BLASTN
NCBI GI
                  g2558961
BLAST score
                  67
E value
                   2.0e-29
Match length
                  75
% identity
                  97
NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds
Seq. No.
                  217783
Seq. ID
                  LIB3148-022-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2827082
BLAST score
                  142
E value
                  1.0e-08
Match length
                  42
% identity
                  69
NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]
Seq. No.
                  217784
                * LIB3148-022-Q1-К1-Н6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2879811
BLAST score
                  276
E value
                  7.0e-26
Match length
                  63
% identity
                  84
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
Seq. No.
                  217785
Seq. ID
                  LIB3148-022-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2245017
BLAST score
                  164
E value
                  9.0e-13
Match length
                  77
% identity
                  49
NCBI Description (Z97341) membrane protein homolog [Arabidopsis thaliana]
```



BLASTX Method NCBI GI a4567197 303 BLAST score E value 4.0e-32 124 Match length % identity 61 (AC007168) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 217787 LIB3148-023-Q1-K1-A10 Seq. ID Method BLASTX NCBI GI g3892051 BLAST score 205 3.0e-16E value Match length 50 % identity 78 (AC002330) predicted NADH dehydrogenase 24 kD subunit NCBI Description [Arabidopsis thaliana] 217788 Seq. No. LIB3148-023-Q1-K1-A11 Seq. ID BLASTX Method g2465015 NCBI GI 156 BLAST score E value 2.0e-10 Match length 128 % identity 34 NCBI Description (AJ001449) ripening-induced protein [Fragaria vesca] 217789 Seq. No. Seq. ID LIB3148-023-Q1-K1-A2 Method BLASTX NCBI GI q232029 BLAST score 201 4.0e-16 E value Match length 45 % identity 87 ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description >gi_100154_pir__S21989 translation elongation factor eEF-1 alpha chain - carrot >gi 18339 emb CAA42843 (X60302) elongation factor 1A [Daucus carota] Seq. No. 217790 LIB3148-023-Q1-K1-A5 Seq. ID Method BLASTX NCBI GI g2695925 BLAST score 301 E value 2.0e-27 77

Match length 75 % identity

NCBI Description (AJ222776) hypothetical protein [Hordeum vulgare]

Seq. No. 217791

Seq. ID LIB3148-023-Q1-K1-A6

Method BLASTX NCBI GI g3914442 BLAST score 374



E value 5.0e-36 Match length 87 % identity 82

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No. 217792

Seq. ID LIB3148-023-Q1-K1-B10

Method BLASTX
NCBI GI g3183088
BLAST score 209
E value 1.0e-16
Match length 71
% identity 56

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

(LTP) >gi_629658_pir__S47084 lipid transfer like protein -cowpea >gi_499034 emb CAA56113 (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 217793

Seq. ID LIB3148-023-Q1-K1-B4

Method BLASTX
NCBI GI g2501102
BLAST score 417
E value 4.0e-41
Match length 123
% identity 69

NCBI Description SYNTAXIN-RELATED PROTEIN KNOLLE >gi 1184165 (U39451)

syntaxin-related [Arabidopsis thaliana] >gi_1184167
(U39452) syntaxin-related [Arabidopsis thaliana]
>gi_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]

>gi_1587182_prf__2206310A syntaxin-related protein

[Arabidopsis thaliana]

Seq. No. 217794

Seq. ID LIB3148-023-Q1-K1-C10

Method BLASTX
NCBI GI g4567229
BLAST score 224
E value 2.0e-18
Match length 84
% identity 48

NCBI Description (AC007119) putative pectin methylesterase [Arabidopsis

thaliana]

Seq. No. 217795

Seq. ID LIB3148-023-Q1-K1-C5

Method BLASTX
NCBI GI g2290532
BLAST score 413
E value 2.0e-40
Match length 124
% identity 65

NCBI Description (U94748) AN11 [Petunia x hybrida]

Seq. No. 217796



```
LIB3148-023-Q1-K1-D1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4006914
 BLAST score
                    416
 E value
                    6.0e-41
                    136
 Match length
 % identity
                    62
                   (Z99708) serine C-palmitoyltransferase like protein
 NCBI Description
                    [Arabidopsis thaliana]
                    217797
 Seq. No.
 Seq. ID
                   LIB3148-023-Q1-K1-D2
 Method
                   BLASTX
                    g4539292
 NCBI GI
                    236
 BLAST score
 E value
                    3.0e-20
                    45
 Match length
                    91
 % identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
 NCBI Description
                    thaliana]
                    217798
 Seq. No.
                   LIB3148-023-Q1-K1-D5
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1174448
 BLAST score
                    423
                    1.0e-41
. E value
                    117
 Match length
                    68
 % identity
                   TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
 NCBI Description
                    (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                    (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative
                    [Arabidopsis thaliana]
                    217799
 Seq. No.
 Seq. ID
                    LIB3148-023-Q1-K1-E11
 Method
                    BLASTX
 NCBI GI
                    q3318615
 BLAST score
                    655
 E value
                    6.0e-69
 Match length
                    133
 % identity
 NCBI Description
                   (AB016065) mitochondrial phosphate transporter [Oryza
                    sativa]
 Seq. No.
                    217800
 Seq. ID
                    LIB3148-023-Q1-K1-E4
 Method
                    BLASTX
 NCBI GI
                    g3914535
 BLAST score
                    373
 E value
                    7.0e-36
 Match length
                    83
                    82
 % identity
 NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283
```

Seq. No. 217801

(AJ223363) ribosomal protein L13a [Lupinus luteus]

```
LIB3148-023-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1103318
BLAST score
                   215
E value
                   2.0e-17
Match length
                   121
                   44
% identity
NCBI Description
                   (X78818) casein kinase I [Arabidopsis thaliana]
                   >gi 2244791_emb_CAB10213.1_ (Z97336) casein kinase I
                   [Arabidopsis thaliana]
                   217802
Seq. No.
Seq. ID
                  LIB3148-023-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                   a1694976
BLAST score
                   370
E value
                   2.0e-35
Match length
                   110
                   65
% identity
NCBI Description
                  (Y09482) HMG1 [Arabidopsis thaliana]
                   >gi 2832361 emb CAA74402_ (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   217803
Seq. No.
Seq. ID
                   LIB3148-023-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   q1652104
BLAST score
                   247
E value
                   4.0e-21
Match length
                  80
                   56
% identity
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]
Seq. No.
                   217804
Seq. ID
                   LIB3148-023-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g3046693
BLAST score
                   254
E value
                   6.0e-22
Match length
                   52
                   88
% identity
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   217805
Seq. ID
                   LIB3148-023-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2924777
BLAST score
                   581
E value
                   3.0e-60
                   138
Match length
% identity
                   80
                  (ACO02334) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
```

30557

217806

LIB3148-023-Q1-K1-H2

Seq. No.

Seq. ID

% identity



```
BLASTX
Method
NCBI GI
                  q2598599
                  288
BLAST score
E value
                   7.0e - 26
                  82
Match length
% identity
                  66
NCBI Description (Y15372) MtN4 [Medicago truncatula]
                  217807
Seq. No.
                  LIB3148-023-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1762634
                   373
BLAST score
                  3.0e-52
E value
Match length
                  120
% identity
                  84
NCBI Description (U64789) AROGP2 [Lycopersicon esculentum]
                  217808
Seq. No.
Seq. ID
                  LIB3148-023-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1350983
BLAST score
                   635
E value
                   1.0e-66
Match length
                  137
% identity
                   89
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   217809
Seq. No.
Seq. ID
                   LIB3148-024-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   g3242704
BLAST score
                   242
                   2.0e-20
E value
Match length
                   65
% identity
                   66
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]
                   217810
Seq. No.
Seq. ID
                   LIB3148-024-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                   g4406384
                   178
BLAST score
E value
                   6.0e-13
Match length
                   57
% identity
                   60
NCBI Description (AF112303) serine acetyltransferase [Arabidopsis thaliana]
                   217811
Seq. No.
Seq. ID
                  LIB3148-024-Q1-K1-B6
                  BLASTX
Method
NCBI GI
                   g2267567
BLAST score
                   394
E value
                   3.0e-38
Match length
                   85
```

30558

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium



x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

217812 Seq. No. LIB3148-024-Q1-K1-C1 Seq. ID Method BLASTX NCBI GI q113515 179 BLAST score 4.0e-13 E value Match length 63 63 % identity FLORAL HOMEOTIC PROTEIN AGL5 >gi_81613_pir__E39534 floral NCBI Description homeotic protein AGL5 - Arabidopsis thaliana >gi 166596 (M55553) transcription factor [Arabidopsis thaliana] 217813 Seq. No. LIB3148-024-Q1-K1-C10 Seq. ID BLASTX Method g3273562 NCBI GI 193 BLAST score E value 1.0e-1480 Match length 42 % identity NCBI Description (AF036707) RAD6 [Candida albicans] 217814 Seq. No. LIB3148-024-Q1-K1-C12 Seq. ID

BLASTX Method NCBI GI q2911886 BLAST score 384

4.0e-37 E value 108 Match length 71 % identity

(AF047663) contains similarity to signal recognition NCBI Description particle subunit 54 (SRP54)-type domains (Pfam; SRP54, score; 71.31); partial CDS [Caenorhabditis elegans]

217815 Seq. No. LIB3148-024-Q1-K1-C2 Seq. ID Method BLASTX

NCBI GI q3702327 BLAST score 208 E value 2.0e-16 Match length 75 % identity

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 217816

LIB3148-024-Q1-K1-C3 Seq. ID

Method BLASTN q303856 NCBI GI BLAST score 44 1.0e-15 E value Match length 60 93 % identity

NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal

protein, complete cds

```
217817
Seq. No.
                  LIB3148-024-Q1-K1-C5
Seq. ID
                  BLASTN
Method
                  g2656031
NCBI GI
                  46
BLAST score
                  1.0e-16
E value
                  118
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
                  217818
Seq. No.
                  LIB3148-024-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  g2262100
NCBI GI
                  143
BLAST score
                  3.0e-09
E value
                  37
Match length
                  76
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                   217819
Seq. No.
                  LIB3148-024-Q1-K1-D2
Seq. ID
                  BLASTN
Method
                   g1928978
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
                   51
Match length
% identity
NCBI Description Vigna unguiculata phospholipase D mRNA, complete cds
                   217820
Seq. No.
                   LIB3148-024-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3426041
BLAST score
                   166
                   1.0e-11
E value
                   52
Match length
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   217821
                   LIB3148-024-Q1-K1-E1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3980416
BLAST score 417
E value 4.0e-41
Match length 121
% identity 68

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 217822

Seq. ID LIB3148-024-Q1-K1-E10

Method BLASTX NCBI GI g2129742



BLAST score 249 E value 2.0e-21 Match length 77 % identity 60

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 217823

Seq. ID LIB3148-024-Q1-K1-E2

Method BLASTX
NCBI GI g2213608
BLAST score 350
E value 4.0e-33
Match length 137
% identity 47

NCBI Description (AC000103) F21J9.2 [Arabidopsis thaliana]

Seq. No. 217824

Seq. ID LIB3148-024-Q1-K1-E3

Method BLASTX
NCBI GI g464985
BLAST score 528
E value 5.0e-54
Match length 99
% identity 98

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN

LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)

>gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating

enzyme homolog [Arabidopsis thaliana]

Seq. No. 217825

Seq. ID LIB3148-024-Q1-K1-F1

Method BLASTX
NCBI GI g4455323 463
E value 2.0e-46
Match length 144
% identity 63

NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis

thaliana]

Seq. No. 217826

Seq. ID LIB3148-024-Q1-K1-F3

Method BLASTX
NCBI GI g1245182
BLAST score 645
E value 1.0e-67
Match length 138
% identity 80

NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No. 217827

Seq. ID LIB3148-024-Q1-K1-F7



```
BLASTX
Method
NCBI GI
                  g2293288
BLAST score
                  157
                  2.0e-10
E value
                  117
Match length
                  37
% identity
                  (AF008220) YtcB [Bacillus subtilis]
NCBI Description
                  >gi 2635571 emb CAB15065 (Z99119) similar to NDP-sugar
                  epimerase [Bacillus subtilis]
                  217828
Seq. No.
Seq. ID
                  LIB3148-024-Q1-K1-G12
                  BLASTX
Method
NCBI GI
                  q485514
                  339
BLAST score
E value
                  8.0e-32
                  72
Match length
                  89
% identity
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
                  217829
Seq. No.
                  LIB3148-024-Q1-K1-G3
Seq. ID
```

Method BLASTX NCBI GI g2565305 BLAST score 480 E value 1.0e-48 Match length 98

91 % identity

NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x

Triticum sp.]

217830 Seq. No.

Seq. ID LIB3148-024-Q1-K1-G6

Method BLASTX NCBI GI q3128210 BLAST score 405 E value 1.0e-39 Match length 118 66 % identity

NCBI Description (AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi 3337378 (AC004481) putative cytochrome P450

protein [Arabidopsis thaliana]

Seq. No. 217831

LIB3148-024-Q1-K1-G8 Seq. ID

Method BLASTX q3046700 NCBI GI BLAST score 357 E value 6.0e-34 Match length 140 % identity 59

NCBI Description (AJ005261) cytidine deaminase [Arabidopsis thaliana]

> >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi 4191787 (AC005917) putative

cytidine deaminase [Arabidopsis thaliana]



```
217832
Seq. No.
Seq. ID
                   LIB3148-024-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                    q3046700
                    218
BLAST score
                    9.0e-18
E value
Match length
                    116
% identity
                    51
                    (AJ005261) cytidine deaminase [Arabidopsis thaliana]
NCBI Description
                   >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative
                    cytidine deaminase [Arabidopsis thaliana]
                    217833
Seq. No.
                   LIB3148-024-Q1-K1-H3
Seq. ID
Method
                   BLASTN
                    g2618602
NCBI GI
BLAST score
                    38
E value
                    6.0e-12
Match length
                    143
                    87
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                    217834
Seq. No.
                    LIB3148-024-Q1-K1-H5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3395432
                    195
BLAST score
E value
                    4.0e-15
Match length
                    43
                    77
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                    217835
Seq. ID
                    LIB3148-024-Q1-K1-H8
Method
                    BLASTX
NCBI GI
                    q3319882
BLAST score
                    694
E value
                    2.0e-73
Match length
                    139
% identity
NCBI Description
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                    arietinum]
Seq. No.
                    217836
Seq. ID
                    LIB3148-025-Q1-K1-A10
Method
                    BLASTX
NCBI GI
                    q3075394
BLAST score
                    376
```

E value 2.0e-36 Match length 106 73 % identity

(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description

thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

% identity

NCBI Description



```
217837
Seq. No.
                  LIB3148-025-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q3860315
NCBI GI
                  285
BLAST score
                  1.0e-25
E value
                  65
Match length
% identity
                  82
NCBI Description (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
                  217838
Seq. No.
                  LIB3148-025-Q1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  217839
Seq. No.
                  LIB3148-025-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829204
BLAST score
                  188
                  3.0e-14
E value
                  52
Match length
% identity
                  62
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  217840
                  LIB3148-025-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543868
                  330
BLAST score
E value
                  5.0e-31
                  70
Match length
% identity
                  84
NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
                  >gi 1076683 pir__B47493 H+-transporting ATP synthase (EC
                   3.6.1.34) epsilon chain - sweet potato
                  >gi 303625 dbj BAA03527 (D14700) F1-ATPase epsilon-subunit
                   [Ipomoea batatas]
Seq. No.
                   217841
                  LIB3148-025-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194124
BLAST score
                  441
E value
                   5.0e-44
Match length
                  105
```

(gb_U63725). [Arabidopsis thaliana]

(AC002062) Similar to Glycine metalloendoproteinase

NCBI Description



```
Seq. No.
                      LIB3148-025-Q1-K1-B11
Seq. ID
Method
                      BLASTX
NCBI GI
                      q464707
BLAST score
                      348
                      3.0e-33
E value
Match length
                      74
                      93
% identity
                     40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                      protein S18.A - Arabidopsis thaliana
                      >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                      [Arabidopsis thaliana] >gi_434343 emb CAA82273 (Z28701)
                      S18 ribosomal protein [Arabidopsis thaliana]
                      >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                      S18 ribosomal protein [Arabidopsis thaliana]
                     >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana FSTS cb_T21121 cb_717755 cb_717755
                      thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                      gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                      protein [Arabidopsis thaliana]
                      217843
Seq. No.
Seq. ID
                      LIB3148-025-Q1-K1-B12
Method
                      BLASTX
NCBI GI
                      q3114901
BLAST score
                      149
                      8.0e-10
E value
Match length
                      36
                      81
% identity
                      (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]
NCBI Description
                      >gi 3114905_emb CAA06709 (AJ005806) pceberh [Populus
                      balsamifera subsp. trichocarpa]
Seq. No.
                      217844
                      LIB3148-025-Q1-K1-C1
Seq. ID
Method
                      BLASTX
NCBI GI
                      q3334261
BLAST score
                      170
                      3.0e-12
E value
                      52
Match length
% identity
                      60
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
                      metallothionein-like protein [Malus domestica]
Seq. No.
                      217845
                      LIB3148-025-Q1-K1-C5
Seq. ID
                      BLASTX
Method
                      q2462761
NCBI GI
                      153
BLAST score
E value
                      3.0e-10
                      70
Match length
% identity
                      46
```

30565

(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]



```
Seq. No.
                  217846
                  LIB3148-025-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g4337210
NCBI GI
                  209
BLAST score
                  8.0e-17
E value
                  98
Match length
                   44
% identity
                  (AC006403) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   217847
                  LIB3148-025-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                   g3169180
NCBI GI
                   558
BLAST score
                   9.0e-58
E value
                   102
Match length
                   100
% identity
                  (AC004401) putative casein kinase II catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   217848
Seq. No.
                   LIB3148-025-Q1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2879811
BLAST score
                   446
                   1.0e-44
E value
                   90
Match length
                   94
% identity
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
                   217849
Seq. No.
                   LIB3148-025-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2626840
BLAST score
                   189
                   2.0e-14
E value
                   93
Match length
                   41
% identity
                   (D89729) CRM1 protein [Homo sapiens]
NCBI Description
                   >gi_4507943_ref_NP_003391.1_pXP01_ exportin 1 (CRM1, yeast,
                   homolog)
                   217850
Seq. No.
                   LIB3148-025-Q1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629864
BLAST score
                   152
                   3.0e-10
E value
Match length
                   72
                   60
% identity
                   histone H2B - garden asparagus >gi_563329_emb_CAA57778_
NCBI Description
```

Seq. No. 217851 Seq. ID LIB3148-025-Q1-K1-E4

30566

(X82362) histone 2B [Asparagus officinalis]



```
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                  416
E value
                  5.0e-41
Match length
                  95
                  86
% identity
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
```

alpha-5 tubulin [Arabidopsis thaliana]
Seq. No. 217852

Seq. ID LIB3148-025-Q1-K1-E8 Method BLASTX NCBI GI g4335751 BLAST score 257 E value 2.0e-22 Match length 84 % identity 52

NCBI Description (AC006284) putative methyltransferase [Arabidopsis

thaliana]

Seq. No. 217853

Seq. ID LIB3148-025-Q1-K1-F10

Method BLASTX
NCBI GI g3193303
BLAST score 303
E value 8.0e-28
Match length 88
% identity 68

NCBI Description (AF069298) sim

(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 217854

Seq. ID LIB3148-025-Q1-K1-F4

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 37

% identity 61

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 217855

Seq. ID LIB3148-025-Q1-K1-F8

Method BLASTX
NCBI GI g3122703
BLAST score 299
E value 2.0e-27
Match length 82
% identity 73

NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal

protein L23a [Fritillaria agrestis]

Seq. No. 217856



```
LIB3148-025-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                  g3548802
NCBI GI
BLAST score
                  185
E value
                   6.0e-14
                  106
Match length
                  40
% identity
                   (ACO05313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                  217857
Seq. No.
                  LIB3148-025-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  q2388565
NCBI GI
BLAST score
                  182
                  1.0e-13
E value
                  76
Match length
                  45
% identity
                  (AC000098) Similar to Prunus pectinesterase (gb X95991).
NCBI Description
                   [Arabidopsis thaliana]
                  217858
Seq. No.
                  LIB3148-025-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  428
                  2.0e-42
E value
                  100
Match length
                   77
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                   >gi_2129500_pir__S52006 polygalacturonase - upland cotton
                  >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                   217859
Seq. ID
                  LIB3148-025-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                   q3549670
BLAST score
                   257
                   2.0e-22
E value
                   66
Match length
% identity
                   70
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                   217860
Seq. No.
                  LIB3148-025-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3068704
BLAST score
                   444
E value
                   2.0e-44
Match length
                  104
                   78
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
```

Seq. No. 217861

Seq. ID LIB3148-025-Q1-K1-G8

Method BLASTX



```
NCBI GI
                  g2781345
BLAST score
                  168
E value
                  5.0e-12
                  97
Match length
% identity
                  44
NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]
                  217862
Seq. No.
Seq. ID
                  LIB3148-025-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q114682
BLAST score
                  276
E value
                  1.0e-24
Match length
                  95
% identity
                  60
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi_168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                  217863
Seq. ID
                  LIB3148-025-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q3687234
BLAST score
                  137
E value
                  1.0e-08
Match length
                  45
% identity
NCBI Description (AC005169) putative copia-like transposable element
                   [Arabidopsis thaliana]
Seq. No.
                   217864
Seq. ID
                  LIB3148-025-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q2160189
BLAST score
                  243
E value
                  8.0e-21
Match length
                  79
% identity
                  54
                  (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb RLK5 ARATH). ESTs gb ATTS0475, gb ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                  217865
Seq. ID
                  LIB3148-025-Q1-K1-H8
                  BLASTX
Method
```

NCBI GI g1621268 BLAST score 166 E value 8.0e-12 43 Match length 72 % identity

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 217866

Seq. ID LIB3148-026-Q1-K1-A12



```
Method
                  BLASTN
NCBI GI
                  q2687434
BLAST score
                  275
E value
                  1.0e-153
                  319
Match length
                  97
% identity
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                  partial sequence
                  217867
Seq. No.
                  LIB3148-026-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157927
                   514
BLAST score
E value
                  2.0e-52
                  134
Match length
% identity
                   75
                   (AC002131) Contains similarity to GDP-dissociation
NCBI Description
                   inhibitor gb_L07918 from Mus musculus. [Arabidopsis
                  thaliana]
                   217868
Seq. No.
Seq. ID
                  LIB3148-026-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3128177
BLAST score
                   504
                   3.0e-51
E value
Match length
                  120
                   82
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
                  217869
Seq. No.
                  LIB3148-026-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1363487
BLAST score
                   473
E value
                   1.0e-47
                   98
Match length
                   91
% identity
NCBI Description IAA7 protein - Arabidopsis thaliana >gi 972917 (U18409)
                   IAA7 [Arabidopsis thaliana]
Seq. No.
                   217870
Seq. ID
                   LIB3148-026-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                   g2618721
BLAST score
                   221
E value
                   9.0e-21
Match length
                  76
% identity
                   61
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
```

217871 Seq. No.

Seq. ID LIB3148-026-Q1-K1-C12

Method BLASTX NCBI GI g586339 BLAST score 383



```
5.0e-37
E value
Match length
                  121
                  57
% identity
                 PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098
NCBI Description
                  probable AMP-binding protein - yeast (Saccharomyces
                  cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c
                  [Saccharomyces cerevisiae]
                  217872
Seq. No.
                  LIB3148-026-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g3264763
NCBI GI
                  297
BLAST score
                  2.0e-33
E value
                  118
Match length
% identity
                  66
                 (AF071891) 40S ribosomal protein S4 [Prunus armeniaca]
NCBI Description
                  217873
Seq. No.
                  LIB3148-026-Q1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2190012
BLAST score
                  239
                  4.0e-20
E value
                  76
Match length
                  64
% identity
NCBI Description (AB004242) din1 [Raphanus sativus]
                  217874
Seq. No.
                  LIB3148-026-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g1345965
NCBI GI
                  223
BLAST score
                  2.0e-18
E value
                  55
Match length
                  75
% identity
NCBI Description FLORAL HOMEOTIC PROTEIN FBP2 (FLORAL BINDING PROTEIN 2)
                  >gi 1181186 (M91666) transcription factor [Petunia hybrida]
                  217875
Seq. No.
Seq. ID
                  LIB3148-026-Q1-K1-D1
Method
                  BLASTX
                  g3493367
NCBI GI
                   364
BLAST score
                   7.0e-35
E value
Match length
                  73
% identity
NCBI Description (AB017159) citrate synthase [Daucus carota]
                   217876
Seq. No.
Seq. ID
                   LIB3148-026-Q1-K1-D2
```

Method BLASTX NCBI GI g2506139 BLAST score 165 1.0e-11 E value 55 Match length % identity 65



NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 217877

Seq. ID LIB3148-026-Q1-K1-D3

Method BLASTX
NCBI GI g1483150
BLAST score 596
E value 6.0e-62
Match length 140
% identity 79

NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis

thaliana]

Seq. No. 217878

Seq. ID LIB3148-026-Q1-K1-D6

Method BLASTN
NCBI GI g169712
BLAST score 50
E value 4.0e-19
Match length 90
% identity 89

NCBI Description Ricinus communis metallothionein (RCMIT) mRNA, complete cds

Seq. No. 217879

Seq. ID LIB3148-026-Q1-K1-E4

Method BLASTX
NCBI GI g2444178
BLAST score 225
E value 7.0e-23
Match length 107
% identity 55

NCBI Description (U94784) unconventional myosin [Helianthus annuus]

Seq. No. 217880

Seq. ID LIB3148-026-Q1-K1-F10

Method BLASTX
NCBI GI g3540181
BLAST score 209
E value 1.0e-16
Match length 116
% identity 43

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 217881

Seq. ID LIB3148-026-Q1-K1-F2

Method BLASTX
NCBI GI 94056489
BLAST score 552
E value 9.0e-57
Match length 129
% identity 73

NCBI Description (AC005896) putative white protein [Arabidopsis thaliana]

Seq. No. 217882

Seq. ID LIB3148-026-Q1-K1-F4

Method

NCBI GI

BLAST score

BLASTX

145

g2407800

```
Method
                  BLASTX
NCBI GI
                  q3522933
BLAST score
                  476
                  6.0e-48
E value
Match length
                  134
                  66
% identity
                  (AC004411) putative anion exchange protein 3 [Arabidopsis
NCBI Description
                  thaliana]
                  217883
Seq. No.
                  LIB3148-026-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1246823
                  211
BLAST score
                  8.0e-17
E value
Match length
                  61
                  67
% identity
                 (X89865) unknown [Phoenix dactylifera]
NCBI Description
                  217884
Seq. No.
                  LIB3148-026-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710530
BLAST score
                  685
E value
                  2.0e-72
                  140
Match length
% identity
                  88
                 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
                  217885
Seq. No.
                  LIB3148-026-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2565275
BLAST score
                  226
                  9.0e-19
E value
Match length
                  57
                  77
% identity
NCBI Description (AF023611) Dimlp homolog [Homo sapiens]
                  217886
Seq. No.
Seq. ID
                  LIB3148-026-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3413167
BLAST score
                  184
E value
                  8.0e-14
Match length
                  70
% identity
NCBI Description (AJ010225) elongation factor 1-alpha [Cicer arietinum]
                   217887
Seq. No.
                  LIB3148-026-Q1-K1-H12
Seq. ID
```



E value 1.0e-09 Match length 32 % identity 88 NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana] 217888 Seq. No. Seq. ID LIB3148-026-Q1-K1-H2 Method BLASTX NCBI GI q4455207 BLAST score 419 E value 3.0e-41Match length 91 % identity 89 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana] 217889 Seq. No. Seq. ID LIB3148-026-Q1-K1-H6 Method BLASTX NCBI GI g479713 BLAST score 344 E value 2.0e-32 Match length 76 % identity 87 NCBI Description aspartate carbamoyltransferase - tomato Seq. No. 217890 Seq. ID LIB3148-026-Q1-K1-H7 Method BLASTX NCBI GI q1944319 BLAST score 260 E value 1.0e-22 Match length 92 55 % identity NCBI Description. (D31700) cysteine proteinase inhibitor [Glycine max] >gi_1944342_dbj_BAA19610_ (D64115) cysteine proteinase inhibitor [Glycine max] 217891 Seq. No. Seq. ID LIB3148-027-Q1-K1-A5 Method BLASTX NCBI GI g4567285

BLAST score 231 E value 3.0e-19

Match length 54 % identity 81

NCBI Description (AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No. 217892

Seq. ID LIB3148-027-Q1-K1-B8

Method BLASTX NCBI GI g3980401 BLAST score 276 2.0e-24 E value Match length 97 % identity 53

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No.

Seq. ID Method

217898

BLASTX

LIB3148-027-Q1-K1-D1



```
217893
Seq. No.
Seq. ID
                  LIB3148-027-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                   433
E value
                   7.0e-43
Match length
                  87
% identity
                   52
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  217894
Seq. ID
                  LIB3148-027-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                   q4115377
BLAST score
                   359
E value
                   2.0e-34
Match length
                  112
% identity
                   59
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   217895
                  LIB3148-027-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3482967
BLAST score
                   576
E value
                   1.0e-59
Match length
                   133
% identity
                   80
NCBI Description
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
                   thaliana] >gi 4559345 gb AAD23006.1 AC006585 1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
                   217896
Seq. No.
Seq. ID
                  LIB3148-027-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                   q3413170
BLAST score
                   151
E value
                   5.0e-10
Match length
                   81
                   55
% identity
NCBI Description (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]
Seq. No.
                   217897
Seq. ID
                  LIB3148-027-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q2982249
BLAST score
                   162
E value
                   3.0e-11
Match length
                   53
% identity
NCBI Description
                  (AF051207) probable 60S ribosomal protein L15 [Picea
                  mariana]
```



```
NCBI GI
                  g3892051
BLAST score
                  319
                  1.0e-29
E value
Match length
                  74
% identity
                  80
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  217899
Seq. ID
                  LIB3148-027-Q1-K1-D11
Method
                  BLASTX
                  g1808656
NCBI GI
                  276
BLAST score
E value
                  2.0e-24
Match length
                  78
% identity
                  67
NCBI Description (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]
                  217900
Seq. No.
Seq. ID
                  LIB3148-027-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q3860317
BLAST score
                  268
E value
                  1.0e-23
Match length
                  57
                  89
% identity
NCBI Description (AJ012685) actin [Cicer arietinum]
                  217901
Seq. No.
                  LIB3148-027-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q684942
BLAST score
                  146
                  1.0e-09
E value
Match length
                  29
% identity
                  90
NCBI Description
                  (U20736) S-adenosyl-L-methionine:trans-caffeoyl-CoA
                  3-O-methyltransferase [Medicago sativa subsp. sativa]
Seq. No.
                  217902
Seq. ID
                  LIB3148-027-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1708191
BLAST score
                  492
E value
                  7.0e-50
Match length
                  123
% identity
                  69
NCBI Description HEXOSE CARRIER PROTEIN HEX6 > gi 467319 (L08188) hexose
                  carrier protein [Ricinus communis]
Seq. No.
                  217903
Seq. ID
                  LIB3148-027-Q1-K1-E12
Method
                  BLASTN
NCBI GI
                  g2832667
BLAST score
                  40
```

30576

τç...

E value

Match length

4.0e-13



% identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project) 217904 Seq. No. Seq. ID LIB3148-027-Q1-K1-E7 Method BLASTX NCBI GI g1906830 BLAST score 445 E value 2.0e-44 Match length 127 % identity 69 NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana] Seq. No. 217905 Seq. ID LIB3148-027-Q1-K1-E9 Method BLASTX NCBI GI g625509 BLAST score 546 E value 3.0e-56 Match length 112 % identity 25 NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment) Seq. No. 217906 Seq. ID LIB3148-027-Q1-K1-F1 Method BLASTN NCBI GI q16172 BLAST score 51 E value 9.0e-20 Match length 119 % identity 86 NCBI Description A.thaliana mRNA for ascorbate peroxidase Seq. No. 217907 Seq. ID LIB3148-027-Q1-K1-F11 Method BLASTX NCBI GI g2462754 BLAST score 241 2.0e-20 E value Match length 121 % identity 47 NCBI Description (AC002292) Unknown protein [Arabidopsis thaliana] Seq. No. 217908 Seq. ID LIB3148-027-Q1-K1-F12 Method BLASTX NCBI GI g3128209 BLAST score 235

1.0e-19 E value Match length 55 75 % identity

NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 217909

Seq. ID LIB3148-027-Q1-K1-F8

Method BLASTX

NCBI GI

E value

BLAST score

g4006877

6.0e-27

297



```
NCBI GI
                   q2341031
BLAST score
                   342
E value
                   6.0e-46
Match length
                   101
                   92
% identity
                  (AC000104) F19P19.10 [Arabidopsis thaliana]
NCBI Description
                  217910
Seq. No.
Seq. ID
                  LIB3148-027-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                   q4220462
BLAST score
                   243
                   9.0e-21
E value
Match length
                   48
                   90
% identity
                   (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
NCBI Description
                   gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF 00170 domains. [Arabidopsis thaliana]
Seq. No.
                   217911
                  LIB3148-027-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2827710
BLAST score
                   409
                   4.0e-40
E value
Match length
                   92
                   74
% identity
                  (AL021684) lysosomal Pro-X carboxypeptidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   217912
Seq. ID
                  LIB3148-027-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g1296816
BLAST score
                   538
E value
                   3.0e-55
Match length
                   110
% identity
                   94
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]
Seq. No.
                   217913
Seq. ID
                  LIB3148-027-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                   g4106515
BLAST score
                   504
E value
                   2.0e-51
Match length
                  112
% identity
                  (AF092743) CAK associated cyclinH homolog [Populus tremula
NCBI Description
                  x Populus tremuloides]
                   217914
Seq. No.
Seq. ID
                  LIB3148-027-Q1-K1-G7
                  BLASTX
Method
```



Match length 82 % identity

NCBI Description (Z99707) RNA-binding like protein [Arabidopsis thaliana]

217915 Seq. No.

LIB3148-027-Q1-K1-H11 Seq. ID

Method BLASTX NCBI GI g3913423 BLAST score 236 5.0e-20 E value Match length 68 % identity 68

S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) NCBI Description

(SAMDC) >gi_1917013 (U91924) S-adenosylmethionine

decarboxylase [Nicotiana tabacum]

217916 Seq. No.

Seq. ID LIB3148-028-Q1-K1-A7

Method BLASTX NCBI GI q2118183 BLAST score 626 E value 1.0e-65 Match length 129 % identity 99

NCBI Description inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating

(clone TVP17), vacuolar membrane - common tobacco (fragment) >gi_790475_emb_CAA58699_ (X83728) inorganic

pyrophosphatase [Nicotiana tabacum]

Seq. No. 217917

Seq. ID LIB3148-028-Q1-K1-B1

Method BLASTX NCBI GI g2462759 BLAST score 360 E value 3.0e - 34Match length 74 % identity

NCBI Description (AC002292) Putative Cytochrome B5 [Arabidopsis thaliana]

Seq. No. 217918

Seq. ID LIB3148-028-Q1-K1-B12

Method BLASTX NCBI GI g82200 BLAST score 502 E value 6.0e-51 Match length 122 77 % identity

NCBI Description hypothetical protein 1244 - common tobacco chloroplast

217919 Seq. No.

Seq. ID LIB3148-028-Q1-K1-C10

Method BLASTX NCBI GI g3355471 BLAST score 373 E value 8.0e-36 Match length 108 % identity 67



```
(AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                  thaliana]
                  217920
Seq. No.
Seq. ID
                  LIB3148-028-Q1-K1-C12
Method
                  BLASTX
                  g2632252
NCBI GI
                  217
BLAST score
                  2.0e-17
E value
                  64
Match length
                  64
% identity
                  (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
Seq. No.
                  217921
                  LIB3148-028-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1766048
                  382
BLAST score
                  7.0e-37
E value
                  91
Match length
                  86
% identity
                  (U81994) NAD+ dependent isocitrate dehydrogenase subunit 2
NCBI Description
                   [Arabidopsis thaliana]
                  217922
Seq. No.
                  LIB3148-028-Q1-K1-C9
Seq. ID
Method
                  BLASTX
                  g2706450
NCBI GI
                  355
BLAST score
E value
                   1.0e-33
Match length
                  79
% identity
                  84
                  (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                  pyrophosphatase [Solanum tuberosum]
Seq. No.
                  217923
Seq. ID
                  LIB3148-028-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                   q633678
BLAST score
                   273
E value
                   3.0e-24
Match length
                   58
                   93
% identity
NCBI Description (X83500) ADP-glucose pyrophosphorylase [Spinacia oleracea]
                   217924
Seq. No.
Seq. ID
                   LIB3148-028-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g1565225
BLAST score
                   268
E value
                   2.0e-23
Match length
                   127
                   48
% identity
                  (X95572) salt-tolerance protein [Arabidopsis thaliana]
NCBI Description
```

30580

217925

LIB3148-028-Q1-K1-E1

Seq. No.

Seq. ID

Match length

% identity

47

47



```
Method
                    BLASTX
  NCBI GI
                    q4204265
  BLAST score
                    172
 E value
                    3.0e-12
 Match length
                    137
                    38
  % identity
 NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
  Seq. No.
                    217926
  Seq. ID
                    LIB3148-028-Q1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    q3868758
  BLAST score
                    560
                    8.0e-58
 E value
 Match length
                    112
  % identity
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
 Seq. No.
                    217927
 Seq. ID
                    LIB3148-028-Q1-K1-E6
 Method
                    BLASTX
 NCBI GI
                    g3885327
 BLAST score
                    297
 E value
                    7.0e-27
 Match length
                    69
  % identity
                    75
 NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
                    217928
  Seq. No.
                    LIB3148-028-Q1-K1-F1
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    g3402672
  BLAST score
                    573
  E value
                    3.0e-59
  Match length
                    131
  % identity
  NCBI Description (AC004697) putative white protein [Arabidopsis thaliana]
  Seq. No.
                    217929
                    LIB3148-028-Q1-K1-F10
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g2687434
  BLAST score
                    173
                    1.0e-92
  E value
  Match length
                    209
  % identity
                    96
  NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                    partial sequence
                    217930
  Seq. No.
  Seq. ID
                    LIB3148-028-Q1-K1-F11
  Method
                    BLASTX
  NCBI GI
                    g4558678
BLAST score
                    145
  E value
                    5.0e-09
```



(AC006586) unknown protein [Arabidopsis thaliana] NCBI Description 217931 Seq. No. LIB3148-028-Q1-K1-G1 Seq. ID Method BLASTX g1781330 NCBI GI BLAST score 206 2.0e-16 E value 64 Match length 58 % identity (Y10466) peroxidase [Spinacia oleracea] NCBI Description 217932 Seq. No. LIB3148-028-Q1-K1-H10 Seq. ID BLASTX Method g3193297 NCBI GI 277 BLAST score E value 7.0e-25 80 Match length 57 % identity (AF069298) similar to epoxide hydrolases [Arabidopsis NCBI Description thaliana] 217933 Seq. No. LIB3148-028-Q1-K1-H5 Seq. ID Method BLASTN NCBI GI q4454731 BLAST score 34 1.0e-09 E value 38 Match length 97 % identity NCBI Description Psychotria berteriana 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence Seq. No. 217934 Seq. ID LIB3148-028-Q1-K1-H9 Method BLASTX NCBI GI q1402883 BLAST score 282 E value 4.0e-25 135 Match length 17 % identity (X98130) unknown [Arabidopsis thaliana] NCBI Description >gi_1495263_emb_CAA66119_ (X97487) orf09 [Arabidopsis thaliana]

Seq. No. 217935

LIB3148-029-Q1-K1-A11 Seq. ID

Method BLASTX NCBI GI q2921213 BLAST score 452 E value 4.0e-45 Match length 99 89 % identity

NCBI Description (AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla

Seq. ID



frutescens]

```
217936
Seq. No.
Seq. ID
                  LIB3148-029-Q1-K1-A2
Method
                  BLASTN
NCBI GI
                  g4139263
BLAST score
                  46
E value
                  5.0e-17
Match length
                  66
                  92
% identity
NCBI Description Brassica napus actin mRNA, complete cds
                  217937
Seq. No.
Seq. ID
                  LIB3148-029-Q1-K1-A9
Method
                  BLASTN
NCBI GI
                  g12292
BLAST score
                  165
                  1.0e-87
E value
Match length
                  255
% identity
                  93
NCBI Description Spinach chloroplast DNA homologous to ARS and ARC elements
                  upstream of rDNA operon
Seq. No.
                  217938
                  LIB3148-029-Q1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618602
BLAST score
                  39
E value
                  1.0e-12
Match length
                  59
% identity
                  92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  217939
Seq. ID
                  LIB3148-029-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3738320
BLAST score
                  371
E value
                  1.0e-35
Match length
                  96
                  77
% identity
NCBI Description
                  (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
                  thaliana]
Seq. No.
                  217940
Seq. ID
                  LIB3148-029-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                  g1945439
BLAST score
                  41
E value
                  7.0e-14
Match length
                  65
% identity
                  91
NCBI Description Medicago sativa salt-inducible protein mRNA, partial cds
Seq. No.
                  217941
```

LIB3148-029-Q1-K1-B3



```
Method
                  BLASTX
NCBI GI
                  g3608481
BLAST score
                  196
                  2.0e-15
E value
Match length
                  43
                  95
% identity
NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]
Seq. No.
                  217942
Seq. ID
                  LIB3148-029-Q1-K1-C11
                  BLASTX
Method
NCBI GI
                  q3334261
BLAST score
                  198
E value
                  2.0e-15
Match length
                  46
                  72
% identity
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
                  metallothionein-like protein [Malus domestica]
Seq. No.
                  217943
Seq. ID
                  LIB3148-029-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2245034
BLAST score
                  178
E value
                  3.0e-13
Match length
                  47
                  70
% identity
NCBI Description (Z97342) enoyl-CoA hydratase [Arabidopsis thaliana]
Seq. No.
                  217944
Seq. ID
                  LIB3148-029-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3297815
BLAST score
                  496
E value
                  5.0e-51
Match length
                  139
                  73
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  217945
Seq. ID
                  LIB3148-029-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g3096935
BLAST score
                  226
E value
                  1.0e-18
                  92
Match length
                  58
% identity
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]
```

Seq. No. 217946

Seq. ID LIB3148-029-Q1-K1-C9

Method BLASTX
NCBI GI g2244835
BLAST score 548
E value 2.0e-56
Match length 118
% identity 79



```
(Z97337) protein kinase homolog [Arabidopsis thaliana]
NCBI Description
                  217947
Seq. No.
                  LIB3148-029-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760836
                  440
BLAST score
                  9.0e-44
E value
                  124
Match length
                  69
% identity
                  (AC003105) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  217948
Seq. No.
                  LIB3148-029-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g730450
NCBI GI
                  340
BLAST score
                  3.0e - 32
E value
                  88
Match length
                  74
% identity
                  60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                  >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
                  >gi 398922 emb CAA80343 (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
Seq. No.
                  217949
                  LIB3148-029-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g872116
NCBI GI
BLAST score
                   646
                   8.0e-68
E value
                  143
Match length
                   33
% identity
NCBI Description (X79770) sti (stress inducible protein) [Glycine max]
Seq. No.
                   217950
                   LIB3148-029-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4417304
BLAST score
                   431
E value
                   1.0e-42
Match length
                   143
                   54
% identity
                   (AC006446) putative beta-1,4-mannosyl-glycoprotein
NCBI Description
                   beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   217951
                   LIB3148-029-Q1-K1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
                   33
BLAST score
                   5.0e-09
E value
```

% identity 58
NCBI Description Xenopus laevis cDNA clone 27A6-1

33

Match length



```
Seq. No.
                  217952
Seq. ID
                  LIB3148-029-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1840425
BLAST score
                  143
                  7.0e-09
E value
Match length
                  36
% identity
                  67
                  (U36586) alcohol dehydrogenase [Vitis vinifera]
NCBI Description
Seq. No.
                  217953
                  LIB3148-029-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3063396
                  500
BLAST score
                  1.0e-50
E value
                  117
Match length
% identity
                  81
NCBI Description
                 (AB012947) vcCyP [Vicia faba]
                  217954
Seq. No.
Seq. ID
                  LIB3148-029-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2511535
BLAST score
                  588
                  5.0e-61
E value
                  120
Match length
                   93
% identity
NCBI Description (AF008122) alpha-tubulin 3 [Eleusine indica]
Seq. No.
                  217955
                  LIB3148-029-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3236254
BLAST score
                  353
                   2.0e-33
E value
Match length
                  112
% identity
                   62
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                  217956
Seq. No.
Seq. ID
                  LIB3148-029-Q1-K1-G4
                  BLASTX
Method
NCBI GI
                  g3337365
BLAST score
                  187
E value
                   5.0e-14
                  75
Match length
% identity
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]
                  217957
Seq. No.
```

Seq. ID LIB3148-029-Q1-K1-G5

Method BLASTX
NCBI GI g4508079
BLAST score 222
E value 3.0e-18

```
Match length
                  56
% identity
                   68
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]
Seq. No.
                  217958
Seq. ID
                  LIB3148-029-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1769898
BLAST score
                  145
E value
                  3.0e-09
Match length
                  61
% identity
                  49
NCBI Description (Y08010) lectin receptor kinase [Arabidopsis thaliana]
Seq. No.
                  217959
Seq. ID
                  LIB3148-029-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3152606
BLAST score
                  192
E value
                  7.0e-15
Match length
                  58
% identity
                  64
NCBI Description (AC004482) putative ring zinc finger protein [Arabidopsis
                  thaliana]
                  217960
Seq. No.
Seq. ID
                  LIB3148-029-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2760320
BLAST score
                  414
E value
                  1.0e-40
Match length
                  142
% identity
                  57
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                  217961
Seq. ID
                  LIB3148-029-Q1-K1-H3
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  217962
Seq. No.
Seq. ID
                  LIB3148-029-Q1-K1-H8
```

Method BLASTX
NCBI GI g3759184
BLAST score 159
E value 7.0e-11
Match length 60
% identity 45

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 217963

Seq. ID LIB3148-029-Q1-K1-H9



Method BLASTX
NCBI GI g1480012
BLAST score 313
E value 8.0e-29
Match length 59
% identity 98
NCBI Description (D78492)
rapa]

NCBI Description (D78492) putative ubiquitin extension protein [Brassica

Seq. No. 217964

Seq. ID LIB3148-030-Q1-K1-A1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 37
% identity 61

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 217965

Seq. ID LIB3148-030-Q1-K1-A12

Method BLASTN
NCBI GI g2618602
BLAST score 38
E value 6.0e-12
Match length 77
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 217966

Seq. ID LIB3148-030-Q1-K1-B11

Method BLASTX
NCBI GI g2244835
BLAST score 437
E value 1.0e-43
Match length 98
% identity 78

NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 217967

Seq. ID LIB3148-030-Q1-K1-B8

Method BLASTX
NCBI GI g2815246
BLAST score 225
E value 2.0e-18
Match length 55
% identity 73

NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No. 217968

Seq. ID LIB3148-030-Q1-K1-B9

Method BLASTX
NCBI GI g1255954
BLAST score 197
E value 3.0e-15
Match length 59



```
% identity
NCBI Description (Z70677) thioredoxin [Ricinus communis]
Seq. No.
                  217969
Seq. ID
                  LIB3148-030-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4415926
BLAST score
                  191
E value
                  1.0e-14
Match length
                  51
% identity
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.
                  217970
Seq. ID
                  LIB3148-030-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2984119
BLAST score
                  180
E value
                  3.0e-13
Match length
                  71
% identity
                  45
NCBI Description
                 (AE000758) peptide chain release factor RF-2 [Aquifex
                  aeolicus]
Seq. No.
                  217971
Seq. ID
                  LIB3148-030-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q82426
BLAST score
                  533
E value
                  1.0e-54
Match length
                  108
% identity
                  46
                  ubiquitin precursor - barley (fragment)
NCBI Description
                  >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
Seq. No.
                  217972
Seq. ID
                  LIB3148-030-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1709453
BLAST score
                  160
E value
                  6.0e-11
Match length
                  41
                  73
% identity
NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
                  PRECURSOR (PDHE1-A) >gi 473169 emb CAA81558 (Z26949) E1
                  alpha subunit of pyruvate dehydrogenase precursor [Solanum
                  tuberosum]
Seq. No.
                  217973
Seq. ID
                  LIB3148-030-Q1-K1-C8
```

BLASTX Method NCBI GI g2262159 BLAST score 278 1.0e-24 E value Match length 85 % identity 64



```
(AC002329) predicted protein similar to S.pombe protein
NCBI Description
                  C5H10.03 [Arabidopsis thaliana]
Seq. No.
                  217974
                  LIB3148-030-Q1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244835
                  452
BLAST score
E value
                  4.0e-45
                  112
Match length
                  71
% identity
NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
                  217975
Seq. No.
                  LIB3148-030-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1914683
                  302
BLAST score
                  2.0e-27
E value
Match length
                  80
% identity
                  76
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
                  217976
Seq. No.
                  LIB3148-030-Q1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062705
                  33
BLAST score
                   6.0e-09
E value
Match length
                  37
% identity
                  59
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  217977
Seq. No.
Seq. ID
                  LIB3148-030-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                   g2833375
BLAST score
                  184
E value
                   9.0e-14
                  39
Match length
% identity
                   90
                  DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)
NCBI Description
                   (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II
                   subunit RPB10 homolog; similar to yeast RNA polymerase II
                   subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica
                  napus]
                   217978
Seq. No.
                  LIB3148-030-Q1-K1-D5
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g485514
BLAST score 390
E value 8.0e-38
Match length 79
% identity 91

NCBI Description ADR11-2 protein - soybean (fragment)

>gi 296443 emb CAA49341 (X69640) auxin down regulated



[Glycine max]

 Seq. No.
 217979

 Seq. ID
 LIB3148-030-Q1-K1-D7

 Method
 BLASTX

 NCBI GI
 g3152587

NCBI GI g3152587 BLAST score 501 E value 8.0e-51 Match length 139 % identity 71

NCBI Description (AC002986) Similar to CREB-binding protein homolog

gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No. 217980

Seq. ID LIB3148-030-Q1-K1-D9

Method BLASTX
NCBI GI g1916290
BLAST score 231
E value 3.0e-19
Match length 103
% identity 47

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 217981

Seq. ID LIB3148-030-Q1-K1-E11

Method BLASTX
NCBI GI g1694976
BLAST score 373
E. value 8.0e-36

E value 8.0e-36 Match length 81 % identity 84

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 217982

Seq. ID LIB3148-030-Q1-K1-E5

Method BLASTX
NCBI GI g2982247
BLAST score 178
E value 6.0e-13
Match length 57
% identity 56

NCBI Description (AF051206) probable thioredoxin H [Picea mariana]

Seq. No. 217983

Seq. ID LIB3148-030-Q1-K1-E6

Method BLASTX
NCBI GI 94220521
BLAST score 215
E value 2.0e-17
Match length 58
% identity 72

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]



Seq. No. 217984 Seq. ID

LIB3148-030-Q1-K1-E8

Method BLASTX NCBI GI g2760830 BLAST score 593 E value 1.0e-61 Match length 131 % identity 88

NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 217985

Seq. ID LIB3148-030-Q1-K1-F2

Method BLASTX NCBI GI q3786008 BLAST score 307 E value 4.0e-28 Match length 120 53 % identity

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

217986 Seq. No.

Seq. ID LIB3148-030-Q1-K1-F5

Method BLASTN NCBI GI q2687439 BLAST score 40 E value 3.0e-13

Match length 40 % identity 100

NCBI Description Peltoboykinia tellimoides large subunit 26S ribosomal RNA

gene, partial sequence

Seq. No. 217987

Seq. ID LIB3148-030-Q1-K1-G11

Method BLASTX NCBI GI g3451075 BLAST score 204 4.0e-16 E value 63 Match length

% identity 59

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 217988

Seq. ID LIB3148-030-Q1-K1-G4

Method BLASTX NCBI GI g1169534 BLAST score 377 E value 3.0e-36 78 Match length % identity 94

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 542019 pir \$39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus

communis]

Seq. No. 217989



Seq. ID LIB3148-030-Q1-K1-G7 Method BLASTX NCBI GI q2642648 BLAST score 605 E value 5.0e-63 Match length 137 87 % identity NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea] 217990 Seq. No. Seq. ID LIB3148-030-Q1-K1-G8 Method BLASTX NCBI GI q643469 BLAST score 321 E value 1.0e-29 Match length 87 % identity 68 NCBI Description (U19886) unknown [Lycopersicon esculentum] Seq. No. 217991 Seq. ID LIB3148-030-Q1-K1-H11 Method BLASTX NCBI GI q543905 BLAST score 664 6.0e-70E value Match length 131 95 % identity NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >qi 347459 (L22162) brassinosteroid-regulated protein [Glycine max] Seq. No. 217992 Seq. ID LIB3148-030-Q1-K1-H3 Method BLASTX NCBI GI q4455225 BLAST score 217 E value 4.0e-18 Match length 46 % identity 85 NCBI Description (AL035440) putative protein [Arabidopsis thaliana] Seq. No. 217993 Seq. ID LIB3148-030-Q1-K1-H4 Method BLASTX NCBI GI q4455225 BLAST score 494

E value 5.0e-50 Match length 136 % identity 68

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 217994

Seq. ID LIB3148-030-Q1-K1-H8

Method BLASTX NCBI GI g3834310



BLAST score 672 E value 7.0e-71 Match length 131 % identity 100

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No. 217995

Seq. ID LIB3148-031-Q1-K1-A10

Method BLASTX
NCBI GI g2511574
BLAST score 422
E value 8.0e-42
Match length 89
% identity 97

NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis

thaliana] >gi_3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 217996

Seq. ID LIB3148-031-Q1-K1-A11

Method BLASTX
NCBI GI g3914360
BLAST score 436
E value 3.0e-43
Match length 89
% identity 88

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_2072351 (U96438) phospholipase D [Pimpinella

brachycarpa]

Seq. No. 217997

Seq. ID LIB3148-031-Q1-K1-A2

Method BLASTX
NCBI GI g3043428
BLAST score 311
E value 9.0e-35
Match length 116
% identity 75

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 217998

Seq. ID LIB3148-031-Q1-K1-A5

Method BLASTX
NCBI GI 9464986
BLAST score 288
E value 4.0e-26
Match length 56
% identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating



enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

217999 Seq. No. LIB3148-031-Q1-K1-A6 Seq. ID BLASTX Method NCBI GI g3176725 BLAST score 183 5.0e-19 E value 70 Match length 53 % identity

NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]

Seq. No. 218000

Seq. ID LIB3148-031-Q1-K1-A7

Method BLASTX
NCBI GI 94539305
BLAST score 488
E value 3.0e-49
Match length 142
% identity 64

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 218001

Seq. ID LIB3148-031-Q1-K1-B11

Method BLASTX
NCBI GI g4455365
BLAST score 165
E value 1.0e-11
Match length 32
% identity 81

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 218002

Seq. ID LIB3148-031-Q1-K1-B12

Method BLASTX
NCBI GI g4337192
BLAST score 187
E value 1.0e-14
Match length 52
% identity 63

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 218003

Seq. ID LIB3148-031-Q1-K1-B5

Method BLASTX
NCBI GI g3832512
BLAST score 263
E value 6.0e-23
Match length 60
% identity 83

NCBI Description (AF097922) granule-bound glycogen (starch) synthase

[Astragalus membranaceus]



```
218004
Seq. No.
                  LIB3148-031-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3337361
BLAST score
                  240
                  3.0e-20
E value
Match length
                  78
                  55
% identity
                 (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  218005
Seq. No.
                  LIB3148-031-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548852
BLAST score
                  291
                  3.0e-26
E value
                  72
Match length
                  75
% identity
                 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
                  218006
Seq. No.
                  LIB3148-031-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3249105
BLAST score
                  377
E value
                  1.0e-36
Match length
                  97
% identity
                  72
                  (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                  218007
Seq. No.
Seq. ID
                  LIB3148-031-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4545262
BLAST score
                  268
E value
                  1.0e-23
Match length
                  61
% identity
                  74
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
                  218008
Seq. No.
Seq. ID
                  LIB3148-031-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4567225
BLAST score
                  284
E value
                  2.0e-25
Match length
                  71
% identity
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
```

30596

218009

LIB3148-031-Q1-K1-C6

Seq. No. Seq. ID

Seq. ID

Method NCBI GI



```
Method
                   BLASTX
NCBI GI
                   q133867
BLAST score
                   589
E value
                   4.0e-61
Match length
                   129
                   87
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi_22470_emb_C\overline{A}A39\overline{43}8 (X55967)
                   ribosomal protein S11 [Zea mays]
Seq. No.
                   218010
                   LIB3148-031-Q1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1350930
BLAST score
                   294
                   8.0e-31
E value
Match length
                   72
                   96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S13
Seq. No.
                   218011
                   LIB3148-031-Q1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3264767
BLAST score
                   339
E value
                   8.0e-32
Match length
                   131
                   53
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   218012
Seq. ID
                   LIB3148-031-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   g1169838
BLAST score
                   182
E value
                   2.0e-13
Match length
                   61
% identity
                   51
NCBI Description GIBBERELLIN-REGULATED PROTEIN 2 PRECURSOR
                   >gi 2129589 pir S60230 GAST1 protein homolog (clone GASA2)
                   - Arabidopsis thaliana >gi_887937 (U11765) GAST1 protein
                   homolog [Arabidopsis thaliana]
                   218013
Seq. No.
Seq. ID
                   LIB3148-031-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   g2275215
BLAST score
                   316
E value
                   3.0e-29
                   111
Match length
% identity
                   60
NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]
                   218014
Seq. No.
```

30597

LIB3148-031-Q1-K1-F10

BLASTX

g1173218

```
BLAST score
                  240
                  2.0e-20
E value
                  83
Match length
                  64
% identity
                 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  218015
Seq. No.
                  LIB3148-031-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g1514977
NCBI GI
BLAST score
                  174
E value
                  5.0e-13
                  39
Match length
% identity
                  90
NCBI Description (D84669) VM23 [Raphanus sativus]
                  218016
Seq. No.
                  LIB3148-031-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023190
BLAST score
                  489
                  1.0e-49
E value
Match length
                  105
                  91
% identity
NCBI Description 14-3-3-LIKE PROTEIN 16R >gi 1888459 emb CAA72381 (Y11685)
                  14-3-3 protein [Solanum tuberosum]
                  218017
Seq. No.
Seq. ID
                  LIB3148-031-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  q555973
BLAST score
                  33
E value
                  4.0e-09
Match length
                  53
% identity
                  91
NCBI Description Pisum sativum 14-3-3-like protein mRNA, complete cds
                  218018
Seq. No.
Seq. ID
                  LIB3148-031-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  g167336
BLAST score
                  44
E value
                  9.0e-16
Match length
                  60
% identity
                  93
```

NCBI Description Gossypium hirsutum Lea4-A gene, complete CDS

 Seq. No.
 218019

 Seq. ID
 LIB3148-031-Q1-K1-G1

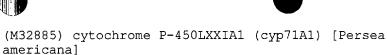
 Method
 BLASTX

 NCBI GI
 g166949

 BLAST score
 442

BLAST score 442 E value 7.0e-44 Match length 140 % identity 56





Seq. No. 218020

NCBI Description

Seq. ID LIB3148-031-Q1-K1-G7

Method BLASTX
NCBI GI g3211989
BLAST score 660
E value 2.0e-69
Match length 146
% identity 86

NCBI Description (AF068260) ADP-glucose pyrophosphorylase large subunit

[Ipomoea batatas]

Seq. No. 218021

Seq. ID LIB3148-031-Q1-K1-G8

Method BLASTX
NCBI GI g2146797
BLAST score 213
E value 5.0e-17
Match length 72
% identity 39

NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean

>gi_1134968 (U41385) protein disulphide isomerase PDI
[Ricinus communis] >gi_1587210_prf__2206331A protein

disulfide isomerase [Ricinus communis]

Seq. No. 218022

Seq. ID LIB3148-031-Q1-K1-G9

Method BLASTN
NCBI GI g2687439
BLAST score 206
E value 1.0e-112
Match length 226
% identity 98

NCBI Description Peltoboykinia tellimoides large subunit 26S ribosomal RNA

gene, partial sequence

Seq. No. 218023

Seq. ID LIB3148-031-Q1-K1-H10

Method BLASTN
NCBI GI g2558943
BLAST score 140
E value 6.0e-73
Match length 247
% identity 95

NCBI Description Gossypium hirsutum histone 3 mRNA, complete cds

Seq. No. 218024

Seq. ID LIB3148-031-Q1-K1-H12

Method BLASTX
NCBI GI g4337025
BLAST score 262
E value 3.0e-23
Match length 84

% identity 61

NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]



```
218025
Seq. No.
                  LIB3148-031-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1174592
                   748
BLAST score
                  8.0e-80
E value
Match length
                  141
                   100
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  218026
Seq. No.
                  LIB3148-031-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  q1841355
NCBI GI
                   315
BLAST score
E value
                   5.0e-29
Match length
                  132
% identity
                   58
                  (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   218027
                  LIB3148-032-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4545262
                  165
BLAST score
                   2.0e-11
E value
Match length
                   44
% identity
                   66
NCBI Description
                   (AF118230) metallothionein-like protein [Gossypium
                   hirsutum]
Seq. No.
                   218028
Seq. ID
                   LIB3148-032-Q1-K1-A4
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   6.0e-11
                   37
Match length
% identity
                   61
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   218029
Seq. ID
                   LIB3148-032-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2253415
BLAST score
                   559
E value
                   1.0e-57
```

133 Match length 76 % identity

(AF007215) stress-induced cysteine proteinase [Lavatera NCBI Description

thuringiaca]

Seq. No. 218030



Seq. ID LIB3148-032-Q1-K1-A7

Method BLASTX NCBI GI q1351365 BLAST score 185 8.0e-14 E value Match length 56 62 % identity

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN NCBI Description

(CR6) >gi_2130002_pir__S68969 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768 (X82325) cytochrome c reductase subunit [Solanum tuberosum]

218031 Seq. No.

LIB3148-032-Q1-K1-A9 Seq. ID

Method BLASTX NCBI GI q2267567 389 BLAST score 6.0e-38 E value Match length 84 % identity 87

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] $>gi_2267569$ (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

Seq. No. 218032

Seq. ID LIB3148-032-Q1-K1-B1

Method BLASTX g464981 NCBI GI 326 BLAST score 2.0e-30 E value Match length 77 78 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 218033

LIB3148-032-Q1-K1-B2 Seq. ID

Method BLASTX NCBI GI q3461884 BLAST score 311 1.0e-28 E value 86 Match length 70 % identity

NCBI Description (AB006082) phosphoribosyl-ATP pyrophosphohydrolase

[Arabidopsis thaliana] >gi_3461886_dbj_BAA32529_ (AB006083)

phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis

thaliana]

218034 Seq. No.

Seq. ID LIB3148-032-Q1-K1-B3

Method BLASTX NCBI GI g2129587 BLAST score 167 E value 1.0e-11 Match length 87 % identity 45



NCBI Description gamma-glutamyltransferase (EC 2.3.2.2) - Arabidopsis thaliana >gi_928934_emb_CAA89206_ (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana] >gi_1585436_prf__2124427C gamma-Glu transpeptidase [Arabidopsis thaliana]

218035 Seq. No. LIB3148-032-Q1-K1-B6 Seq. ID Method BLASTX NCBI GI q2833375 BLAST score 187 4.0e-14 E value Match length 39 % identity 92

NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II

subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica

napus]

Seq. No. 218036

Seq. ID LIB3148-032-Q1-K1-B7

Method BLASTX
NCBI GI g3046700
BLAST score 350
E value 4.0e-33
Match length 135
% identity 56

NCBI Description (AJ005261) cytidine deaminase [Arabidopsis thaliana]

>gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative

cytidine deaminase [Arabidopsis thaliana]

Seq. No. 218037

Seq. ID LIB3148-032-Q1-K1-B8

Method BLASTX
NCBI GI 94097547
BLAST score 293
E value 2.0e-26
Match length 65
% identity 45

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

Seq. No. 218038

Seq. ID LIB3148-032-Q1-K1-B9

Method BLASTX
NCBI GI g2494076
BLAST score 301
E value 8.0e-28
Match length 67
% identity 84

NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase

[Nicotiana plumbaginifolia]



Seq. No. 218039

Seq. ID LIB3148-032-Q1-K1-C1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 218040

Seq. ID LIB3148-032-Q1-K1-C5

Method BLASTX
NCBI GI 94426565
BLAST score 164
E value 1.0e-11
Match length 81
% identity 43

NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 218041

Seq. ID LIB3148-032-Q1-K1-C8

Method BLASTX
NCBI GI g3660467
BLAST score 342
E value 3.0e-32
Match length 80
% identity 84

NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis

thaliana]

Seq. No. 218042

Seq. ID LIB3148-032-Q1-K1-D7

Method BLASTX
NCBI GI g4115920
BLAST score 154
E value 4.0e-10
Match length 78
% identity 45

NCBI Description (AF118222) similar to the subtilase family of serine

proteases (Pfam: PF00082, score; 45.8, E=1.1e-11, n=2)

[Arabidopsis thaliana]

Seq. No. 218043

Seq. ID LIB3148-032-Q1-K1-E12

Method BLASTX
NCBI GI g4105097
BLAST score 473
E value 1.0e-47
Match length 121
% identity 75

NCBI Description (AF043255) MADS box protein 26 [Cucumis sativus]

Seq. No. 218044

Seq. ID LIB3148-032-Q1-K1-E2

Method BLASTX



```
NCBI GI
                  g1172873
BLAST score
                  348
E value
                  5.0e-33
Match length
                  82
% identity
                  66
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  218045
                  LIB3148-032-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2146727
BLAST score
                  490
E value
                  1.0e-49
                  136
Match length
% identity
                  68
NCBI Description
                  cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 -
                  Arabidopsis thaliana (fragment) >gi 598069 (L37884)
                  cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  218046
                  LIB3148-032-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133793
BLAST score
                  249
                  2.0e-21
E value
Match length
                  100
                  56
% identity
                 40S RIBOSOMAL PROTEIN S15A (PPCB8) >gi_99825_pir__S20945
NCBI Description
                  ribosomal protein S15a - rape >gi_17863_emb_CAA42599_
                  (X59983) r-protein BnS15a [Brassica napus]
Seq. No.
                  218047
Seq. ID
                  LIB3148-032-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3068704
BLAST score
                  591
E value
                  2.0e-61
Match length
                  137
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  218048
Seq. ID
                  LIB3148-032-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2346986
BLAST score
                  142
E value
                  9.0e-09
Match length
                  74
% identity
                  49
```

NCBI Description (AB006605) ZPT3-3 [Petunia x hybrida]

Seq. No. 218049

Seq. ID LIB3148-032-Q1-K1-F4

Method BLASTX



```
NCBI GI
                  g2119279
BLAST score
                   627
E value
                   1.0e-65
Match length
                  118
% identity
                  100
NCBI Description tubulin beta-2 chain - rice
                  218050
Seq. No.
Seq. ID
                  LIB3148-032-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q4490309
BLAST score
                   323
E value
                   6.0e-30
Match length
                  98
% identity
                   66
NCBI Description
                  (AL035678) peroxidase ATP17a-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  218051
Seq. ID
                  LIB3148-032-Q1-K1-F9
Method
                  BLASTN
NCBI GI
                  q4104241
BLAST score
                  69
E value
                   6.0e - 31
Match length
                  125
% identity
                   89
NCBI Description Gossypium hirsutum palmitoyl-acyl carrier protein
                  thioesterase (FatB1) mRNA, partial cds
Seq. No.
                   218052
Seq. ID
                  LIB3148-032-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                   g2865522
BLAST score
                  34
E value
                   2.0e-09
Match length
                  103
                   91
% identity
NCBI Description Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
                  complete cds
Seq. No.
                   218053
Seq. ID
                  LIB3148-032-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                   g3152618
BLAST score
                   444
E value
                   4.0e-44
Match length
                  132
% identity
                   60
```

(AC004482) putative pectinesterase [Arabidopsis thaliana] NCBI Description

>gi 3242724 (AC003040) putative pectinesterase [Arabidopsis

thaliana]

218054 Seq. No.

Seq. ID LIB3148-032-Q1-K1-G6

Method BLASTX NCBI GI g4490704 169 BLAST score



```
6.0e-12
E value
Match length
                  63
                  49
% identity
                 (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                  218055
Seq. No.
                  LIB3148-032-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g441457
                  690
BLAST score
E value
                  5.0e-73
Match length
                  131
% identity
                  97
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  218056
                  LIB3148-032-Q1-K1-G8
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g3334413
BLAST score
                  452
E value
                  4.0e-45
Match length
                  123
                  78
% identity
                 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 2502087
NCBI Description
                   (AF022926) adenosine triphosphatase; c-subunit of V-ATPase
                   [Vigna radiata]
Seq. No.
                  218057
                  LIB3148-032-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1130682
BLAST score
                  325
E value
                   3.0e - 30
Match length
                  93
% identity
                   67
NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
Seq. No.
                  218058
                  LIB3148-032-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3600058
                   282
BLAST score
E value
                   1.0e-25
                  70
Match length
% identity
                  (AF080120) similar to vacuolar ATPases [Arabidopsis
NCBI Description
                  thaliana]
                   218059
Seq. No.
Seq. ID
                  LIB3148-032-Q1-K1-H10
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3121829
BLAST score 157
E value 2.0e-10
Match length 64
% identity 45



NCBI Description CHROMATIN ASSEMBLY FACTOR I P60 SUBUNIT (CAF-I 60 KD SUBUNIT) >gi_2134915_pir__B56731 chromatin assembly factor

I p60 chain - human $\overline{>}$ gi_882260 (U20980) chromatin assembly

factor-I p60 subunit [Homo sapiens]

Seq. No. 218060

Seq. ID LIB3148-032-Q1-K1-H3

Method BLASTX
NCBI GI g3152614
BLAST score 220
E value 6.0e-18
Match length 112
% identity 41

NCBI Description (AC004482) unknown protein [Arabidopsis thaliana]

Seq. No. 218061

Seq. ID LIB3148-032-Q1-K1-H4

Method BLASTX
NCBI GI 94455208
BLAST score 344
E value 2.0e-32
Match length 124
% identity 60

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 218062

Seq. ID LIB3148-033-Q1-K1-A10

Method BLASTX
NCBI GI 94510417
BLAST score 357
E value 5.0e-34
Match length 87
% identity 79

NCBI Description (AC006929) putative BEL1 homeotic protein [Arabidopsis

thaliana]

Seq. No. 218063

Seq. ID LIB3148-033-Q1-K1-A4

Method BLASTX
NCBI GI g3080389
BLAST score 411
E value 2.0e-40
Match length 96
% identity 82

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 218064

Seq. ID LIB3148-033-Q1-K1-A8

Method BLASTX
NCBI GI 94539307
BLAST score 179
E value 2.0e-13
Match length 46
% identity 74

NCBI Description (AL049480) putative acidic ribosomal protein [Arabidopsis

thaliana]

```
218065
Seq. No.
                  LIB3148-033-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  295
E value
                   1.0e-26
Match length
                  77
                   70
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                   218066
Seq. ID
                  LIB3148-033-Q1-K1-B3
Method
                  BLASTX
                  g3158476
NCBI GI
BLAST score
                  258
E value
                   6.0e-23
Match length
                  59
                  86
% identity
NCBI Description
                 (AF067185) aquaporin 2 [Samanea saman]
                  218067
Seq. No.
                  LIB3148-033-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885884
BLAST score
                  280
E value
                   4.0e-25
Match length
                  59
% identity
                   90
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  218068
Seq. No.
Seq. ID
                  LIB3148-033-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2262159
BLAST score
                  281
E value
                   2.0e-25
Match length
                  86
% identity
                   63
NCBI Description
                  (AC002329) predicted protein similar to S.pombe protein
                  C5H10.03 [Arabidopsis thaliana]
Seq. No.
                  218069
Seq. ID
                  LIB3148-033-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2760830
BLAST score
                  585
E value
                  1.0e-60
Match length
                  129
% identity
                  87
NCBI Description
                  (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana]
```

30608

218070

BLASTX

LIB3148-033-Q1-K1-C10

Seq. No. Seq. ID

Method



```
NCBI GI
                  q2583128
BLAST score
                  222
E value
                  4.0e-18
Match length
                  53
% identity
                  77
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
                  218071
Seq. No.
                  LIB3148-033-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2116599
BLAST score
                  257
E value
                  3.0e-22
Match length
                  70
                  71
% identity
NCBI Description (AB003779) leucoanthocyanidin dioxygenase [Perilla
                  frutescens]
Seq. No.
                  218072
Seq. ID
                  LIB3148-033-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g421941
BLAST score
                  237
E value
                  7.0e-20
Match length
                  54
% identity
                  83
NCBI Description GTP-binding protein, ras-related - common tobacco
                  >gi_296878_emb_CAA50609 (X71609) ras-related GTP-binding
                  protein [Nicotiana tabacum]
Seq. No.
                  218073
                  LIB3148-033-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3182981
BLAST score
                  679
E value
                  1.0e-71
Match length
                  142
% identity
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096
                  (D86494) diminuto [Pisum sativum]
Seq. No.
                  218074
Seq. ID
                  LIB3148-033-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1710546
BLAST score
                  351
E value
                  3.0e-33
Match length
                  81
                  86
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
                  ribosomal protein [Daucus carota]
Seq. No.
                  218075
```

Seq. ID LIB3148-033-Q1-K1-E8

Method BLASTX NCBI GI g3413704 BLAST score 327

```
2.0e-30
E value
Match length
                  74
% identity
                  74
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  218076
                  LIB3148-033-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4105633
BLAST score
                  335
E value
                  2.0e-31
Match length
                  138
% identity
                  50
NCBI Description
                  (AF048982) putative ethylene receptor [Arabidopsis
                  thaliana]
Seq. No.
                  218077
Seq. ID
                  LIB3148-033-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4185140
BLAST score
                  309
E value
                  2.0e-28
Match length
                  70
% identity
                  87
NCBI Description
                  (AC005724) putative small nuclear ribonucleoprotein E
                   (snRNP-E) [Arabidopsis thaliana]
```

Seq. No. 218078

LIB3148-033-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI g4165018 BLAST score 207 E value 2.0e-16 93 Match length

% identity 45

NCBI Description (D89053) Acyl-CoA synthetase 3 [Homo sapiens]

Seq. No. 218079

Seq. ID LIB3148-033-Q1-K1-G12

Method BLASTN NCBI GI g166919 BLAST score 55 E value 2.0e-22 Match length 67 % identity 96

NCBI Description Arabidopsis thaliana alpha-6 tubulin (TUA6) gene, complete

cds

Seq. No. 218080

Seq. ID LIB3148-033-Q1-K1-G2

Method BLASTX NCBI GI g134612 BLAST score 328 E value 2.0e-30 Match length 69 % identity

NCBI Description SUPEROXIDE DISMUTASE 1 (CU-ZN) >gi 100254 pir S08350

% identity

NCBI Description

96

crispum]



superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - tomato
>gi_19197_emb_CAA32199_ (X14040) Cu-Zn superoxide dismutase
(AA 1-152) [Lycopersicon esculentum] >gi_170512 (M37150)
superoxide dismutase (SOD) [Lycopersicon esculentum]

Seq. No. 218081 LIB3148-033-Q1-K1-G4 Seq. ID Method BLASTX NCBI GI g2832681 BLAST score 474 E value 1.0e-47Match length 91 % identity 91 NCBI Description (AL021712) putative protein [Arabidopsis thaliana] Seq. No. 218082 LIB3148-033-Q1-K1-G7 Seq. ID Method BLASTX NCBI GI g1362093 BLAST score 165 E value 2.0e-11 Match length 69 55 % identity NCBI Description hypothetical protein (clone TPP15) - tomato (fragment) >gi 924632 (U20595) unknown [Solanum lycopersicum] 218083 Seq. No. LIB3148-033-Q1-K1-H11 Seq. ID Method BLASTN NCBI GI q4098126 BLAST score 153 E value 7.0e-81 Match length 161 99 % identity NCBI Description Gossypium hirsutum sucrose synthase mRNA, partial cds Seq. No. 218084 Seq. ID LIB3148-033-Q1-K1-H2 Method BLASTX NCBI GI g2632252 BLAST score 263 E value 6.0e-23 Match length 124 % identity NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor] Seq. No. 218085 LIB3148-033-Q1-K1-H3 Seq. ID Method BLASTX NCBI GI g2809385 BLAST score 295 E value 8.0e-27 Match length 57

(AF024634) NADPH cytochrome P450 reductase [Petroselinum



```
Seq. No.
                  218086
Seq. ID
                  LIB3148-033-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3643608
BLAST score
                  176
E value
                  1.0e-12
Match length
                  66
                  55
% identity
NCBI Description
                 (AC005395) hypothetical protein [Arabidopsis thaliana]
                  218087
Seq. No.
                  LIB3148-033-Q1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4539447
BLAST score
                  173
E value
                  2.0e-12
Match length
                  139
% identity
                  32
NCBI Description
                  (AL049523) retrotransposon like protein [Arabidopsis
                  thaliana]
Seq. No.
                  218088
Seq. ID
                  LIB3148-034-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  q3928090
BLAST score
                  203
E value
                  1.0e-17
Match length
                  84
% identity
                  52
NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]
                  218089
Seq. No.
Seq. ID
                  LIB3148-034-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  g3449312
BLAST score
                  36
E value
                  9.0e-11
Match length
                  72
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K16L22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  218090
                  LIB3148-034-Q1-K1-B12
Seq. ID
                  BLASTX
                  g1351014
                  168
                  6.0e-12
```

Method

NCBI GI BLAST score E value 33 Match length 91 % identity

40S RIBOSOMAL PROTEIN S8 >gi_968902 dbj_BAA07207_ (D38010) NCBI Description

ribosomal protein S8 [Oryza sativa]

Seq. No. 218091

Seq. ID LIB3148-034-Q1-K1-B3

Method BLASTX NCBI GI g3021357

NCBI GI

BLAST score

```
BLAST score
                  163
E value
                   3.0e-11
Match length
                  27
% identity
                  96
                  (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                  tetragonoloba]
                  218092
Seq. No.
Seq. ID
                  LIB3148-034-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  443
E value
                  2.0e-44
Match length
                  81
% identity
                  100
                  TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                  218093
Seq. ID
                  LIB3148-034-Q1-K1-B7
Method
                  BLASTX
                  g3549670
NCBI GI
BLAST score
                  171
E value
                  4.0e-12
Match length
                  35
% identity
                  86
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                  218094
Seq. No.
Seq. ID
                  LIB3148-034-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2493052
BLAST score
                  326
E value
                  2.0e-30
Match length
                  69
% identity
                  84
NCBI Description
                  ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
                  >gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of
                  mitochondrial FI-ATPase [Arabidopsis thaliana]
Seq. No.
                  218095
Seq. ID
                  LIB3148-034-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4558552
BLAST score
                  305
E value
                  6.0e-28
Match length
                  108
% identity
                  36
NCBI Description (AC007138) putative P-glycoprotein-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  218096
Seq. ID
                  LIB3148-034-Q1-K1-C5
Method
                  BLASTX
```

30613

g2501353



E value 2.0e-33 Match length 79 % identity 87

NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase

[Craterostigma plantagineum]

Seq. No. 218097

Seq. ID LIB3148-034-Q1-K1-D12

Method BLASTX
NCBI GI 94508073
BLAST score 347
E value 5.0e-33
Match length 97
% identity 64

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 218098

Seq. ID LIB3148-034-Q1-K1-D6

Method BLASTX
NCBI GI g3287683
BLAST score 154
E value 4.0e-10
Match length 65
% identity 18

NCBI Description (AC003979) Similar to apoptosis protein MA-3 gb D50465 from

Mus musculus. [Arabidopsis thaliana]

Seq. No. 218099

Seq. ID LIB3148-034-Q1-K1-D9

Method BLASTX
NCBI GI g1172874
BLAST score 405
E value 1.0e-39
Match length 129
% identity 64

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 218100

Seq. ID LIB3148-034-Q1-K1-E1

Method BLASTX
NCBI GI g1085595
BLAST score 164
E value 2.0e-11
Match length 51

% identity 63

NCBI Description 1-aminocyclopropane-1-carboxylate oxidase - Prunus persica

>gi_452671_emb CAA54449 (X77232)

1-aminocyclopropane-1-carboxylate oxidase [Prunus persica] >gi 3510500 (AF026793) 1-aminocyclopropane-1-carboxylate

oxidase; ACC oxidase [Prunus armeniaca]

```
Seq. No.
                   218101
Seq. ID
                   LIB3148-034-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3559814
BLAST score
                   400
E value
                   2.0e-39
Match length
                   97
                   81
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
Seq. No.
                  218102
Seq. ID
                  LIB3148-034-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                   q2252871
BLAST score
                   178
E value
                   4.0e-13
Match length
                  104
                   43
% identity
NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]
                   218103
Seq. No.
Seq. ID
                  LIB3148-034-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1565225
BLAST score
                   212
E value
                   6.0e-17
Match length
                  84
                   52
% identity
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                   218104
Seq. ID
                  LIB3148-034-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                   g1707017
BLAST score
                  196
E value
                   1.0e-16
Match length
                   60
% identity
                   75
NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.
                   218105
Seq. ID
                  LIB3148-034-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2147328
BLAST score
                  247
E value
                   4.0e-21
Match length
                  126
                   41
% identity
NCBI Description dioscorin class B - Dioscorea cayenensis (fragment)
```

Seq. No. 218106

Seq. ID LIB3148-034-Q1-K1-F3 Method BLASTX

NCBI GI g2880049 BLAST score 325 E value 3.0e-30 Match length 124



```
% identity
                  55
NCBI Description
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
                  218107
Seq. No.
                  LIB3148-034-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2880049
BLAST score
                  204
                  5.0e-16
E value
                  126
Match length
% identity
                   41
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  218108
Seq. ID
                  LIB3148-034-Q1-K1-H10
Method
                  BLASTN
NCBI GI
                  g414831
BLAST score
                  33
                  6.0e-09
E value
                  53
Match length
% identity
                  91
NCBI Description Glycine max (Rablp) mRNA, complete cds
Seq. No.
                  218109
                  LIB3148-034-Q1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  5.0e-11
E value
                  48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  218110
Seq. No.
                  LIB3148-034-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2688830
BLAST score
                   277
E value
                   1.0e-38
Match length
                   117
                   71
% identity
NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]
Seq. No.
                   218111
Seq. ID
                  LIB3148-034-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                   g4432866
BLAST score
                   189
E value
                   3.0e-14
```

Match length 115 % identity 36

NCBI Description (AC006300) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 218112

Seq. ID LIB3148-034-Q1-K1-H4

Method BLASTX

Match length

% identity

36

67



```
NCBI GI
                  g4457221
BLAST score
                  237
E value
                  6.0e-20
                  63
Match length
                  78
% identity
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum
                  chinense]
                  218113
Seq. No.
Seq. ID
                  LIB3148-034-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                  q3659907
BLAST score
                  293
E value
                  2.0e-26
                  73
Match length
                  75
% identity
NCBI Description (AF091857) protein translation factor SUI1 homolog
                  [Pimpinella brachycarpa]
Seq. No.
                  218114
Seq. ID
                  LIB3148-035-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4105798
BLAST score
                  443
E value
                  4.0e-44
Match length
                  124
                  55
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
                  218115
Seq. No.
Seq. ID
                  LIB3148-035-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4559334
BLAST score
                  225
E value
                  2.0e-18
Match length
                  120
                  37
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218116
                  LIB3148-035-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128181
BLAST score
                  408
                  6.0e-40
E value
Match length
                  111
% identity
                  76
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218117
                  LIB3148-035-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1840425
BLAST score
                  140
E value
                  1.0e-08
```

```
NCBI Description
                 (U36586) alcohol dehydrogenase [Vitis vinifera]
Seq. No.
                  218118
Seq. ID
                  LIB3148-035-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  q3869074
BLAST score
                  63
E value
                  7.0e-27
Match length
                  83
% identity
                  94
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMI9, complete sequence [Arabidopsis thaliana]
                  218119
Seq. No.
                  LIB3148-035-Q1-K1-B12
Seq. ID
Method
                  BLASTX
                  g461735
NCBI GI
BLAST score
                  424
E value
                  4.0e-42
Match length
                  88
% identity
                  99
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
                  >gi_478785_pir__S29315 chaperonin 60 - cucurbit
                  >gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita
                  sp.]
Seq. No.
                  218120
Seq. ID
                  LIB3148-035-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2583123
BLAST score
                  217
                  1.0e-17
E value
Match length
                  128
% identity
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                  218121
Seq. ID
                  LIB3148-035-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1717975
```

Method BLASTX
NCBI GI g1717975
BLAST score 286
E value 1.0e-25
Match length 97
% identity 54

NCBI Description 14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG) >gi_1177435_emb_CAA64670_ (X95384) 14.5

kDa translational inhibitor protein, p14.5 [Homo sapiens]

Seq. No. 218122

Seq. ID LIB3148-035-Q1-K1-B8

Method BLASTX
NCBI GI 94105097
BLAST score 542
E value 1.0e-55
Match length 120
% identity 85





```
NCBI Description (AF043255) MADS box protein 26 [Cucumis sativus]
Seq. No.
                   218123
                   LIB3148-035-Q1-K1-C10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   5.0e-11
Match length
                   48
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   218124
Seq. No.
Seq. ID
                  LIB3148-035-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                   g3928142
BLAST score
                   472
E value
                   2.0e-47
Match length
                   130
% identity
                   18
NCBI Description (AJ131045) protein phosphatase [Cicer arietinum]
Seq. No.
                   218125
Seq. ID
                  LIB3148-035-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                   q2191187
BLAST score
                   237
E value
                   7.0e-20
Match length
                   131
% identity
                   20
NCBI Description
                  (AF007271) contains similarity to a DNAJ-like domain
                   [Arabidopsis thaliana]
Seq. No.
                   218126
Seq. ID
                  LIB3148-035-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                   q4512664
BLAST score
                  270
E value
                   9.0e-24
Match length
                   67
% identity
NCBI Description
                  (AC006931) putative ribose phosphate pyrophosphokinase
                   [Arabidopsis thaliana]
                  >gi_4544471 gb AAD22378.1 AC006580 10 (AC006580) putative
                  ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
Seq. No.
                   218127
Seq. ID
                  LIB3148-035-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  392
E value
                  2.0e-38
Match length
                  105
                  73
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir $46302
NCBI Description
```

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi 397482 emb CAA52684 (X74604) heat shock protein 70



cognate [Arabidopsis thaliana]

```
Seq. No.
                   218128
Seq. ID
                   LIB3148-035-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4539350
BLAST score
                   368
E value
                   3.0e - 35
                   80
Match length
% identity
                   80
NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                   218129
Seq. ID
                   LIB3148-035-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2500378
BLAST score
                   274
E value
                   2.0e-31
                   78
Match length
                   75
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                   218130
Seq. ID
                   LIB3148-035-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g543868
BLAST score
                   185
E value
                   5.0e-14
Match length
                   41
% identity
                   80
NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
                   >gi_1076683_pir__B47493 H+-transporting ATP synthase (EC
                   3.6.1.34) epsilon chain - sweet potato >gi_303625_dbj_BAA03527_ (D14700) F1-ATPase epsilon-subunit
                   [Ipomoea batatas]
Seq. No.
                   218131
Seq. ID
                   LIB3148-035-Q1-K1-E9
Method
                   BLASTX
                   g189422
NCBI GI
BLAST score
                   391
                   3.0e-42
E value
                   135
Match length
% identity
                   59
NCBI Description (M32110) proliferating cell nuclear protein P120 [Homo
                   sapiens]
                   218132
Seq. No.
Seq. ID
                   LIB3148-035-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2500981
BLAST score
                   551
E value
                   1.0e-56
Match length
                   126
% identity
                   80
NCBI Description GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)
                   >gi 1084418 pir S51685 glutamate--tRNA ligase (EC
```



6.1.1.17) - common tobacco >gi_603867_emb_CAA58506_(X83524) glutamate--tRNA ligase [Nicotiana tabacum]

Seq. No. 218133

Seq. ID LIB3148-035-Q1-K1-F10

Method BLASTX
NCBI GI g3386614
BLAST score 564
E value 3.0e-58
Match length 134
% identity 42

NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis

thaliana]

Seq. No. 218134

Seq. ID LIB3148-035-Q1-K1-F12

Method BLASTX
NCBI GI g4559334
BLAST score 293
E value 1.0e-26
Match length 95
% identity 48

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 218135

Seq. ID LIB3148-035-Q1-K1-F2

Method BLASTX
NCBI GI g3549681
BLAST score 309
E value 2.0e-28
Match length 119
% identity 52

NCBI Description (AL031394) male sterility 2-like protein [Arabidopsis

thaliana]

Seq. No. 218136

Seq. ID LIB3148-035-Q1-K1-F4

Method BLASTX
NCBI GI g1617206
BLAST score 354
E value 1.0e-33
Match length 77
% identity 82

NCBI Description (Z72489) CP12 [Pisum sativum]

Seq. No. 218137

Seq. ID LIB3148-035-Q1-K1-G1

Method BLASTX
NCBI GI g3242704
BLAST score 272
E value 4.0e-24
Match length 82
% identity 59

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 218138

Seq. ID LIB3148-035-Q1-K1-G10

```
Method
                  BLASTX
NCBI GI
                  q4371280
BLAST score
                  435
E value
                  4.0e-43
Match length
                  133
                  67
% identity
NCBI Description
                 (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  218139
                  LIB3148-035-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1800281
                  198
BLAST score
                  2.0e-24
E value
Match length
                  89
% identity
                  14
NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]
                  218140
Seq. No.
Seq. ID
                  LIB3148-035-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g485514
BLAST score
                  354
E value
                  1.0e-33
                  79
Match length
                  86
% identity
                  ADR11-2 protein - soybean (fragment)
NCBI Description
                  >gi_296443_emb_CAA49341_ (X69640) auxin down regulated
                   [Glycine max]
                   218141
Seq. No.
                  LIB3148-035-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2493146
BLAST score
                  157
E value
                   5.0e-11
Match length
                  47
                   70
% identity
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >qi 755148
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                   [Gossypium hirsutum] >gi 4519415 dbj BAA75542.1_ (AB024275)
                   vacuolar H+-ATPase c subunit [Citrus unshiu]
                   218142
Seq. No.
Seq. ID
                  LIB3148-035-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                   g4193382
BLAST score
                  319
E value
                   1.0e-29
Match length
                  86
                   72
% identity
NCBI Description
                   (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
                   >qi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                   thaliana]
```

Seq. No. 218143

Seq. ID LIB3148-035-Q1-K1-H5

Method

NCBI GI



```
Method
                  BLASTX
NCBI GI
                   q3914394
                  174
BLAST score
E value
                  1.0e-12
Match length
                  37
                  86
% identity
NCBI Description
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_2118335_pir__S60473 phosphoglycerate mutase (EC
                   5.4.2.1) - common ice plant >gi_602426 (U16021)
                  phosphoglyceromutase [Mesembryanthemum crystallinum]
                  218144
Seq. No.
Seq. ID
                  LIB3148-035-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g2104680
BLAST score
                  35
E value
                   4.0e-10
Match length
                  94
                  85
% identity
NCBI Description V.faba mRNA for putative transciption factor (1556bp)
Seq. No.
                  218145
                  LIB3148-035-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1498053
BLAST score
                  284
                  2.0e-44
E value
Match length
                  101
                   92
% identity
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  218146
                  LIB3148-036-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935167
BLAST score
                  507
E value
                   1.0e-51
Match length
                  113
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                   218147
Seq. ID
                  LIB3148-036-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   q3033385
BLAST score
                  291
E value
                   3.0e-26
Match length
                  122
% identity
NCBI Description
                  (AC004238) similar to Human XE169 protein (escapes
                  X-chromosome inactivation) [Arabidopsis thaliana]
Seq. No.
                   218148
Seq. ID
```

30623

LIB3148-036-Q1-K1-A6

BLASTX

g2281649



```
BLAST score
                   377
                   2.0e-36
E value
Match length
                  132
                   60
% identity
NCBI Description
                  (AF003105) AP2 domain containing protein RAP2.12
                   [Arabidopsis thaliana]
                  218149
Seq. No.
                  LIB3148-036-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006924
BLAST score
                  527
E value
                  5.0e-54
Match length
                  117
% identity
                  80
NCBI Description
                  (Z99708) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  218150
Seq. No.
                  LIB3148-036-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334261
BLAST score
                  141
                  1.0e-08
E value
Match length
                  48
                  56
% identity
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
                  metallothionein-like protein [Malus domestica]
                  218151
Seq. No.
Seq. ID
                  LIB3148-036-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q417360
BLAST score
                  239
E value
                  3.0e-20
Match length
                  90
% identity
                  44
NCBI Description
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
                  >gi_2131280_pir__S67767 high mobility group-like protein
                  NHP2 - yeast (Saccharomyces cerevisiae)
                  >gi_666101_emb_CAA40885 (X57714) high mobility group-like
                  nuclear protein 2 [Saccharomyces cerevisiae]
                  >gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like
                  protein [Saccharomyces cerevisiae]
                  >gi 1431346 emb CAA98786 (Z74256) ORF YDL208w
                   [Saccharomyces cerevisiae]
Seq. No.
                  218152
Seq. ID
                  LIB3148-036-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1362065
BLAST score
                  381
E value
                  9.0e-37
```

Match length 93 82

NCBI Description small GTP-binding protein - garden pea >gi_871506_emb_CAA90081_ (Z49901) small GTP-binding protein



[Pisum sativum]

Seq. No. 218153

Seq. ID LIB3148-036-Q1-K1-C11

Method BLASTX NCBI GI q461903 BLAST score 146 2.0e-09 E value Match length 33 % identity 88

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 405129

(L14844) cyclophilin [Arabidopsis thaliana]

>gi_4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl isomerase ROC1 [Arabidopsis thaliana]

Seq. No. 218154

LIB3148-036-Q1-K1-C8 Seq. ID

Method BLASTX NCBI GI q119354 BLAST score 550 E value 1.0e-56 Match length 116 94 % identity

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 82082 pir JQ1185

phosphopyruvate hydratase (EC 4.2.1.11) - tomato

>gi_19281_emb_CAA41115 (X58108) enolase [Lycopersicon

esculentum]

Seq. No. 218155

Seq. ID LIB3148-036-Q1-K1-D12

Method BLASTX NCBI GI q1703380 BLAST score 572 E value 4.0e-59 Match length 109 % identity 99

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)

ADP-ribosylation factor [Oryza sativa]

Seq. No. 218156

Seq. ID LIB3148-036-Q1-K1-D7

Method BLASTN NCBI GI g296442 BLAST score 33 E value 6.0e-09 Match length 65 88 % identity

NCBI Description G.max ADR11 mRNA

Seq. No. 218157

Seq. ID LIB3148-036-Q1-K1-D8

Method BLASTX NCBI GI g3790567 BLAST score 220 E value 7.0e-18



```
Match length
                  91
% identity
                   47
NCBI Description
                  (AF078821) RING-H2 finger protein RHAlb [Arabidopsis
                  thaliana]
Seq. No.
                  218158
Seq. ID
                  LIB3148-036-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2829896
BLAST score
                  104
E value
                  8.0e-09
Match length
                  109
                  37
% identity
NCBI Description
                  (AC002311) highly similar to auxin-regulated protein GH3,
                  gp X60033 18591 [Arabidopsis thaliana]
                  218159
Seq. No.
Seq. ID
                  LIB3148-036-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2160155
BLAST score
                  38
E value
                  6.0e-12
Match length
                  74
% identity
                  88
NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  218160
Seq. ID
                  LIB3148-036-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3851636
BLAST score
                  375
E value
                  5.0e-36
                  85
Match length
% identity
                  85
NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  218161
Seq. ID
                  LIB3148-036-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1172004
BLAST score
                  711
E value
                  2.0e-75
Match length
                  148
% identity
                  95
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 1345583 emb CAA53581
                   (X75967) phenylalanine ammonium lyase [Vitis vinifera]
Seq. No.
                  218162
Seq. ID
                  LIB3148-036-Q1-K1-G10
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2781345
BLAST score 252
E value 9.0e-22
Match length 108

49

% identity



NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

218163 Seq. No.

Seq. ID LIB3148-036-Q1-K1-G11

Method BLASTX NCBI GI g2129552 511 BLAST score E value 5.0e-52 Match length 118 % identity 54

NCBI Description calcium-dependent protein kinase 19 - Arabidopsis thaliana

(fragment)

218164 Seq. No.

LIB3148-036-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI q3080402 274 BLAST score E value 3.0e-24Match length 69 77 % identity

NCBI Description (AL022603) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana]

Seq. No. 218165

LIB3148-036-Q1-K1-G6 Seq. ID

Method BLASTX NCBI GI g3860258 BLAST score 198 E value 3.0e-15 Match length 58

% identity 67

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 218166

Seq. ID LIB3148-036-Q1-K1-G9

Method BLASTN NCBI GI g2264318 BLAST score 34 E value 2.0e-09 Match length 219 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MUP24, complete sequence [Arabidopsis thaliana]

Seq. No. 218167

Seq. ID LIB3148-036-Q1-K1-H11

Method BLASTX NCBI GI q3080393 BLAST score 258 E value 2.0e-22 Match length 51 % identity

NCBI Description (AL022603) NADH dehydrogenase like protein [Arabidopsis

thaliana]

```
Seq. No.
                   218168
Seq. ID
                   LIB3148-036-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   q4454042
BLAST score
                   597
E value
                   5.0e-62
                   148
Match length
% identity
                   72
NCBI Description
                  (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                   218169
                  LIB3148-037-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2801536
                   379
BLAST score
E value
                   1.0e-36
Match length
                   118
                   61
% identity
NCBI Description
                  (AF039531) lysophospholipase homolog [Oryza sativa]
                   218170
Seq. No.
Seq. ID
                  LIB3148-037-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                   g3851636
BLAST score
                   317
                   2.0e-36
E value
Match length
                   92
% identity
                   86
NCBI Description
                  (AF098519) unknown [Avicennia marina] >gi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   218171
Seq. No.
Seq. ID
                  LIB3148-037-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   q1632831
BLAST score
                   397
E value
                   8.0e-39
Match length
                  88
                                               5--
% identity
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                   218172
                   LIB3148-037-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g485514
BLAST score
                   350
E value
                   4.0e-33
Match length
                  132
% identity
                   58
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                   >gi 296443 emb CAA49341 (X69640) auxin down regulated
                   [Glycine max]
                   218173
Seq. No.
Seq. ID
                  LIB3148-037-Q1-K1-A8
Method
                  BLASTX
```



NCBI GI g584794 BLAST score 561 E value 7.0e-58 Match length 143 % identity 77

NCBI Description PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)

>gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
- curled-leaved tobacco >gi_170289 (M80489) plasma membrane

H+ ATPase [Nicotiana plumbaginifolia]

Seq. No. 218174

Seq. ID LIB3148-037-Q1-K1-A9

Method BLASTX
NCBI GI g3150415
BLAST score 656
E value 5.0e-69
Match length 140
% identity 37

NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana]

>gi 3420046 (AC004680) sec13-related protein [Arabidopsis

thaliana]

Seq. No. 218175

Seq. ID LIB3148-037-Q1-K1-B1

Method BLASTX
NCBI GI g3388157
BLAST score 168
E value 8.0e-12
Match length 104
% identity 44

NCBI Description (AF079556) poly(ADP-ribose) glycohydrolase [Drosophila

melanogaster]

Seq. No. 218176

Seq. ID LIB3148-037-Q1-K1-B11

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 5.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 218177

Seq. ID LIB3148-037-Q1-K1-B2

Method BLASTX
NCBI GI g3367517
BLAST score 163
E value 3.0e-11
Match length 37
% identity 76

NCBI Description (AC004392) Similar to F4I1.26 putative beta-glucosidase

gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene.

[Arabidopsis thaliana]

Seq. No. 218178

E value

Match length

4.0e-48

109

```
LIB3148-037-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924520
BLAST score
                  490
                  1.0e-49
E value
Match length
                  121
                  82
% identity
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  218179
Seq. No.
                  LIB3148-037-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3309170
                  251
BLAST score
                  1.0e-21
E value
                  119
Match length
                  47
% identity
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]
Seq. No.
                  218180
                  LIB3148-037-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3329368
BLAST score
                  314
                   4.0e-29
E value
Match length
                  96
                   67
% identity
NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  218181
                  LIB3148-037-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2980793
BLAST score
                   436
E value
                  2.0e-43
Match length
                  113
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  218182
                  LIB3148-037-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2980770
BLAST score
                  371
E value
                  9.0e-36
                  79
Match length
                  87
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  218183
Seq. ID
                  LIB3148-037-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                   476
```

```
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  218184
                  LIB3148-037-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461753
BLAST score
                  362
E value
                  2.0e-34
Match length
                  115
% identity
                  69
NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
                  PRECURSOR >gi_419773_pir_S31164 ATP-dependent ClpB
                  proteinase regulatory chain homolog precursor, chloroplast
                  - garden pea >gi 169128 (L09547) nuclear encoded precursor
                  to chloroplast protein [Pisum sativum]
Seq. No.
                  218185
Seq. ID
                  LIB3148-037-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3335375
BLAST score
                  187
E value
                  5.0e-14
Match length
                  39
% identity
                  77
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.
                  218186
Seq. ID
                  LIB3148-037-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3719211
BLAST score
                  165
E value
                  2.0e-11
```

Match length 42 % identity 76

218187

NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. ID LIB3148-037-Q1-K1-D7 Method BLASTX NCBI GI g4567249 BLAST score 543 E value 9.0e-56 Match length 141 % identity 71

Seq. No.

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 218188

Seq. ID LIB3148-037-Q1-K1-E1

BLASTX Method NCBI GI g4033467 BLAST score 247 5.0e-21 E value Match length 84 % identity 67

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi_1707366_emb CAA67798 (X99435) splicing factor



[Arabidopsis thaliana]

```
Seq. No.
                  218189
                  LIB3148-037-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3329368
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  97
Match length
                  69
% identity
NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]
                  218190
Seq. No.
                  LIB3148-037-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2204236
                  404
BLAST score
                  1.0e-39
E value
                  92
Match length
                  87
% identity
NCBI Description (Y13861) enoyl-ACP reductase [Nicotiana tabacum]
                  218191
Seq. No.
                  LIB3148-037-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084391
BLAST score
                  395
                  2.0e-38
E value
                  113
Match length
                  61
% identity
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG2)
NCBI Description
                  - common nasturtium (fragment) >gi 311837 emb CAA48325
                   (X68255) cellulase [Tropaeolum majus]
Seq. No.
                  218192
Seq. ID
                  LIB3148-037-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                  q1777669
BLAST score
                  55
E value
                  2.0e-22
Match length
                  55
% identity
                  100
                  Kalanchoe daigremontiana 18S ribosomal RNA gene, partial
NCBI Description
                  sequence
                  218193
Seq. No.
Seq. ID
                  LIB3148-037-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3237190
BLAST score
                  170
E value
                  4.0e-12
Match length
                  60
% identity
NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]
```

218194

LIB3148-037-Q1-K1-F1

Seq. No. Seq. ID



```
BLASTX
Method
                  g4006875
NCBI GI
BLAST score
                  148
                  1.0e-09
E value
Match length
                  61
                  57
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                  218195
                  LIB3148-037-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3236242
BLAST score
                  377
E value
                  2.0e-36
Match length
                  95
                  80
% identity
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis
                  thaliana]
Seq. No.
                  218196
Seq. ID
                  LIB3148-037-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3850569
BLAST score
                  141
E value
                  1.0e-08
Match length
                  44
% identity
NCBI Description (AC005278) ESTs gb T21276, gb T45403, and gb AA586113 come
                  from this gene. [Arabidopsis thaliana]
                  218197
Seq. No.
                  LIB3148-037-Q1-K1-F8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  33
E value
                  6.0e-09
Match length
                  33
                  58
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   218198
Seq. ID
                  LIB3148-037-Q1-K1-G1
                  BLASTX
Method
NCBI GI
                  g1694976
BLAST score
                  358
                   2.0e-34
E value
Match length
                  76
                  86
% identity
NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]
                   >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   218199
Seq. No.
Seq. ID
                  LIB3148-037-Q1-K1-G3
```

Method BLASTX NCBI GI g1362010 BLAST score 297



```
4.0e-27
E value
Match length
% identity
                  19
NCBI Description ubiquitin-like protein 9 - Arabidopsis thaliana
                  218200
Seq. No.
                  LIB3148-037-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  529
                  4.0e-54
E value
Match length
                  116
% identity
                  85
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                  218201
Seq. No.
                  LIB3148-037-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709535
BLAST score
                  545
E value
                  5.0e-56
Match length
                  135
                  79
% identity
NCBI Description DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447]
                   (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                  thaliana] >gi_1669658_emb_CAA70527_ (Y09355)
                  pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
Seq. No.
                  218202
                  LIB3148-037-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4138109
BLAST score
                  357
E value
                  3.0e - 34
Match length
                  100
% identity
NCBI Description (AJ006414) spermidine synthase [Lycopersicon esculentum]
Seq. No.
                  218203
Seq. ID
                  LIB3148-037-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1518113
BLAST score
                  162
E value
                  2.0e-11
Match length
                  62
% identity
```

NCBI Description (U66193) SLL2 [Brassica napus] 218204

Seq. ID LIB3148-037-Q1-K1-H11

Method BLASTX NCBI GI g2921340 BLAST score 660

Seq. No.

```
E value
                   2.0e-69
Match length
                   139
% identity
NCBI Description
                  (AF034134) MYB-like DNA-binding domain protein [Gossypium
Seq. No.
                   218205
Seq. ID
                   LIB3148-037-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                   q2465925
BLAST score
                  294
E value
                   2.0e-26
Match length
                  127
% identity
                   50
NCBI Description (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                  218206
Seq. ID
                  LIB3148-037-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4091806
BLAST score
                  262
E value
                   9.0e-23
Match length
                  109
% identity
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                  218207
Seq. ID
                  LIB3148-038-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4558678
BLAST score
                  200
E value
                  1.0e-15
                  93
Match length
% identity
NCBI Description (AC006586) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218208
Seq. ID
                  LIB3148-038-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3746069
BLAST score
                  147
E value
                  2.0e-09
Match length
                  97
% identity
                  33
NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  218209
Seq. ID
                  LIB3148-038-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2909781
BLAST score
                  495
E value
                  4.0e-50
Match length
                  133
% identity
NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump
```

NCBI Description

thalianal

[Arabidopsis thaliana]

```
Seq. No.
                     218210
   Seq. ID
                     LIB3148-038-Q1-K1-B2
  Method
                     BLASTX
  NCBI GI
                     g4096662
  BLAST score
                     665
  E value
                     4.0e-70
  Match length
                     130
   % identity
                     98
  NCBI Description (U35026) Rab1-like small GTP-binding protein [Petunia x
                     hybrida]
  Seq. No.
                     218211
  Seq. ID
                     LIB3148-038-Q1-K1-B9
  Method
                     BLASTN
  NCBI GI
                     g3687405
  BLAST score
                     55
  E value
                     3.0e-22
                     99
  Match length
  % identity
                     89
  NCBI Description Lycopersicon esculentum mRNA for hypothetical protein
  Seq. No.
                     218212
  Seq. ID
                     LIB3148-038-Q1-K1-C1
  Method
                     BLASTX
  NCBI GI
                     g2274859
  BLAST score
                     396
  E value
                     2.0e-38
  Match length
                     73
  % identity
                     97
  NCBI Description (AJ000016) Cks1 protein [Arabidopsis thaliana]
                     >gi_4510420_gb_AAD21506.1_ (AC006929) putative
                     cyclin-dependent kinase regulatory subunit [Arabidopsis
                     thaliana]
  Seq. No.
                     218213
Seq. ID
                     LIB3148-038-Q1-K1-C11
  Method
                    BLASTX
  NCBI GI
                     g1009363
  BLAST score
                     324
  E value
                     4.0e-30
  Match length
                     98
  % identity
  NCBI Description (D67086) RGP-3 [Nicotiana sylvestris]
  Seq. No.
                     218214
  Seq. ID
                     LIB3148-038-Q1-K1-C3
  Method
                     BLASTX
  NCBI GI
                     q4406807
  BLAST score
                     389
  E value
                     1.0e-37
  Match length
                     83
  % identity
                     88
```

(AC006201) putative elongation factor beta-1 [Arabidopsis



```
218215
Seq. No.
Seq. ID
                  LIB3148-038-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q464621
BLAST score
                  158
                  1.0e-10
E value
Match length
                  37
                  81
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                  [Mesembryanthemum crystallinum]
                  218216
Seq. No.
Seq. ID
                  LIB3148-038-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4455246
BLAST score
                  546
E value
                  4.0e-56
Match length
                  135
% identity
                  75
NCBI Description
                 (AL035523) putative protein [Arabidopsis thaliana]
                  218217
Seq. No.
Seq. ID
                  LIB3148-038-Q1-K1-D3
Method
                  BLASTN
                  q3985955
NCBI GI
BLAST score
                  39
E value
                  1.0e-12
Match length
                  83
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTH16, complete sequence [Arabidopsis thaliana]
                  218218
Seq. No.
Seq. ID
                  LIB3148-038-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q2507442
BLAST score
                  215
E value
                  1.0e-17
Match length
                  42
% identity
                  90
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi_1419685_emb_CAA67207_ (X98618) TCTP-like protein
                  [Medicago sativa]
Seq. No.
                  218219
Seq. ID
                  LIB3148-038-Q1-K1-D6
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3790100
BLAST score 362
E value 1.0e-34
Match length 73
% identity 89

NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta

subunit [Citrus X paradisi]

NCBI Description

```
Seq. No.
                   218220
Seq. ID
                  LIB3148-038-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q1703380
BLAST score
                  568
E value
                   1.0e-58
Match length
                  108
                  99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                  218221
Seq. No.
Seq. ID
                  LIB3148-038-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2497543
BLAST score
                  268
E value
                  1.0e-23
Match length
                  128
% identity
                  45
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
                  pyruvate kinase - common tobacco >gi_444023_emb_CAA82628
                  (Z29492) pyruvate kinase [Nicotiana tabacum]
Seq. No.
                  218222
Seq. ID
                  LIB3148-038-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  a3879543
BLAST score
                  180
E value
                  3.0e-13
Match length
                  67
% identity
                  54
NCBI Description (Z50071) similar to ATP-dependent helicase; cDNA EST
                  EMBL:D73826 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  218223
Seq. ID
                  LIB3148-038-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1354849
BLAST score
                  232
E value
                  3.0e-19
Match length
                  66
% identity
                  65
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.
                  218224
Seq. ID
                  LIB3148-038-Q1-K1-F2
                  BLASTX
Method
NCBI GI
                  g730290
BLAST score
                  456
E value
                  1.0e-45
Match length
                  128
% identity
                  62
```

PECTATE LYASE PRECURSOR >gi_322883_pir_ S29612 pectate lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328) pectate lyase [Lilium longiflorum] >gi_308902 (L18911)

pectate lyase [Lilium longiflorum]



```
Seq. No.
                  218225
                  LIB3148-038-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512667
BLAST score
                  403
                  2.0e-39
E value
Match length
                  118
% identity
                  65
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  218226
                  LIB3148-038-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201617
BLAST score
                  167
E value
                  5.0e-12
                  43
Match length
                  65
% identity
NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]
                  218227
Seq. No.
                  LIB3148-038-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244732
BLAST score
                  265
                  9.0e-24
E value
Match length
                  54
                  94
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                  218228
Seq. No.
                  LIB3148-038-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076331
BLAST score
                  308
E value
                  3.0e-28
Match length
                  74
                  80
% identity
                  histidine transport protein - Arabidopsis thaliana
NCBI Description
                  >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
                  1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His
                  transporter [Arabidopsis thaliana]
Seq. No.
                  218229
Seq. ID
                  LIB3148-038-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g606942
BLAST score
                  282
E value
                  6.0e-26
Match length
                  97
% identity
                  57
NCBI Description (U13760) unknown [Gossypium hirsutum]
```

Seq. No. 218230

Seq. ID LIB3148-038-Q1-K1-H11

Method BLASTX NCBI GI g1483563

Method

NCBI GI

BLAST score

BLASTX

141

g3334261

```
BLAST score
                   248
E value
                   8.0e-31
                   85
Match length
                   87
% identity
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.
                   218231
Seq. ID
                   LIB3148-038-Q1-K1-H12
Method
                   BLASTX
NCBI GI
                   g1703282
BLAST score
                   217
E value
                   8.0e-18
Match length
                   62
% identity
                   84
NCBI Description CHLOROPLAST AMINOPEPTIDASE PRECURSOR (LEUCINE
                   AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE
                   AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE)
                   >gi_542082_pir__S41376 leucyl aminopeptidase (EC 3.4.11.1)
- potato >gi_443979_emb_CAA54314_ (X77015) leucine
                   aminopeptidase [Solanum tuberosum]
Seq. No.
                   218232
Seq. ID
                   LIB3148-038-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g1658197
BLAST score
                   576
E value
                   1.0e-59
Match length
                   135
                   78
% identity
NCBI Description (U74630) calreticulin [Ricinus communis] >gi 1763297
                   (U74631) calreticulin [Ricinus communis]
Seq. No.
                   218233
Seq. ID
                   LIB3148-038-Q1-K1-H9
Method
                   BLASTX
NCBI GI
                   g606942
BLAST score
                   477
E value
                   5.0e-48
Match length
                   120
% identity
                   74
NCBI Description (U13760) unknown [Gossypium hirsutum]
Seq. No.
                   218234
Seq. ID
                   LIB3148-039-Q1-K1-A8
Method
                   BLASTN
NCBI GI
                   g2275090
BLAST score
                   173
E value
                   1.0e-92
Match length
                   193
% identity
                   97
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
Seq. No.
                   218235
Seq. ID
                   LIB3148-039-Q1-K1-A9
```



E value 1.0e-08 Match length 48 % identity 56

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)

metallothionein-like protein [Malus domestica]

Seq. No. 218236

Seq. ID LIB3148-039-Q1-K1-B11

Method BLASTX
NCBI GI 94220483
BLAST score 374
E value 6.0e-36
Match length 92
% identity 80

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 218237

Seq. ID LIB3148-039-Q1-K1-B2

Method BLASTX
NCBI GI g4544403
BLAST score 249
E value 3.0e-21
Match length 58
% identity 71

NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase

precursor [Arabidopsis thaliana]

Seq. No. 218238

Seq. ID LIB3148-039-Q1-K1-B8

Method BLASTX
NCBI GI g3334346
BLAST score 413
E value 1.0e-43
Match length 111
% identity 87

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG

>gi_2852445_dbj_BAA24697_ (AB003378) SUI1 homolog [Salix

bakko]

Seq. No. 218239

Seq. ID LIB3148-039-Q1-K1-C1

Method BLASTN
NCBI GI g12212
BLAST score 293
E value 1.0e-164
Match length 329
% identity 98

NCBI Description S.alba chloroplast rp123 and rp12 genes for ribosomal

proteins L23 and L2

Seq. No. 218240

Seq. ID LIB3148-039-Q1-K1-C2

Method BLASTN
NCBI GI g1922250
BLAST score 159
E value 1.0e-84
Match length 166

```
% identity 99
NCBI Description G.arboreum mRNA for farnesyl pyrophosphate synthase
Seq. No. 218241
Seq. ID LIB3148-039-Q1-K1-C5
Method BLASTX
NCBI GI 9730450
BLAST score 396
```

% identity 78
NCBI Description 60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
>gi_480649_pir__S37134 cold-induced protein BnC24B - ra

>gi_480649_pir__S37134 cold-induced protein BnC24B - rape
>gi_398922_emb_CAA80343_ (Z22620) cold induced protein

(BnC24B) [Brassica napus]

9.0e-39

98

E value

Match length

NCBI Description (AC000106) Similar to Saccharomyces hypothetical protein

YDR051c (gb_Z49209). ESTs gb_T44436,gb_42252 come from this

gene. [Arabīdopsis thaliana]

 Seq. No.
 218243

 Seq. ID
 LIB3148-039-Q1-K1-D1

 Method
 BLASTX

 NCBI GI
 g2500139

 BLAST score
 302

 E value
 1.0e-27

Match length 94 % identity 60

NCBI Description PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)

>gi_1653916_dbj_BAA18826_ (D90917) peptide chain release

factor [Synechocystis sp.]

Seq. No. 218244

Seq. ID LIB3148-039-Q1-K1-D10

Method BLASTX
NCBI GI g131384
BLAST score 564
E value 3.0e-58
Match length 125
% identity 86

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__\$04132

photosystem II oxygen-evolving complex protein 1 precursor
- garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_(D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf_1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. ID

```
Seq. No.
                   218245
Seq. ID
                   LIB3148-039-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                   g799005
BLAST score
                   88
E value
                   6.0e-42
Match length
                   88
% identity
                   100
NCBI Description S.rotundifolia Nutt. nrDNA (Oxelman 2231 (GB))
Seq. No.
                   218246
Seq. ID
                  LIB3148-039-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                   q3236251
BLAST score
                   549
E value
                   2.0e-56
Match length
                   143
% identity
                   74
NCBI Description
                  (AC004684) putative phosphoribosylaminoimidazole
                  carboxylase [Arabidopsis thaliana]
Seq. No.
                   218247
Seq. ID
                  LIB3148-039-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   33
E value
                   5.0e-09
Match length
                   33
% identity
                   58
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   218248
Seq. ID
                   LIB3148-039-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                   g4455172
BLAST score
                  286
E value
                   1.0e-25
                  80
Match length
% identity
                   68
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   218249
Seq. ID
                  LIB3148-039-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                   g3834304
BLAST score
                   524
E value
                   1.0e-53
Match length
                  120
                   78
% identity
NCBI Description
                  (AC005679) Contains similarity to gi 1786244 hypothetical
                  24.9 kD protein in surA-hepA intergenic region yab0 from
                  Escherichia coli genome gb AE000116, and to hypothetical
                  YABO family PF_00849. [Arabidopsis thaliana]
Seq. No.
                  218250
```

30643

LIB3148-039-Q1-K1-F2

```
BLASTX
Method
NCBI GI
                   q486757
                   148
BLAST score
E value
                   2.0e-09
Match length
                   79
                   54
% identity
                   anther-specific protein (clone Bgp1) - field mustard
NCBI Description
                   >gi_311938_emb_CAA48292 (X68210) bgp1 [Brassica rapa]
>gi_448272_prf__1916399A Bgp1 gene [Brassica rapa]
Seq. No.
                   218251
                   LIB3148-039-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1169534
BLAST score
                   440
E value
                   6.0e-44
                   100
Match length
                   89
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                   phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                   >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus
                   communis]
Seq. No.
                   218252
Seq. ID
                   LIB3148-039-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g2146727
                   534
BLAST score
                   1.0e-54
E value
Match length
                   136
                   76
% identity
NCBI Description
                   cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 -
                   Arabidopsis thaliana (fragment) >gi 598069 (L37884)
                   cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                    218253
                   LIB3148-039-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g117954
BLAST score
                   260
E value
                    1.0e-22
Match length
                   51
% identity
                    92
NCBI Description CYTOCHROME C >gi 65509 pir CCLK cytochrome c - leek
Seq. No.
                    218254
Seq. ID
                   LIB3148-039-Q1-K1-G1
Method
                   BLASTX
```

NCBI GI g730557 BLAST score 406 7.0e-40 E value 90 Match length 90 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal

protein L34 - garden pea >gi 498908 (U10047) ribosomal

protein L34 homolog [Pisum sativum]

Seq. No.

218260

```
Seq. No.
                   218255
Seq. ID
                  LIB3148-039-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q1399265
BLAST score
                  146
E value
                   3.0e-09
Match length
                   94
% identity
                   35
NCBI Description
                   (U31751) calmodulin-domain protein kinase CDPK isoform 9
                   [Arabidopsis thaliana]
Seq. No.
                  218256
Seq. ID
                  LIB3148-039-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1408471
BLAST score
                  240
                  3.0e-20
E value
Match length
                  57
% identity
                  74
NCBI Description
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
Seq. No.
                  218257
Seq. ID
                  LIB3148-039-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g4325342
BLAST score
                  160
E value
                  8.0e-11
Match length
                  33
% identity
NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]
Seq. No.
                  218258
Seq. ID
                  LIB3148-039-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g285286
BLAST score
                  267
E value
                  2.0e-23
Match length
                  91
% identity
                  55
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
Seq. No.
                  218259
Seq. ID
                  LIB3148-039-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1408471
BLAST score
                  521
E value
                  4.0e-53
Match length
                  115
% identity
                  82
NCBI Description
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
```

Match length

% identity

104

47

NCBI Description (X80472) sts15 [Solanum tuberosum]



```
Seq. ID
                   LIB3148-039-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   q4467146
BLAST score
                   426
E value
                   4.0e-42
Match length
                   103
% identity
NCBI Description
                  (AL035540) galactosidase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   218261
Seq. ID
                   LIB3148-039-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   g1350707
BLAST score
                   212
E value
                   6.0e-17
Match length
                   52
% identity
                   73
NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal
                   protein 17K - mouse >gi 404766 (L08651) ribosomal protein
                   [Mus musculus]
Seq. No.
                   218262
Seq. ID
                  LIB3148-039-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q133406
BLAST score
                  518
E value
                   9.0e-53
Match length
                  150
% identity
                   69
NCBI Description DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN
                   >gi_81501_pir__C23525 DNA-directed RNA polymerase (EC
                   2.7.7.6) alpha chain - spinach chloroplast
                  >gi_12265_emb_CAA27214_ (X03496) pot. RNA polymerase alpha
                   subunit (aa 1-335) [Spinacia oleracea]
Seq. No.
                  218263
Seq. ID
                  LIB3148-040-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3548801
BLAST score
                  199
E value
                  1.0e-15
                  90
Match length
                  47
% identity
NCBI Description
                  (AC005313) putative transmembrane protein [Arabidopsis
                  thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative
                  integral membrane protein [Arabidopsis thaliana]
Seq. No.
                  218264
Seq. ID
                  LIB3148-040-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g1616628
BLAST score
                  212
E value
                  5.0e-17
```

NCBI GI

```
Seq. No.
                   218265
Seq. ID
                   LIB3148-040-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g1220196
BLAST score
                   186
E value
                   6.0e-14
Match length
                   38
% identity
                   97
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                   218266
Seq. ID
                   LIB3148-040-Q1-K1-B9
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   32
E value
                   9.0e-09
Match length
                   48
% identity
                   65
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   218267
Seq. ID
                   LIB3148-040-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g4512685
BLAST score
                   209
E value
                   1.0e-16
Match length
                   95
% identity
                   41
NCBI Description
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
                   >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   218268
Seq. ID
                  LIB3148-040-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1888485
BLAST score
                  274
E value
                  3.0e-24
Match length
                  65
% identity
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
Seq. No.
                  218269
Seq. ID
                  LIB3148-040-Q1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  38
% identity
                  61
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  218270
Seq. ID
                  LIB3148-040-Q1-K1-D2
Method
                  BLASTX
```

30647

g3461846

NCBI GI

E value

BLAST score

Match length

% identity

g2959781

1.0e-71

679

133

92

```
BLAST score
                   481
E value
                   2.0e-48
Match length
                   138
% identity
                   32
NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis
                  thaliana]
Seq. No.
                   218271
Seq. ID
                  LIB3148-040-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4567282
BLAST score
                  224
E value
                   2.0e-18
Match length
                  69
% identity
NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]
Seq. No.
                  218272
Seq. ID
                  LIB3148-040-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2499613
BLAST score
                  222
E value
                   4.0e-18
Match length
                  48
% identity
                  90
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2
                  >gi_1204129_emb_CAA57719_ (X82268) protein kinase [Medicago
                  satival
Seq. No.
                  218273
Seq. ID
                  LIB3148-040-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4539369
BLAST score
                  295
E value
                  1.0e-26
Match length
                  84
% identity
                  65
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  218274
Seq. ID
                  LIB3148-040-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g2570118
BLAST score
                  55
E value
                  3.0e-22
Match length
                  83
% identity
                  92
NCBI Description S.latifolia mRNA, clone CCLS
Seq. No.
                  218275
Seq. ID
                  LIB3148-040-Q1-K1-F4
Method
                  BLASTX
```

Seq. ID

```
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                  218276
Seq. No.
Seq. ID
                  LIB3148-040-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2190012
BLAST score
                  160
E value
                  7.0e-11
Match length
                  42
% identity
                  67
NCBI Description (AB004242) din1 [Raphanus sativus]
Seq. No.
                  218277
                  LIB3148-040-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  g3915873
NCBI GI
BLAST score
                  614
E value
                  4.0e-64
Match length
                  128
                  91
% identity
NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
                  (NODULIN-100) >gi 2606081 (AF030231) sucrose synthase
                  [Glycine max]
Seq. No.
                  218278
Seq. ID
                  LIB3148-040-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  260
E value
                  1.0e-22
Match length
                  86
% identity
                  62
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  218279
Seq. ID
                  LIB3148-040-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4454032
BLAST score
                  425
E value
                  6.0e-42
Match length
                  116
% identity
                  70
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                  218280
Seq. No.
Seq. ID
                  LIB3148-040-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2462754
BLAST score
                  332
E value
                  4.0e-31
Match length
                  126
% identity
                  60
NCBI Description (AC002292) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  218281
```

30649

LIB3148-040-Q1-K1-H4

```
BLASTX
Method
NCBI GI
                  q627281
                  196
BLAST score
E value
                  4.0e-15
Match length
                  91
                  46
% identity
NCBI Description allantoinase (EC 3.5.2.5) precursor - bullfrog
                  218282
Seq. No.
                  LIB3148-040-Q1-K1-H6
Seq. ID
Method
                  BLASTX
                  g3493172
NCBI GI
BLAST score
                  161
E value
                  2.0e-11
Match length
                  54
                  63
% identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
                  218283
Seq. No.
                  LIB3148-040-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g133867
NCBI GI
BLAST score
                  503
E value
                  4.0e-51
Match length
                  115
                  83
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                  protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
                  218284
Seq. No.
                  LIB3148-040-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2598575
BLAST score
                  143
E value
                  7.0e-09
Match length
                  84
% identity
                  36
NCBI Description (Y15293) MtN21 [Medicago truncatula]
                  218285
Seq. No.
Seq. ID
                  LIB3148-041-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  g1439608
BLAST score
                  175
E value
                  5.0e-94
```

Match length 179 % identity 99

NCBI Description Gossypium hirsutum delta-tonoplast intrinsic protein mRNA,

complete cds

Seq. No. 218286

Seq. ID LIB3148-041-Q1-K1-A10

Method BLASTN NCBI GI g1732362 BLAST score 41 E value 6.0e-14

```
Match length
% identity
                   92
NCBI Description Malus domestica pAFD103 mRNA, partial cds
Seq. No.
                   218287
Seq. ID
                  LIB3148-041-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1912286
BLAST score
                  403
E value
                   1.0e-39
Match length
                  77
                   95
% identity
NCBI Description
                  (U39568) type 2A serine/threonine protein phosphatase
                   [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to
                  Arabidopsis protein phosphatase PP2A (gb U39568). EST
                   gb_T41959 comes from this gene. [Arabidopsis thaliana]
                   218288
Seq. No.
Seq. ID
                  LIB3148-041-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g310587
BLAST score
                  169
E value
                   4.0e-12
Match length
                  56
% identity
                  62
NCBI Description
                  (L20864) ascorbate peroxidase [Spinacia oleracea]
                  >gi_1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate
                  peroxidase [Spinacia oleracea]
Seq. No.
                  218289
Seq. ID
                  LIB3148-041-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  q4098126
BLAST score
                  82
E value
                  2.0e-38
Match length
                  160
                  994
% identity
NCBI Description Gossypium hirsutum sucrose synthase mRNA, partial cds
Seq. No.
                  218290
Seq. ID
                  LIB3148-041-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g2369713
BLAST score
                  34
E value
                  1.0e-09
Match length
                  38
                  97
% identity
NCBI Description Beta vulgaris cDNA for elongation factor
```

 Seq. No.
 218291

 Seq. ID
 LIB3148-041-Q1-K1-B2

 Method
 BLASTN

 NCBI GI
 g3449334

BLAST score 56
E value 8.0e-23
Match length 140
% identity 85



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  218292
Seq. ID
                  LIB3148-041-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g571519
BLAST score
                  201
E value
                   4.0e-16
Match length
                  70
% identity
                  10
NCBI Description
                  (U16852) polyubiquitin [Gracilaria verrucosa]
                  >gi_1095488_prf__2109223A poly-ubiquitin [Gracilaria
                  verrucosal
Seq. No.
                  218293
Seq. ID
                  LIB3148-041-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1346180
BLAST score
                  349
E value
                  3.0e - 33
Match length
                  78
% identity
                  83
                  GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374)
NCBI Description
                  homology with RNA-binding proteins in meristematic tissue
                  [Sinapis alba]
Seq. No.
                  218294
Seq. ID
                  LIB3148-041-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1076678
BLAST score
                  366
E value
                  2.0e-35
Match length
                  82
% identity
                  91
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  218295
Seq. ID
                  LIB3148-041-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3080415
BLAST score
                  438
E value
                  1.0e-43
Match length
                  97
% identity
                  80
                 (AL022604) cysteine proteinase - like protein [Arabidopsis
                  thaliana]
```

NCBI Description

Seq. No. 218296

Seq. ID LIB3148-041-Q1-K1-C11

Method BLASTX NCBI GI q2495365 BLAST score 389 E value 6.0e-38 Match length 97 % identity 80

NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B

NCBI Description

thaliana]



heat shock protein HSP81-2 [Arabidopsis thaliana]

```
Seq. No.
                  218297
Seq. ID
                  LIB3148-041-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3334346
BLAST score
                  305
E value
                  4.0e-28
Match length
                  60
% identity
                  97
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
                  >gi_2852445_dbj_BAA24697 (AB003378) SUI1 homolog [Salix
                  bakko]
Seq. No.
                  218298
Seq. ID
                  LIB3148-041-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  425
E value
                  3.0e-42
Match length
                  89
% identity
                  89
NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                  >gi_2129500_pir S52006 polygalacturonase - upland cotton
                  >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  218299
Seq. ID
                  LIB3148-041-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  159
E value
                  6.0e-11
Match length
                  51
% identity
                  63
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                  218300
Seq. ID
                  LIB3148-041-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2252841
BLAST score
                  187
E value
                  3.0e-14
Match length
                  89
% identity
                  46
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  218301
Seq. ID
                  LIB3148-041-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4455170
BLAST score
                  209
E value
                  7.0e-17
Match length
                  55
% identity
```

30653

(AL035521) fatty acid elongase-like protein [Arabidopsis



```
Seq. No.
                   218302
Seq. ID
                   LIB3148-041-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   g2500047
BLAST score
                   463
E value
                   1.0e-46
                   97
Match length
% identity
                   87
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                   PHOSPHO-HYDROLASE) (PPASE) >gi_534916_emb_CAA85362
                   (Z36894) soluble inorganic pyrophosphatase [Solanum
                   tuberosum]
Seq. No.
                   218303
Seq. ID .
                  LIB3148-041-01-K1-F8
Method
                  BLASTX
NCBI GI
                  g2832664
BLAST score
                  160
E value
                   4.0e-11
Match length
                  88
% identity
NCBI Description (AL021710) pollen-specific protein - like [Arabidopsis
                  thaliana]
Seq. No.
                  218304
Seq. ID
                  LIB3148-041-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4406759
BLAST score
                  200
E value
                  7.0e-16
                  76
Match length
% identity
                  57
NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  218305
Seq. ID
                  LIB3148-041-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q4468798
BLAST score
                  206
E value
                  2.0e-16
Match length
                  92
% identity
                  45
NCBI Description (AJ010440) GST7 protein [Zea mays]
Seq. No.
                  218306
Seq. ID
                  LIB3148-042-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3914473
```

Method BLASTX
NCBI GI g3914473
BLAST score 440
E value 8.0e-44
Match length 108
% identity 77

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_479684_pir__S35151 photosystem I chain XI - spinach >gi_396275_emb_CAA45775_ (X64445) subunit XI of

photosystem I reaction center [Spinacia oleracea]

Method

NCBI GI

BLASTN

g2264317

```
Seq. No.
                   218307
Seq. ID
                   LIB3148-042-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2529229
BLAST score
                   401
E value
                   2.0e-39
Match length
                  85
% identity
                   88
NCBI Description (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
Seq. No.
                   218308
Seq. ID
                  LIB3148-042-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q1710807
BLAST score
                  266
E value
                   3.0e-23
Match length
                  71
% identity
                   75
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390
                   (U21105) alphacpn60 [Pisum sativum]
Seq. No.
                  218309
Seq. ID
                  LIB3148-042-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                  q407800
BLAST score
                  210
E value
                  1.0e-114
Match length
                  258
% identity
                  96
NCBI Description G.hirsutum mRNA for ribosomal protein 41, large subunit
                   (RL41)
Seq. No.
                  218310
Seq. ID
                  LIB3148-042-Q1-K1-A8
Method
                  BLASTN
NCBI GI
                  g18511
BLAST score
                  232
E value
                  1.0e-128
Match length
                  232
% identity
                  100
NCBI Description G.hirsutum light regulated unknown reading frame DNA
Seq. No.
                  218311
Seq. ID
                  LIB3148-042-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3821780
                  33
BLAST score
E value
                  3.0e-09
Match length
                  38
% identity
                  45
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  218312
Seq. ID
                  LIB3148-042-Q1-K1-B9
```



BLAST score 48
E value 4.0e-18
Match length 80
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 218313

Seq. ID LIB3148-042-Q1-K1-C1

Method BLASTX
NCBI GI g122007
BLAST score 268
E value 1.0e-23
Match length 60
% identity 93

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley

>gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 218314

Seq. ID LIB3148-042-Q1-K1-C11

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 218315

Seq. ID LIB3148-042-Q1-K1-C2

Method BLASTX
NCBI GI g1480027
BLAST score 508
E value 8.0e-52
Match length 115
% identity 89

NCBI Description (D78500) putative aldolase [Brassica rapa]

Seq. No. 218316

Seq. ID LIB3148-042-Q1-K1-C3

Method BLASTX
NCBI GI g2130073
BLAST score 237
E value 2.0e-20
Match length 63
% identity 75

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase

C-1 [Oryza sativa] $\overline{>}$ gi 7909 $\overline{7}$ 0 dbj BAA088 $\overline{3}$ 0 (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 218317

Seq. ID LIB3148-042-Q1-K1-C4

Method BLASTX NCBI GI g1336084 BLAST score 456

% identity

75

```
E value
                   9.0e-46
Match length
                   97
% identity
                   86
NCBI Description (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
                   (GDH2) mRNA, complete cds. [Arabidopsis thaliana]
Seq. No.
                   218318
Seq. ID
                   LIB3148-042-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   g4455365
BLAST score
                   366
E value
                   3.0e-35
                   74
Match length
                   86
% identity
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   218319
Seq. ID
                   LIB3148-042-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g1845567
BLAST score
                   154
E value
                   2.0e-10
Match length
                   51
% identity
                   57
NCBI Description (D89435) cytochrome P450 [Glycyrrhiza echinata]
Seq. No.
                   218320
Seq. ID
                   LIB3148-042-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g730290
BLAST score
                   363
E value
                   1.0e-34
Match length
                   119
% identity
                   55
NCBI Description PECTATE LYASE PRECURSOR >gi_322883_pir__S29612 pectate
                   lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328) pectate lyase [Lilium longiflorum] >gi_308902 (L18911)
                   pectate lyase [Lilium longiflorum]
                   218321
Seq. No.
Seq. ID
                   LIB3148-042-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g533256
BLAST score
                   322
E value
                   5.0e-30
Match length
                   103
% identity
                   59
NCBI Description (L27101) pectinesterase [Petunia inflata]
Seq. No.
                   218322
Seq. ID
                   LIB3148-042-Q1-K1-E11
Method
                   BLASTX
NCBI GI
                   g1171978
BLAST score
                   249
E value
                   3.0e-21
Match length
                   59
```



```
NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                  (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                  [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                  218323
                  LIB3148-042-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3355480
BLAST score
                  226
E value
                  1.0e-18
Match length
                  91
                  49
% identity
NCBI Description
                  (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  218324
Seq. ID
                  LIB3148-042-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q4220524
BLAST score
                  270
E value
                  7.0e-24
Match length
                  61
% identity
                  77
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  218325
Seq. No.
Seq. ID
                  LIB3148-042-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2529683
BLAST score
                  535
E value
                  6.0e-55
Match length
                  121
% identity
                  79
NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]
                  218326
Seq. No.
Seq. ID
                  LIB3148-042-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3264759
BLAST score
                  134
E value
                  6.0e-11
                  63
Match length
% identity
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
Seq. No.
                  218327
Seq. ID
                  LIB3148-042-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q2829869
```

Method BLASTX
NCBI GI g2829869
BLAST score 195
E value 4.0e-15
Match length 49
% identity 71

NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

```
Seq. No.
                    218328
Seq. ID
                   LIB3148-042-Q1-K1-F9
Method
                   BLASTN
NCBI GI
                   g2623909
BLAST score
                   154
E value
                   2.0e-81
Match length
                   181
% identity
                   95
NCBI Description
                   Gossypium arboreum ATPase B subunit (atpB) and ribulose
                   1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL)
                   genes, chloroplast genes encoding chloroplast proteins,
                   partial cds, and atpB-rbcL intergenic spacer
Seq. No.
                   218329
Seq. ID
                   LIB3148-042-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g3024127
BLAST score
                   649
E value
                   3.0e-68
Match length
                   126
% identity
                   94
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
Seq. No.
                   218330
Seq. ID
                   LIB3148-042-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   q135860
BLAST score
                   308
E value
                   1.0e-36
                   98
Match length
% identity
                   80
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic
                   protein gamma - Arabidopsis thaliana
                   >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                   protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                   >gi_445129_prf _1908432B tonoplast intrinsic protein gamma
                   [Arabidopsis thaliana]
Seq. No.
                   218331
Seq. ID
                   LIB3148-042-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1113861
BLAST score
                   248
E value
                   2.0e-21
Match length
                   100
% identity
                   50
```

Seq. No. 218332

Seq. ID LIB3148-042-Q1-K1-G5

Method BLASTX

NCBI Description (U39930) nitrate reductase [Chlorella vulgaris] >gi_1113863 (U39931) nitrate reductase [Chlorella vulgaris]



NCBI GI g1928981 BLAST score 469 E value 3.0e-47 Match length 120 % identity 76

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 218333

Seq. ID LIB3148-042-Q1-K1-G6

Method BLASTX
NCBI GI g1709825
BLAST score 291
E value 2.0e-26
Match length 93
% identity 67

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 218334

Seq. ID LIB3148-042-Q1-K1-H11

Method BLASTX
NCBI GI g1237080
BLAST score 394
E value 3.0e-38
Match length 83
% identity 93

NCBI Description (X96764) ADP-glucose pyrophosphorylase [Pisum sativum]

Seq. No. 218335

Seq. ID LIB3148-042-Q1-K1-H3

Method BLASTX
NCBI GI g2281098
BLAST score 441
E value 7.0e-44
Match length 122
% identity 64

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 218336

Seq. ID LIB3148-042-Q1-K1-H4

Method BLASTX
NCBI GI g4512679
BLAST score 336
E value 2.0e-31
Match length 83
% identity 78

NCBI Description (AC006931) putative 60S ribosomal protein L11B [Arabidopsis

thaliana]

Seq. No. 218337

Seq. ID LIB3148-042-Q1-K1-H5

Method BLASTX
NCBI GI g4539662
BLAST score 166
E value 8.0e-12
Match length 90

```
% identity
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                  218338
Seq. ID
                  LIB3148-043-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3548801
BLAST score
                  148
E value
                   2.0e-09
Match length
                  66
% identity
                  41
                  (AC005313) putative transmembrane protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4335768_gb_AAD17445_ (AC006284) putative
                  integral membrane protein [Arabidopsis thaliana]
Seq. No.
                  218339
Seq. ID
                  LIB3148-043-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4263790
BLAST score
                  226
E value
                  1.0e-18
Match length
                  53
% identity
                  83
NCBI Description (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
Seq. No.
                  218340
Seq. ID
                  LIB3148-043-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3355466
BLAST score
                  186
E value
                  6.0e-14
Match length
                  104
% identity
                  38
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218341
Seq. ID
                  LIB3148-043-Q1-K1-B1
Method
                  BLASTX
                  q2997694
                  359
                  3.0e-34
                  114
% identity
                  55
```

NCBI GI BLAST score E value Match length

NCBI Description (AF053721) putative retrovirus-related polyprotein

[Lithospermum erythrorhizon]

Seq. No. 218342

Seq. ID LIB3148-043-Q1-K1-B3

Method BLASTX NCBI GI q1076579 BLAST score 217 E value 5.0e-18 Match length 51 % identity 73

NCBI Description alcohol dehydrogenase homolog ADH3a - tomato

Seq. No. 218343

```
Seq. ID
                  LIB3148-043-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q3413716
BLAST score
                  157
E value
                  2.0e-10
Match length
                  134
% identity
                  15
NCBI Description
                  (AC004747) unknown protein [Arabidopsis thaliana]
                  >gi 3643589 (AC005395) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  218344
Seq. ID
                  LIB3148-043-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q4138912
BLAST score
                  336
E value
                  2.0e-31
Match length
                  69
% identity
NCBI Description (AF059487) expansin precursor [Lycopersicon esculentum]
                  218345
Seq. No.
Seq. ID
                  LIB3148-043-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3372233
BLAST-score
                  375
E value
                  4.0e-36
Match length
                  82
% identity
                  87
NCBI Description
                 (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
                  [Arabidopsis thaliana]
Seq. No.
                  218346
Seq. ID
                  LIB3148-043-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3021355
BLAST score
                  277
E value
                  1.0e-24
Match length
                  51
% identity
                  90
NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
                  tetragonoloba]
                  218347
Seq. No.
Seq. ID
                  LIB3148-043-Q1-K1-D2
                  BLASTX
Method
NCBI GI
                  q3335349
BLAST score
                  188
E value
                  4.0e-14
Match length
                  97
% identity
                  45
NCBI Description
                  (AC004512) Similar to gb U46691 putative chromatin
                  structure regulator (SUPT6H) from Homo sapiens. ESTs
                  gb_T42908, gb_AA586170 and gb_AA395125 come from this gene.
```

[Arabidopsis thaliana]



```
LIB3148-043-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g122007
BLAST score
                   346
                   5.0e-33
E value
Match length
                   91
                   76
% identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
Seq. No.
                   218349
Seq. ID
                   LIB3148-043-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   g3334765
BLAST score
                   319
E value
                   1.0e-29
Match length
                   102
                   64
% identity
                  (AJ225047) Hsp19.9 protein [Lycopersicon peruvianum]
NCBI Description
Seq. No.
                   218350
                   LIB3148-043-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3128175
BLAST score
                   157
                   2.0e-10
E value
                   114
Match length
% identity
                   33
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   218351
                   LIB3148-043-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464849
BLAST score
                   595
E value
                   7.0e-62
Match length
                   112
                   100
% identity
                   TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 2041\overline{3} emb \overline{CAA47635} (X67162)
                   alpha-tubulin [Prunus dulcis]
Seq. No.
                   218352
Seq. ID
                   LIB3148-043-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   q4105800
BLAST score
                   350
E value
                   1.0e-38
Match length
                   119
% identity
NCBI Description (AF049931) PGP301 [Petunia x hybrida]
```

Seq. ID LIB3148-043-Q1-K1-F7

Method BLASTX NCBI GI g2495365



```
BLAST score
                  304
                  9.0e-28
E value
Match length
                  92
% identity
                  72
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  218354
Seq. No.
Seq. ID
                  LIB3148-043-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q4056462
BLAST score
                  162
E value
                  1.0e-17
Match length
                  76
% identity
                  59
NCBI Description
                  (AC005990) Strong similarity to gb Y09876 aldehyde
                  dehydrogenase (NAD+) from Nicotiana tabacum and a member of
                  the aldehyde dehydrogenase family PF 00171. ESTs
                  gb_F15117, gb_R83958 and gb_586262 come from this gene.
                  [Arabidopsis thaliana]
                  218355
Seq. No.
Seq. ID
                  LIB3148-043-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q625509
BLAST score
                  361
E value
                  5.0e - 35
                  72
Match length
% identity
                  25
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.
                  218356
                  LIB3148-043-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512591
BLAST score
                  163
E value
                  3.0e-11
                  34
Match length
% identity
                  88
NCBI Description (AB023789) flavanone 3-hydroxyrase [Ipomoea batatas]
Seq. No.
                  218357
Seq. ID
                  LIB3148-043-Q1-K1-G4
                  BLASTN
Method
                  g3242658
                  38
```

NCBI GI BLAST score 5.0e-12 E value Match length 62 90 % identity

NCBI Description Coffea arabica mRNA for spermidine synthase, complete cds

218358 Seq. No.

Seq. ID LIB3148-043-Q1-K1-G6

Method BLASTN NCBI GI q287810 BLAST score 38 E value 5.0e-12



```
Match length
% identity
                  96
NCBI Description M.sativa mRNA for phosphoprotein phosphatase type 2A
Seq. No.
                  218359
Seq. ID
                  LIB3148-043-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2119042
BLAST score
                  199
E value
                  2.0e-15
Match length
                  40
                  95
% identity
NCBI Description glycine-rich RNA-binding protein RGP-la - wood tobacco
                  >gi_469070_dbj_BAA03741_ (D16204) RNA-binding glycine-rich
                  protein-1 (RGP-1a) [Nicotiana sylvestris]
Seq. No.
                  218360
Seq. ID
                  LIB3148-043-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3128168
BLAST score
                  407
E value
                  8.0e-40
Match length
                  123
% identity.
                  56
NCBI Description (AC004521) putative carboxyl-terminal peptidase
                  [Arabidopsis thaliana]
                  218361
Seq. No.
Seq. ID
                  LIB3148-043-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1708191
BLAST score
                  484
E value
                  6.0e-49
Match length
                  123
% identity
                  68
NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
                  carrier protein [Ricinus communis]
Seq. No.
                  218362
Seq. ID
                  LIB3148-044-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  157
E value
                  2.0e-10
Match length
                  110
% identity
                  29
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
```

Seq. ID LIB3148-044-Q1-K1-A3

Method BLASTX NCBI GI g4510417 BLAST score 236 E value 2.0e-28 Match length 82

% identity

NCBI Description (AC006929) putative BEL1 homeotic protein [Arabidopsis

Seq. ID

218369

LIB3148-044-Q1-K1-B9



thaliana]

```
218364
Seq. No.
Seq. ID
                  LIB3148-044-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1362078
BLAST score
                  185
                  4.0e-14
E value
Match length
                  48
% identity
                  65
NCBI Description
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
                   - common nasturtium >gi_311835_emb_CAA48324_ (X68254)
                  cellulase [Tropaeolum majus]
                  218365
Seq. No.
                  LIB3148-044-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829894
BLAST score
                   461
E value
                   4.0e-46
Match length
                  128
                  72
% identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   218366
Seq. ID
                  LIB3148-044-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                   g3033380
                   523
BLAST score
E value
                   2.0e-53
Match length
                   134
                   76
% identity
                  (AC004238) putative coatomer epsilon subunit [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   218367
Seq. ID
                  LIB3148-044-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1276977
BLAST score
                   597
E value
                   4.0e-62
                   135
Match length
                   87
% identity
NCBI Description (U47143) nonsymbiotic hemoglobin [Glycine max]
Seq. No.
                   218368
Seq. ID
                   LIB3148-044-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   q1762148
BLAST score
                   648
E value
                   4.0e-68
Match length
                   134
% identity
                   91
NCBI Description (U48695) glutamate dehydrogenase [Solanum lycopersicum]
```

Method

NCBI GI

BLASTX

g4567302



```
Method
                  BLASTX
NCBI GI
                  q992706
BLAST score
                  153
E value
                  5.0e-10
Match length
                  34
% identity
                  85
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]
Seq. No.
                  218370
Seq. ID
                  LIB3148-044-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q4406780
BLAST score
                  597
E value
                  4.0e-62
Match length
                  138
% identity
                  85
NCBI Description (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  218371
Seq. ID
                  LIB3148-044-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g231509
BLAST score
                  501
E value
                  8.0e-51
Match length
                  114
% identity
                  81
NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935
                  actin-depolymerizing factor - trumpet lily
                  >gi 22748 emb CAA78483 (Z14110) actin depolymerizing
                  factor [Lilium longiflorum]
                  218372
Seq. No.
Seq. ID
                  LIB3148-044-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q139780
BLAST score
                  195
                  5.0e-15
E value
                  75
Match length
                  56
% identity
NCBI Description WOUND-INDUCED PROTEIN 1 >gi 82293 pir JQ0398 wun1 protein
                  - potato
Seq. No.
                  218373
Seq. ID
                  LIB3148-044-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4220524
BLAST score
                  251
E value
                  2.0e-21
Match length
                  62
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  218374
Seq. ID
                  LIB3148-044-Q1-K1-E11
```

```
BLAST score
                  3.0e-30
E value
Match length
                  80
% identity
                  85
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218375
Seq. ID
                  LIB3148-044-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1279598
BLAST score
                  217
E value
                  2.0e-17
Match length
                  120
% identity
                  38
NCBI Description (Z71752) pectin methylesterase [Nicotiana plumbaginifolia]
Seq. No.
                  218376
Seq. ID
                  LIB3148-044-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4325367
BLAST score
                  193
E value
                  1.0e-14
Match length
                  98
% identity
                  49
NCBI Description (AF128396) contains similarity to Nicotiana tabacum B-type
                  cyclin (GB:D50737) [Arabidopsis thaliana]
Seq. No.
                  218377
Seq. ID
                  LIB3148-044-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g729477
BLAST score
                  641
E value
                  3.0e-67
Match length
                  131
% identity
                  92
NCBI Description
                 FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                  >gi 320548 pir A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi 167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >gi_226768 prf_1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
Seq. No.
                  218378
Seq. ID
                  LIB3148-044-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g462567
BLAST score
                  165
E value
                  2.0e-11
Match length
                  40
% identity
                  72
NCBI Description MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE)
                  (PMI) (PHOSPHOHEXOMUTASE) >gi_631328_pir__S41122
                  mannose-6-phosphate isomerase (EC 5.3.1.8) - human
                  >gi 416017 emb CAA53657 (X76057) phosphomannose isomerase
                  [Homo sapiens] >gi_740967_prf 2006245A phosphomannose
                  isomerase [Homo sapiens] >gi 4505235 ref NP 002426.1 pMPI
```

30668

mannose phosphate isomerase

Seq. ID

```
218379
Seq. No.
                  LIB3148-044-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3834330
BLAST score
                  150
                  1.0e-09
E value
Match length
                  81
% identity
                  49
NCBI Description (AC005679) F9K20.17 [Arabidopsis thaliana]
Seq. No.
                  218380
                  LIB3148-044-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707955
BLAST score
                  665
                  4.0e-70
E value
Match length
                  132
% identity
                  95
NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
                  (GLUTAMATE--AMMONIA LIGASE) >gi 1134896 emb CAA63981
                  (X94320) glutamine synthetase [Vitis vinifera]
Seq. No.
                  218381
Seq. ID
                  LIB3148-044-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4467119
BLAST score
                  310
E value
                  5.0e-29
Match length
                  68
% identity
                  84
NCBI Description (AL035538) Histone deacetylase [Arabidopsis thaliana]
Seq. No.
                  218382
Seq. ID
                  LIB3148-044-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1173027
BLAST score
                  209
E value
                  1.0e-16
                  74
Match length
                  59
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                  218383
Seq. ID
                  LIB3148-044-Q1-K1-G8
                  BLASTX
Method
NCBI GI
                  g2454182
BLAST score
                  201
E value
                  8.0e-16
Match length
                  42
% identity
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
Seq. No.
                  218384
```

30669

LIB3148-044-Q1-K1-H7

```
Method
                  BLASTX
NCBI GI
                  g2244806
BLAST score
                  258
E value
                   2.0e-22
Match length
                  98
                  55
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  218385
                  LIB3148-045-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2104681
BLAST score
                  249
E value
                  2.0e-21
Match length
                  119
% identity
                  51
NCBI Description (X97907) transcription factor [Vicia faba]
                  218386
Seq. No.
Seq. ID
                  LIB3148-045-Q1-K1-A8
Method
                  BLASTX
                  g3881507
NCBI GI
BLAST score
                  301
E value
                  2.0e-27
Match length
                  91
% identity
                  55
NCBI Description (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
                  yk375c3.3 comes from this gene [Caenorhabditis elegans]
                  218387
Seq. No.
Seq. ID
                  LIB3148-045-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g4008159
BLAST score
                  636
E value
                  1.0e-66
Match length
                  143
                  84
% identity
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                  218388
Seq. ID
                  LIB3148-045-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3869075
BLAST score
                  33
E value
                  5.0e-09
Match length
                  41
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
```

218389

Seq. ID LIB3148-045-Q1-K1-B12 Method BLASTX NCBI GI g2129622 BLAST score 329 E value 1.0e-30 Match length 74

Seq. No.

```
% identity
NCBI Description
                  immunophilin FKBP15-1 - Arabidopsis thaliana >qi 1272406
                   (U52046) immunophilin [Arabidopsis thaliana]
                  218390
Seq. No.
Seq. ID
                  LIB3148-045-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3193303
BLAST score
                  160
E value
                  7.0e-11
                  75
Match length
% identity
                  45
NCBI Description (AF069298) similar to several proteins containing a tandem
                  repeat region such as Plasmodium falciparum GGM tandem
                  repeat protein (GB:U27807); partial CDS [Arabidopsis
                  thaliana]
Seq. No.
                  218391
Seq. ID
                  LIB3148-045-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1684855
BLAST score
                  319
E value
                  1.0e-29
Match length
                  65
% identity
                  22
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]
Seq. No.
                  218392
Seq. ID
                  LIB3148-045-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g951427
BLAST score
                  583
E value
                  2.0e-60
Match length
                  134
% identity
                  80
NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                  communis]
Seq. No.
                  218393
Seq. ID
                  LIB3148-045-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4150974
BLAST score
                  373
E value
                  8.0e-36
                  95
Match length
                  71
% identity
NCBI Description (AJ224331) cystatin [Castanea sativa]
Seq. No.
                  218394
Seq. ID
                  LIB3148-045-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g464840
BLAST score
                  700
E value
                  3.0e-74
Match length
                  134
% identity
                  99
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
```

```
alpha-1 chain - fern (Anemia phyllitidis)
>gi 296494 emb CAA48927 (X69183) alpha tubulin [Anemia
phyllitidis]
```

Seq. ID LIB3148-045-Q1-K1-C4 Method BLASTX NCBI GI g2160180 BLAST score 174 E value 1.0e-12 44 Match length 73 % identity

Seq. No.

218395

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 218396 Seq. ID LIB3148-045-Q1-K1-C5 Method BLASTX NCBI GI g3540181 178 5.0e-13

BLAST score E value Match length 63 % identity 49

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 218397

LIB3148-045-Q1-K1-D1 Seq. ID

Method BLASTX NCBI GI g2500354 BLAST score 677 E value 2.0e-71 Match length 142 90 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_

(AB001891) QM family protein [Solanum melongena]

218398 Seq. No.

Seq. ID LIB3148-045-Q1-K1-D11

Method BLASTX NCBI GI g1350742 BLAST score 161 E value 4.0e-11 Match length 49 59 % identity

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C.

elegans cDNA yk51f3.5; coded for by C. elegans cDNA

yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA

yk64g1

218399 Seq. No.

Seq. ID LIB3148-045-Q1-K1-D2

Method BLASTX NCBI GI q1743354 BLAST score 441 E value 5.0e-44Match length 101

% identity

72



```
% identity
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
NCBI Description
                  218400
Seq. No.
                  LIB3148-045-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  g303732
NCBI GI
                  166
BLAST score
                  1.0e-11
E value
                  34
Match length
                  88
% identity
                  (D12549) GTP-binding protein [Pisum sativum]
NCBI Description
                  >gi 738941 prf 2001457J GTP-binding protein [Pisum
                  sativum]
                  218401
Seq. No.
                  LIB3148-045-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g1296816
NCBI GI
                  252
BLAST score
                  1.0e-21
E value
Match length
                  64
                  80
% identity
                 (X94995) naringenin-chalcone synthase [Juglans sp.]
NCBI Description
Seq. No.
                  218402
Seq. ID
                  LIB3148-045-Q1-K1-D6
                  BLASTX
Method
                  g2832625
NCBI GI
                  142
BLAST score
                  3.0e-09
E value
Match length
                  59
                  49
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                  218403
Seq. No.
Seq. ID
                  LIB3148-045-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                  q4038055
BLAST score
                   469
E value
                   4.0e-47
Match length
                  116
                   75
% identity
                   (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   >qi 4557077 gb AAD22516.1 AC007045 16 (AC007045) putative
                   cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                   218404
                   LIB3148-045-Q1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4580523
BLAST score
                   486
E value
                   4.0e-49
Match length
                  130
```

NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]



```
LIB3148-045-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g170354
BLAST score
                  287
                  9.0e-26
E value
                  65
Match length
                  18
% identity
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
                  218406
Seq. No.
                  LIB3148-045-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g945081
BLAST score
                  518
                  8.0e-53
E value
Match length
                  140
                  74
% identity
NCBI Description (U31094) P21 [Petunia hybrida]
                  218407
Seq. No.
                  LIB3148-045-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567225
                  294
BLAST score
                  1.0e-26
E value
Match length
                  78
% identity
                  72
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
                  218408
Seq. No.
                  LIB3148-045-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g1085384
NCBI GI
                  318
BLAST score
E value
                  2.0e-29
Match length
                  74
% identity
                  74
NCBI Description Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm
                  protein F [Homo sapiens]
                  >gi_4507131_ref_NP_003086.1_pSNRPF_ small nuclear
                  ribonucleoprotein polypeptide F
                  218409
Seq. No.
                  LIB3148-045-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455207
BLAST score
                  432
E value
                  1.0e-42
Match length
                  91
% identity
                  90
NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                  218410
                  LIB3148-045-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545262
```



BLAST score 159 E value 1.0e-10 Match length 44 % identity 64

NCBI Description (AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No. 218411

Seq. ID LIB3148-045-Q1-K1-F8

Method BLASTX
NCBI GI g122070
BLAST score 360
E value 1.0e-34
Match length 80
% identity 91

NCBI Description HISTONE H3 >gi_82483_pir__A25564 histone H3 - rice

>gi 169793 (M15664) histone 3 [Oryza sativa] >gi 940018

(U25664) histone H3 [Oryza sativa]

Seq. No. 218412

Seq. ID LIB3148-045-Q1-K1-G8

Method BLASTX
NCBI GI g2492782
BLAST score 460
E value 5.0e-46
Match length 125
% identity 69

NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi 504489 (L27992)

alpha-galactosidase [Coffea arabica]

Seq. No. 218413

Seq. ID LIB3148-045-Q1-K1-H10

Method BLASTX
NCBI GI g2290683
BLAST score 625
E value 2.0e-65
Match length 141
% identity 82

NCBI Description (AF000136) basic cellulase [Citrus sinensis]

Seq. No. 218414

Seq. ID LIB3148-045-Q1-K1-H12

Method BLASTX
NCBI GI g3287270
BLAST score 455
E value 2.0e-45
Match length 109
% identity 80

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 218415

Seq. ID LIB3148-045-Q1-K1-H9

Method BLASTX
NCBI GI g3334244
BLAST score 511
E value 5.0e-52



121 Match length 76 % identity

LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) NCBI Description

> (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi 2113825 emb CAA73691 (Y13239) Glyoxalase I [Brassica

juncea]

Seq. No.

218416

Seq. ID LIB3148-046-Q1-K1-A11

Method BLASTX NCBI GI q2960120 BLAST score 401 4.0e-39 E value Match length 142 % identity 53

NCBI Description (AL022121) qlpK [Mycobacterium tuberculosis]

Seq. No.

218417

Seq. ID LIB3148-046-Q1-K1-A2

Method BLASTX NCBI GI q2829204 BLAST score 363 E value 1.0e-34 Match length 96 % identity 66

(AF044204) lipid transfer protein precursor [Gossypium NCBI Description

hirsutum]

Seq. No. 218418

LIB3148-046-Q1-K1-A3 Seq. ID

Method BLASTX NCBI GI g122084 BLAST score 313 E value 6.0e-29 Match length 63 % identity 100

NCBI Description HISTONE H3 >gi_70754_pir_ HSBH3 histone H3 - barley (fragment) >gi_167061 (M34928) histone H3 protein [Hordeum

vulgare] >gi_225348_prf__1301219A histone H3 [Hordeum vulgare var. distichum]

Seq. No. 218419

LIB3148-046-Q1-K1-B11 Seq. ID

Method BLASTX NCBI GI g114974 BLAST score 141 E value 9.0e-09 79 Match length 34 % identity

NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR NCBI Description

>gi 67491 pir GLJY31 beta-glucosidase (EC 3.2.1.21)

precursor (clone TRE361) - white clover

>gi 21955 emb CAA40058.1 (X56734) beta-glucosidase

[Trifolium repens]

Seq. No. 218420



```
LIB3148-046-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120663
BLAST score
                  485
E value
                  5.0e-49
Match length
                  96
                  92
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_66027_pir__DEPMNB
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                  garden pea >gi 309671 (M55147) glyceraldehyde-3-phosphate
                  dehydrogenase B subunit [Pisum sativum]
                  218421
Seq. No.
Seq. ID
                  LIB3148-046-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g567893
BLAST score
                  180
E value
                  2.0e-13
Match length
                  104
                  39
% identity
NCBI Description (L37382) beta-galactosidase-complementation protein
                  [Cloning vector]
                  218422
Seq. No.
Seq. ID
                  LIB3148-046-Q1-K1-D1
                  BLASTX
Method
NCBI GI
                  g4337192
BLAST score
                  384
E value
                  4.0e-37
                  120
Match length
% identity
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  218423
Seq. ID
                  LIB3148-046-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                  g4204575
BLAST score
                  218
E value
                  1.0e-17
                  82
Match length
                  57
% identity
NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
Seq. No.
                  218424
Seq. ID
                  LIB3148-046-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q542200
BLAST score
                  373
```

Method BLASTX
NCBI GI g542200
BLAST score 373
E value 8.0e-36
Match length 99
% identity 70

NCBI Description hypothetical protein - garden asparagus

>gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus

officinalis]



```
Seq. No.
                  218425
Seq. ID
                  LIB3148-046-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  32
E value
                  1.0e-08
Match length
                  44
                  49
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  218426
Seq. ID
                  LIB3148-046-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2244756
BLAST score
                  384
E value
                  4.0e-37
Match length
                  98
                  73
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  218427
Seq. ID
                  LIB3148-046-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                  g2315210
BLAST score
                  58
                  7.0e-24
E value
Match length
                  130
% identity
NCBI Description Lycopersicon esculentum mRNA for proteasome, alpha subunit
Seq. No.
                   218428
                  LIB3148-046-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006915
BLAST score
                  339
E value
                  8.0e-32
Match length
                  117
% identity
                  61
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   218429
Seq. ID
                  LIB3148-046-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g547683
BLAST score
                  469
E value
                   4.0e-47
Match length
                  110
% identity
                  84
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >qi 170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                   >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
```

Seq. ID LIB3148-046-Q1-K1-F10

Method BLASTX NCBI GI g3281853



```
BLAST score
                    615
                    3.0e-64
E value
Match length
                   145
                    92
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   218431
Seq. No.
                   LIB3148-046-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                    g131015
NCBI GI
BLAST score
                    330
                    8.0e-31
E value
                    77
Match length
                    73
% identity
                   PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR
NCBI Description
                    (THAUMATIN-LIKE PROTEIN E22) >gi_100385_pir__JH0230
                    pathogenesis-related protein R precursor - common tobacco
                   >gi_19855_emb_CAA33293_ (X15224) thaumatin-like protein
[Nicotiana tabacum] >gi_19980_emb_CAA31235_ (X12739)
                    pathogenesis-related protein \overline{R} (A\overline{A} 1 - 226) [Nicotiana
                    tabacum]
                    218432
Seq. No.
                    LIB3148-046-Q1-K1-F2
Seq. ID
Method
                    BLASTX
                    q3434971
NCBI GI
                    171
BLAST score
                    4.0e-12
E value
                    113
Match length
                    47
% identity
                    (AB008105) ethylene responsive element binding factor 3
NCBI Description
                    [Arabidopsis thaliana]
                    218433
Seq. No.
                    LIB3148-046-Q1-K1-G5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4567225
BLAST score
                    274
                    3.0e-24
E value
Match length
                    69
% identity
                    71
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.
                    218434
                    LIB3148-046-Q1-K1-G7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4406807
                    157
BLAST score
                    4.0e-11
E value
                    63
Match length
                    56
% identity
                    (AC006201) putative elongation factor beta-1 [Arabidopsis
NCBI Description
                    thaliana]
```

Seq. ID LIB3148-046-Q1-K1-G9

Method BLASTX



```
g2116599
NCBI GI
                  199
BLAST score
                  7.0e-17
E value
Match length
                  72
                  69
% identity
                  (AB003779) leucoanthocyanidin dioxygenase [Perilla
NCBI Description
                  frutescens]
                  218436
Seq. No.
                  LIB3148-046-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  g2911043
NCBI GI
                  230
BLAST score
                  5.0e-19
E value
                  121
Match length
                  46
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  218437
Seq. No.
                  LIB3148-046-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g2459435
NCBI GI
                  453
BLAST score
                  3.0e-45
E value
                  124
Match length
                  69
% identity
                 (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  218438
Seq. No.
                  LIB3148-047-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  g3335366
NCBI GI
                  223
BLAST score
                  2.0e-18
E value
                  93
Match length
% identity
                  44
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
                  218439
Seq. No.
                  LIB3148-047-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  q1174592
NCBI GI
                   595
BLAST score
                  8.0e-62
E value
Match length
                  112
                   100
% identity
                  TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
```

sativum]

218440 Seq. No.

Seq. ID LIB3148-047-Q1-K1-B11

BLASTX Method NCBI GI g2129709 BLAST score 179 E value 2.0e-13



```
69
Match length
                   52
% identity
NCBI Description reverse transcriptase - Arabidopsis thaliana retrotransposon Tall-1 >gi_976278 (L47193) reverse
                   transcriptase [Arabidopsis thaliana]
                   218441
Seq. No.
                   LIB3148-047-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2738949
BLAST score
                   568
E value
                   1.0e-58
                   118
Match length
                   87
% identity
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                   ananassa]
                   218442
Seq. No.
                   LIB3148-047-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3098571
BLAST score
                   217
E value
                   2.0e-17
Match length
                   116
% identity
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
                   218443
Seq. No.
                   LIB3148-047-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1085384
BLAST score
                   313
                   1.0e-28
E value
Match length
                   74
                   73
% identity
NCBI Description Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm
                   protein F [Homo sapiens]
                   >qi 4507131 ref NP 003086.1 pSNRPF small nuclear
                   ribonucleoprotein polypeptide F
Seq. No.
                   218444
                   LIB3148-047-Q1-K1-C1
Seq. ID
Method
                   BLASTX
                   g1174847
NCBI GI
                   206
BLAST score
E value
                   1.0e-16
Match length
                   41
                   95
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-21 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 4) (UBIQUITIN CARRIER PROTEIN 4) >gi_431266 (L19354)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
```

Seq. ID LIB3148-047-Q1-K1-C3

Method BLASTX NCBI GI g4455326 BLAST score 557



2.0e-57 E value Match length 131 % identity 75

(AL035525) putative protein [Arabidopsis thaliana] NCBI Description

218446 Seq. No.

LIB3148-047-Q1-K1-C7 Seq. ID

Method BLASTN NCBI GI q167346 BLAST score 50 E value 4.0e-19 Match length 189 84 % identity

NCBI Description Gossypium hirsutum Lea5-A late embryogenesis-abundant

protein (Lea5-A) gene, complete cds

218447 Seq. No.

Seq. ID LIB3148-047-Q1-K1-C9

Method BLASTX NCBI GI q2765837 BLAST score 209 1.0e-16 E value Match length 85 % identity 54

NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

218448 Seq. No.

LIB3148-047-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI g1170939 BLAST score 660 E value 2.0e-69 Match length 130 95

% identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi_1084408_pir__S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867 (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 218449

Seq. ID LIB3148-047-Q1-K1-D11

Method BLASTN NCBI GI g3821780 BLAST score 37 E value 2.0e-11 Match length 37 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 218450

Seq. ID LIB3148-047-Q1-K1-D2

Method BLASTX NCBI GI g2781362 BLAST score 234 E value 1.0e-19

E value

Match length

% identity

7.0e-29

103 64



```
Match length
                  121
                   19
% identity
NCBI Description (AC003113) F2401.18 [Arabidopsis thaliana]
                  218451
Seq. No.
Seq. ID
                  LIB3148-047-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2088647
BLAST score
                  578
E value
                   7.0e-60
Match length
                  137
                   79
% identity
                  (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   218452
Seq. No.
                  LIB3148-047-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3169182
                  207
BLAST score
                   2.0e-16
E value
Match length
                   40
                   88
% identity
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
Seq. No.
                   218453
                  LIB3148-047-01-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4539359
BLAST score
                   235
                   1.0e-19
E value
Match length
                   118
                   47
% identity
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                   218454
                   LIB3148-047-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g118514
BLAST score
                   179
E value
                   4.0e-13
Match length
                   33
% identity
                   100
                  TURGOR-RESPONSIVE PROTEIN 26G >gi 100051 pir S11863
NCBI Description
                   aldehyde dehydrogenase homolog - garden pea
                   >gi 20681 emb CAA38243 (X54359) 508 aa peptide [Pisum
                   sativum]
                   218455
Seq. No.
Seq. ID
                   LIB3148-047-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g717142
BLAST score
                   313
```



```
(U21801) alcohol dehydrogenase homolog [Solanum
NCBI Description
                  lycopersicum]
Seq. No.
                  218456
                  LIB3148-047-Q1-K1-F9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  48
                  67
% identity
                 Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  218457
                  LIB3148-047-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118926
BLAST score
                  349
E value
                  4.0e-33
                  119
Match length
                  55
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >qi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi 227781 prf 1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
                  218458
Seq. No.
Seq. ID
                  LIB3148-047-Q1-K1-G12
                  BLASTX
Method
NCBI GI
                  g4105794
BLAST score
                  174
                  5.0e-16
E value
Match length
                  80
% identity
                  54
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
                   218459
Seq. No.
Seq. ID
                  LIB3148-047-Q1-K1-G3
                  BLASTX
Method
NCBI GI
                  g3482971
BLAST score
                   466
E value
                   8.0e-47
Match length
                   94
% identity
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
                   218460
Seq. No.
                  LIB3148-047-Q1-K1-G5
Seq. ID
Method
                  BLASTX
```

NCBI GI g1076800
BLAST score 311
E value 4.0e-29
Match length 64
% identity 89

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -



maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
peroxidase [Zea mays]

218461 Seq. No. LIB3148-047-Q1-K1-G6 Seq. ID Method BLASTN g4038468 NCBI GI BLAST score 47 3.0e-17 E value Match length 123 % identity 85 NCBI Description Porteresia coarctata histone H3 mRNA, complete cds 218462 Seq. No. LIB3148-047-Q1-K1-G8 Seq. ID Method BLASTX NCBI GI q541816 185 BLAST score 5.0e-14E value Match length 69 59 % identity protein kinase - common ice plant >gi_457689_emb_CAA82990_ NCBI Description (Z30329) protein kinase [Mesembryanthemum crystallinum] 218463 Seq. No. LIB3148-047-Q1-K1-H11 Seq. ID BLASTX Method NCBI GI q1848212 BLAST score 222 E value 4.0e-18 59 Match length 76 % identity (Y11209) protein disulfide-isomerase precursor [Nicotiana NCBI Description tabacum] Seq. No. 218464 LIB3148-047-Q1-K1-H12 Seq. ID Method BLASTX NCBI GI q4544408 BLAST score 390 E value 6.0e-38 Match length 97 73 % identity NCBI Description (AC006955) unknown protein [Arabidopsis thaliana] Seq. No. 218465 LIB3148-047-Q1-K1-H6 Seq. ID Method BLASTX q2388689 NCBI GI 332 BLAST score E value 5.0e-31 71 Match length 86 % identity (AF016633) GH1 protein [Glycine max] NCBI Description

Seq. No. 218466



```
Seq. ID
                  LIB3148-048-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3183094
BLAST score
                  585
E value
                   1.0e-60
Match length
                  131
% identity
                  82
NCBI Description ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
                   (ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine
                  carbamoyltransferase [Pisum sativum]
Seq. No.
                  218467
Seq. ID
                  LIB3148-048-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q2462748
BLAST score
                  461
E value
                  3.0e-46
Match length
                  96
% identity
                  92
NCBI Description (AC002292) putative Clathrin Coat Assembly protein
                  [Arabidopsis thaliana]
Seq. No.
                  218468
Seq. ID
                  LIB3148-048-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q4468812
BLAST score
                  270
E value
                  6.0e-24
Match length
                  71
% identity
                  66
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  218469
Seq. ID
                  LIB3148-048-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3914685
BLAST score
                  580
E value
                  4.0e-60
Match length
                  124
% identity
                  89
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
Seq. No.
                  218470
Seq. ID
                  LIB3148-048-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4567225
BLAST score
                  295
E value
                  1.0e-26
Match length
                  78
% identity
                  72
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3148-048-Q1-K1-B5

Method BLASTX NCBI GI g4455208

```
BLAST score
                   340
                   4.0e-32
E value
                   81
Match length
% identity
                   77
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   218472
Seq. No.
                   LIB3148-048-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4508069
BLAST score
                   365
E value
                   6.0e-35
Match length
                   123
                   58
% identity
NCBI Description (AC005882) 12246 [Arabidopsis thaliana]
                   218473
Seq. No.
                   LIB3148-048-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3548810
BLAST score
                   167
E value
                   1.0e-11
Match length
                   130
                   35
% identity
NCBI Description
                   (AC005313) putative chloroplast nucleoid DNA binding
                   protein [Arabidopsis thaliana]
                   218474
Seq. No.
                   LIB3148-048-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832709
                   170
BLAST score
E value
                   4.0e-12
Match length
                   45
                   71
% identity
NCBI Description
                    (AL021713) neoxanthin cleavage enzyme-like protein
                    [Arabidopsis thaliana]
Seq. No.
                    218475
Seq. ID
                   LIB3148-048-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   g481384
BLAST score
                   162
E value
                    4.0e-11
Match length
                   121
% identity
                    36
NCBI Description
                   outer envelope protein omp24, chloroplast - spinach
                   >gi 1076265 pir S46542 chloroplast outer envelope 24 kD
                   protein - spinach >gi_414200_emb_CAA53243_ (X75563) chloroplast outer envelope 24 kD protein (omp24) [Spinacia
                   oleracea]
```

Seq. ID LIB3148-048-Q1-K1-C10

Method BLASTX NCBI GI g399182 BLAST score 321



E value 1.0e-29 Match length 69 % identity 90 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME

(PEPCASE) >gi_320128_pir__S28428 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - soybean

>gi_218267_dbj_BAA01560_ (D10717) phosphoenolpyruvate

carboxylase [Glycine max]

Seq. No. 218477

Seq. ID LIB3148-048-Q1-K1-C4

Method BLASTX NCBI GI g100551 BLAST score 279 E value 8.0e-25 Match length 55 % identity 96

NCBI Description tubulin beta chain - oat

Seq. No. 218478

Seq. ID LIB3148-048-Q1-K1-D11

Method BLASTX NCBI GI q2076884 BLAST score 435 E value 4.0e-43 Match length 121 % identity 70

NCBI Description (U90522) lysine-ketoglutarate reductase/saccharopine

dehydrogenase [Arabidopsis thaliana]

Seq. No. 218479

Seq. ID LIB3148-048-Q1-K1-D4

Method BLASTX NCBI GI g3023419 BLAST score 300 E value 2.0e-27 107 Match length 57 % identity

NCBI Description CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)

>gi 1934859 emb CAA72911 (Y12228) caffeoyl-CoA

O-methyltransferase [Eucalyptus gunnii]

218480 Seq. No.

Seq. ID LIB3148-048-Q1-K1-D9

Method BLASTX NCBI GI g2851508 BLAST score 477 E value 4.0e-48 Match length 97 % identity 89

NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to

ribosomal protein L21 (gb_L38826). ESTs

gb AA395597, gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 (AC003970) Putative ribosomal protein

L21 [Arabidopsis thaliana]

Method

NCBI GI

BLAST score



```
218481
Seq. No.
Seq. ID
                  LIB3148-048-Q1-K1-E12
Method
                  BLASTX
                  g3355486
NCBI GI
BLAST score
                  464
                  2.0e-46
E value
                  120
Match length
% identity
                  75
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218482
                  LIB3148-048-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567225
BLAST score
                  268
E value
                  1.0e-23
                  73
Match length
                  67
% identity
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218483
Seq. ID
                  LIB3148-048-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q4539293
BLAST score
                  277
E value
                  9.0e-25
                  74
Match length
% identity
                  68
NCBI Description (AL049480) putative membrane transporter [Arabidopsis
                  thaliana]
                   218484
Seq. No.
                  LIB3148-048-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982243
BLAST score
                  277
                  1.0e-24
E value
                  73
Match length
                   67
% identity
NCBI Description (AF051204) hypothetical protein [Picea mariana]
                   218485
Seq. No.
                  LIB3148-048-Q1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3360289
BLAST score
                  425
E value
                   4.0e-49
Match length
                  122
                   78
% identity
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase
                   1 [Zea mays]
Seq. No.
                   218486
Seq. ID
                   LIB3148-048-Q1-K1-G12
```

630

BLASTX

g266945



```
E value
                  6.0e-66
Match length
                  137
                  88
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                  >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                  >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
                  218487
Seq. No.
Seq. ID
                  LIB3148-048-Q1-K1-G2
Method
                  BLASTN
NCBI GI
                  q2760164
BLAST score
                  35
E value
                  2.0e-10
Match length
                  71
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  218488
Seq. ID
                  LIB3148-048-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1771780
BLAST score
                  413
E value
                  1.0e-40
Match length
                  110
                  79
% identity
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
Seq. No.
                  218489
Seq. ID
                  LIB3148-048-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q1168746
BLAST score
                  154
E value
                  1.0e-12
Match length
                  60
                  63
% identity
                  CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE)
NCBI Description
                  >gi 2147169 pir S61882 carbonate dehydratase (EC 4.2.1.1)
                  - Flaveria brownii >gi 606813 (U08402) carbonic anhydrase
                  [Flaveria brownii]
                  218490
Seq. No.
Seq. ID
                  LIB3148-048-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3894194
BLAST score
                  276
E value
                  1.0e-24
Match length
                  86
                  62
% identity
                  (AC005662) putative strictosidine synthase [Arabidopsis
NCBI Description
```

thaliana]

218491 Seq. No.

Seq. ID LIB3148-048-Q1-K1-H4

Method BLASTX



```
q2492953
NCBI GI
                   316
BLAST score
                   3.0e-29
E value
Match length
                   77
                   78
% identity
NCBI Description
                   CHORISMATE SYNTHASE 2 PRECURSOR
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2)
                   >gi_542027_pir_S40409 chorismate synthase (EC 4.6.1.4) 2
                   precursor - tomato >gi_410484_emb_CAA79854_ (Z21791) chorismate synthase 2 [Lycopersicon esculentum]
Seq. No.
                   218492
                   LIB3148-048-Q1-K1-H6
Seq. ID
Method
                   BLASTN
                   g606649
NCBI GI
BLAST score
                   33
                   2.0e-09
E value
Match length
                   33
                   100
% identity
NCBI Description Gossypium hirsutum polygalacturonase mRNA, complete cds
                   218493
Seq. No.
                   LIB3148-048-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   g2398831
NCBI GI
                   587
BLAST score
E value
                   5.0e-61
Match length
                   127
                   87
% identity
NCBI Description (X75542) 4-coumarate:CoA ligase [Vanilla planifolia]
                   218494
Seq. No.
                   LIB3148-048-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q170507
BLAST score
                   180
E value
                    3.0e-13
Match length
                   73
                   53
% identity
                   (M59251) ORF [Lycopersicon esculentum] >gi 1172167 (U44386)
NCBI Description
                   heat shock protein [Solanum lycopersicum]
                    218495
Seq. No.
                   LIB3148-049-Q1-K1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                    8.0e-11
E value
                   36
Match length
                    100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Seq. ID LIB3148-049-Q1-K1-A5

Method BLASTX NCBI GI g4239845 BLAST score 180

E value

Match length

% identity

1.0e-34

119 55



```
E value
                    3.0e-13
  Match length
                    79
                    47
  % identity
  NCBI Description
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
  Seq. No.
                    218497
                    LIB3148-049-Q1-K1-A6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q1928981
  BLAST score
                    618
  E value
                    1.0e-64
  Match length
                    139
  % identity
                    63
  NCBI Description
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                    oleracea var. botrytis]
  Seq. No.
                    218498
                    LIB3148-049-Q1-K1-A7
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4557062
 BLAST score
                    258
                    2.0e-22
  E value
 Match length
                    94
  % identity
                    54
NCBI Description (AC007045) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                    218499
                    LIB3148-049-Q1-K1-A9
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    q2765837
  BLAST score
                    246
  E value
                    6.0e-21
 Match length
                    83
                    64
  % identity
  NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]
  Seq. No.
                    218500
  Seq. ID
                    LIB3148-049-Q1-K1-B3
  Method
                    BLASTX
  NCBI GI
                    g2494034
  BLAST score
                    486
  E value
                    5.0e-49
  Match length
                    108
  % identity
                    89
  NCBI Description
                    DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
                    KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase -
                    Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                    diacylglycerol kinase [Arabidopsis thaliana]
  Seq. No.
                    218501
  Seq. ID
                    LIB3148-049-Q1-K1-B4
  Method
                    BLASTX
 NCBI GI
                    q730290
BLAST score
                    363
```



NCBI Description PECTATE LYASE PRECURSOR >gi_322883_pir__S29612 pectate lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328) pectate lyase [Lilium longiflorum] >gi_308902 (L18911) pectate lyase [Lilium longiflorum]

Seq. No. 218502

Seq. ID LIB3148-049-Q1-K1-B5

Method BLASTX
NCBI GI g4454480
BLAST score 241
E value 2.0e-20
Match length 98
% identity 46

NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase

[Arabidopsis thaliana]

Seq. No. 218503

Seq. ID LIB3148-049-Q1-K1-B6

Method BLASTX
NCBI GI g1174592
BLAST score 746
E value 1.0e-79
Match length 141
% identity 100

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir___S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 218504

Seq. ID LIB3148-049-Q1-K1-B9

Method BLASTX
NCBI GI g4567225
BLAST score 284
E value 2.0e-25
Match length 71
% identity 72

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 218505

Seq. ID LIB3148-049-Q1-K1-C1

Method BLASTX
NCBI GI g1174870
BLAST score 273
E value 4.0e-24
Match length 72
% identity 74

NCBI Description : UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN

>gi 633685 emb CAA55861 (X79274) ubiquinol--cytochrome c

reductase [Solanum tuberosum]

Seq. No. 218506

Seq. ID LIB3148-049-Q1-K1-D7

Method BLASTX
NCBI GI 94567243
BLAST score 392
E value 5.0e-38
Match length 138



```
% identity
                  (AC007070) putative synaptobrevin protein [Arabidopsis
NCBI Description
                  thaliana]
                  218507
Seq. No.
Seq. ID
                  LIB3148-049-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4469020
BLAST score
                  149
E value
                  8.0e-10
Match length
                  39
                  74
% identity
NCBI Description (AL035602) putative protein (fragment) [Arabidopsis
                  thaliana]
                  218508
Seq. No.
Seq. ID
                  LIB3148-049-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  296
E value
                  9.0e-27
Match length
                  143
% identity
                  42
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                  218509
Seq. No.
Seq. ID
                  LIB3148-049-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1694976
BLAST score
                  275
E value
                  2.0e-24
Match length
                  106
% identity
                  52
                 (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                  thaliana]
                  218510
Seq. No.
Seq. ID
                  LIB3148-049-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3986750
BLAST score
                  747
E value
                  1.0e-79
Match length
                  138
% identity
                  97
NCBI Description (AF107464) serine/threonine protein phosphatase type 2A
                  [Hevea brasiliensis]
Seq. No.
                  218511
Seq. ID
                  LIB3148-049-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
```

100

NCBI Description Xenopus laevis cDNA clone 27A6-1

% identity



```
218512
Seq. No.
Seq. ID
                  LIB3148-049-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                   489
                   2.0e-49
E value
Match length
                   98
% identity
                   86
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   218513
Seq. No.
                  LIB3148-049-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  196
E value
                   2.0e-26
Match length
                   94
% identity
                   65
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
Seq. No.
                   218514
                  LIB3148-049-Q1-K1-F1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3510339
                   34
BLAST score
                   1.0e-09
E value
Match length
                   157
                   83
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   218515
Seq. ID
                   LIB3148-049-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   q3776559
BLAST score
                   447
E value
                   2.0e-44
Match length
                   130
% identity
NCBI Description
                   (AC005388) Strong similarity to gene F14J9.26 gi_3482933
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   218516
Seq. ID
                   LIB3148-049-Q1-K1-F4
```

Method BLASTX

NCBI GI g135535 BLAST score 360 E value 2.0e-34Match length 118 67 % identity



NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana] Seq. No. 218517 Seq. ID LIB3148-049-Q1-K1-F5 Method BLASTX g3885515

NCBI GI BLAST score 274 E value 3.0e-24Match length 72 % identity 74

NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago

satival

Seq. No. 218518 Seq. ID LIB3148-049-Q1-K1-G10

Method BLASTX NCBI GI g3056601 BLAST score 250

E value 2.0e-21 Match length 122 48 % identity

NCBI Description (AC004255) T1F9.22 [Arabidopsis thaliana]

Seq. No. 218519

LIB3148-049-Q1-K1-G12 Seq. ID

Method BLASTX NCBI GI q4467123 BLAST score 303 E value 1.0e-27 Match length 129 % identity 53

NCBI Description (AL035538) hypothetical pretein [Arabidopsis thaliana]

Seq. No. 218520

LIB3148-049-Q1-K1-G2 Seq. ID

Method BLASTX NCBI GI g4309732 220 BLAST score 7.0e-18 E value 64 Match length % identity

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 218521

Seq. ID LIB3148-049-Q1-K1-G3

Method BLASTN NCBI GI g2244733 BLAST score 169 E value 3.0e-90 Match length 251 % identity 97

NCBI Description Cotton mRNA for actin, clone CF456, partial cds

```
Seq. No.
                   218522
Seq. ID
                  LIB3148-049-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g544184
BLAST score
                  233
E value
                   2.0e-19
Match length
                  66
% identity
                  67
NCBI Description
                  4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)
                   (DISPROPORTIONATING ENZYME) (D-ENZYME)
                  >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC
                   2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664)
                   4-alpha-glucanotransferase [Solanum tuberosum]
Seq. No.
                  218523
Seq. ID
                  LIB3148-049-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g485512
BLAST score
                  211
E value
                  5.0e-17
Match length
                  79
% identity
                  52
NCBI Description salt-associated protein csaA - sweet orange
Seq. No.
                  218524
Seq. ID
                  LIB3148-049-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  466
E value
                  9.0e-47
Match length
                  111
                  79
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  218525
Seq. ID
                  LIB3148-049-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4567205
BLAST score
                  178
E value
                  1.0e-25
Match length
                  78
% identity
                  81
NCBI Description (AC007168) putative trehalose-6-phosphate phosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  218526
Seq. ID
                  LIB3148-050-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q1944575
BLAST score
                  645
E value
                  1.0e-67
Match length
                  142
% identity
                  81
NCBI Description
                 (Z94058) pectinesterase [Lycopersicon esculentum]
Seq. No.
                  218527
```

NCBI GI

```
Seq. ID
                  LIB3148-050-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q1439609
BLAST score
                  178
E value
                   8.0e-19
Match length
                   66
% identity
                  79
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
                   218528
Seq. No.
                  LIB3148-050-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829871
BLAST score
                  173
E value
                   2.0e-12
Match length
                  37
                   73
% identity
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   218529
                  LIB3148-050-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3687245
BLAST score
                   477
E value
                   5.0e-48
Match length
                  110
% identity
                   78
                  (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                   218530
Seq. No.
Seq. ID
                  LIB3148-050-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                   q4510381
BLAST score
                   185
E value
                   8.0e-14
Match length
                  102
% identity
                   48
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   218531
Seq. ID
                  LIB3148-050-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                   g1076510
BLAST score
                   235
E value
                   1.0e-19
Match length
                  101
% identity
                   51
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
NCBI Description
                  >gi 829119 emb CAA52414 (X74403) cyclophilin [Phaseolus
                   vulgaris]
                   218532
Seq. No.
Seq. ID
                  LIB3148-050-Q1-K1-C7
Method
                  BLASTX
```

30698

g4539292



BLAST score 6.0e-27 E value 100 Match length 61 % identity

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

218533 Seq. No.

LIB3148-050-Q1-K1-C8 Seq. ID

Method BLASTX NCBI GI g2828147 BLAST score 297 5.0e-27 E value 96 Match length 58 % identity

NCBI Description (AF042384) BC-2 protein [Homo sapiens]

Seq. No. 218534

LIB3148-050-Q1-K1-D3 Seq. ID

Method BLASTX NCBI GI g3882081 BLAST score 618 E value 1.0e-64 Match length 123 % identity 33

NCBI Description (AJ012552) polyubiquitin [Vicia faba]

218535 Seq. No.

LIB3148-050-Q1-K1-E11 Seq. ID

Method BLASTX NCBI GI g113512 BLAST score 182 E value 2.0e-13 Match length 50 70 % identity

FLORAL HOMEOTIC PROTEIN AGL2 >gi 81610 pir B39534 floral NCBI Description

homeotic protein AGL2 - Arabidopsis thaliana >gi 166591 (M55551) transcription factor [Arabidopsis thaliana]

218536 Seq. No.

Seq. ID LIB3148-050-Q1-K1-E3

Method BLASTX NCBI GI g1684851 BLAST score 313 E value 9.0e-29 Match length 108

% identity 57

NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

218537 Seq. No.

Seq. ID LIB3148-050-Q1-K1-E5

Method BLASTX NCBI GI g2507421 BLAST score 137 E value 1.0e-08 Match length 31 87 % identity



NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana] 218538 Seq. No. LIB3148-050-Q1-K1-E6 Seq. ID Method BLASTX NCBI GI g730290 BLAST score 568

1.0e-58 E value 140 Match length 71 % identity NCBI Description PECTATE LYASE PRECURSOR >gi_322883_pir__S29612 pectate lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328)

pectate lyase [Lilium longiflorum] >gi_308902 (L18911)

pectate lyase [Lilium longiflorum]

218539 Seq. No.

LIB3148-050-Q1-K1-E7 Seq. ID

BLASTX Method g3860259 NCBI GI 196 BLAST score 3.0e-15 E value 108 Match length % identity 43

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

218540 Seq. No.

LIB3148-050-Q1-K1-E8 Seq. ID

Method BLASTX NCBI GI g3482931 BLAST score 343 2.0e-32E value Match length 108 64 % identity

NCBI Description (AC003970) germin-like protein [Arabidopsis thaliana]

218541 Seq. No.

LIB3148-050-Q1-K1-F10 Seq. ID

Method BLASTX NCBI GI q464987 265 BLAST score 3.0e-23 E value 51 Match length % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana

>gi 297878 emb CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 218542

Seq. ID LIB3148-050-Q1-K1-F11

Method BLASTX

BLAST score

E value

472 2.0e-47



```
q3702317
NCBI GI
BLAST score
                  161
                   5.0e-11
E value
Match length
                  37
% identity
                  92
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  218543
                  LIB3148-050-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3080427
BLAST score
                  494
                  4.0e-50
E value
Match length
                  117
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  218544
Seq. No.
                  LIB3148-050-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3334261
BLAST score
                   143
                   3.0e-09
E value
Match length
                   39
                   67
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 > gi 1655851 (U61973)
NCBI Description
                   metallothionein-like protein [Malus domestica]
Seq. No.
                   218545
                   LIB3148-050-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3790554
BLAST score
                   222
E value
                   4.0e-18
Match length
                   97
                   47
% identity
                  (AF078683) RING-H2 finger protein RHA1a [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   218546
                   LIB3148-050-Q1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643607
BLAST score
                   573
E value
                   3.0e-59
Match length
                   118
                   87
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   218547
Seq. ID
                   LIB3148-050-Q1-K1-H4
                   BLASTX
Method
NCBI GI
                   g3024017
```

```
Match length
% identity
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                  (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
                  218548
Seq. No.
                  LIB3148-050-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1408471
BLAST score
                  418
E value
                  4.0e-41
                  93
Match length
                  84
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
                  218549
Seq. No.
                  LIB3148-050-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080395
BLAST score
                  281
E value
                   5.0e-25
                  120
Match length
                   55
% identity
NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]
                   218550
Seq. No.
                  LIB3148-051-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2244732
BLAST score
                   577
E value
                   9.0e-60
Match length
                  107
% identity
                   92
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                   218551
                   LIB3148-051-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2459412
BLAST score
                   265
E value
                   3.0e-23
                   97
Match length
% identity
                   52
NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana]
Seq. No.
                   218552
Seq. ID
                   LIB3148-051-Q1-K1-A9
```

 ${\tt BLASTX}$ Method NCBI GI g3024386 BLAST score 606 4.0e-63 E value Match length 130 % identity 87

NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)

```
Seq. No.
                  218553
                  LIB3148-051-Q1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2760326
BLAST score
                  197
E value
                   3.0e-15
                  97
Match length
% identity
                   43
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                  218554
Seq. No.
                  LIB3148-051-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                   q170354
NCBI GI
                   449
BLAST score
                   1.0e-44
E value
Match length
                   90
% identity
                   21
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
                   218555
Seq. No.
                   LIB3148-051-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   a3377764
                   398
BLAST score
                   8.0e-39
E value
Match length
                   84
% identity
                   88
NCBI Description (AF079851) nodule-enhanced sucrose synthase [Pisum sativum]
                   218556
Seq. No.
                   LIB3148-051-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2809253
BLAST score
                   188
E value
                   4.0e-14
Match length
                   70
% identity
                   50
NCBI Description (AC002560) F21B7.22 [Arabidopsis thaliana]
Seq. No.
                   218557
                   LIB3148-051-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703380
                   377
BLAST score
                   2.0e-36
E value
Match length
                   72
                   100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj BAA04607_ (D17760)
                   ADP-ribosylation factor [Oryza sativa]
```

>gi_2129500_pir__S52006 polygalacturonase - upland cotton >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]

30703

218558

BLASTX

LIB3148-051-Q1-K1-C1

Seq. No. Seq. ID

Method



```
g2244905
NCBI GI
                    346
BLAST score
                    8.0e-33
E value
Match length
                    112
                    57
% identity
                    (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                    [Arabidopsis thaliana]
                    218559
Seq. No.
                    LIB3148-051-Q1-K1-C11
Seq. ID
Method
                    BLASTX
                    g1169534
NCBI GI
                    390
BLAST score
                    8.0e-38
E value
Match length
                    81
% identity
                    94
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                    >gi 433609 emb CAA82232_ (Z28386) enolase [Ricinus
                    communis]
                    218560
Seq. No.
                    LIB3148-051-Q1-K1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2804278
                    620
BLAST score
                    8.0e-65
E value
                    139
Match length
% identity
NCBI Description (AB003516) squalene epoxidase [Panax ginseng]
                    218561
Seq. No.
                    LIB3148-051-Q1-K1-C4
Seq. ID
Method
                    BLASTX
NCBI GI
                     q584865
BLAST score
                     405
                     1.0e-39
E value
Match length
                     127
% identity
                    CYTOCHROME P450 76A2 (CYPLXXVIA2) (P-450EG7)
NCBI Description
                     >gi_542073_pir__S38534_cytochrome P450 76A2 - eggplant
>gi_415911_emb_CAA50648_ (X71657) P450 hydroxylase [Solanum]
                     melongena]
Seq. No.
                     218562
Seq. ID
                     LIB3148-051-Q1-K1-D1
Method
                     BLASTX
                     q1076511
NCBI GI
BLAST score
                     594
E value
                     9.0e-62
```

136 Match length 82 % identity

H+-transporting ATPase (EC 3.6.1.35) - kidney bean NCBI Description

>gi 758250 emb_CAA59799_ (X85804) H(+)-transporting ATPase

[Phaseolus vulgaris]



```
218563
Seq. No.
                   LIB3148-051-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   q3913518
NCBI GI
                   211
BLAST score
                   8.0e-17
E value
                   54
Match length
                   83
% identity
                   3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                    (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate
                   nucleotidase [Arabidopsis thaliana]
                    218564
Seq. No.
                   LIB3148-051-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   g2134385
NCBI GI
                    544
BLAST score
                    7.0e-56
E value
                    137
Match length
                    73
% identity
                   protein kinase - chicken >gi_571460 (U16656) protein kinase
NCBI Description
                    [Gallus gallus]
                    218565
Seq. No.
                    LIB3148-051-Q1-K1-D2
Seq. ID
                    BLASTX
Method
                    g3688170
NCBI GI
                    394
BLAST score
                    3.0e-38
E value
                    110
Match length
                    70
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                    218566
Seq. No.
                    LIB3148-051-Q1-K1-D5
Seq. ID
Method
                    BLASTX
                    g567893
NCBI GI
BLAST score
                    201
                    1.0e-15
E value
                    100
Match length
% identity
                    29
                   (L37382) beta-galactosidase-complementation protein
NCBI Description
                    [Cloning vector]
                    218567
Seq. No.
Seq. ID
                    LIB3148-051-Q1-K1-D6
Method
                    BLASTN
NCBI GI
                    g2687435
BLAST score
                    85
```

NCBI GI g2687435
BLAST score 85
E value 5.0e-40
Match length 105
% identity 95

NCBI Description Hamamelis virginiana large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 218568



BLASTX

Seq. ID

Method

LIB3148-051-Q1-K1-D8

```
g4033467
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
                   82
Match length
                   57
% identity
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
NCBI Description
                   >gi_1707366_emb_CAA67798_ (X99435) splicing factor
                   [Arabidopsis thaliana]
                   218569
Seq. No.
                   LIB3148-051-Q1-K1-F1
Seq. ID
Method
                   BLASTX
                   g832876
NCBI GI
                   314
BLAST score
                   9.0e - 39
E value
                   99
Match length
                   78
% identity
                  (L41345) ascorbate free radical reductase [Solanum
NCBI Description
                   lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                   radical reductase [Lycopersicon esculentum]
                   218570
Seq. No.
                   LIB3148-051-Q1-K1-F10
Seq. ID
                   BLASTX.
Method
NCBI GI
                   g2281115
                   598
BLAST score
                   3.0e-62
E value
                   140
Match length
                   77
% identity
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
                   218571
Seq. No.
Seq. ID
                   LIB3148-051-Q1-K1-F11
Method
                   BLASTX
                   g2281115
NCBI GI
                   433
BLAST score
                   8.0e-44
E value
                   121
Match length
% identity
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
                   218572
Seq. No.
Seq. ID
                   LIB3148-051-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2244732
BLAST score
                   731
                   8.0e-78
E value
Match length
                   139
% identity
                   95
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                   218573
Seq. ID
                   LIB3148-051-Q1-K1-F5
```

Match length

% identity

48

58



```
BLASTX
Method
NCBI GI
                  q2970051
                  460
BLAST score
                  5.0e-46
E value
                  95
Match length
                  92
% identity
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
                  218574
Seq. No.
                  LIB3148-051-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q3738297
NCBI GI
                  159
BLAST score
                   1.0e-10
E value
                   60
Match length
                  13
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                   218575
Seq. No.
                   LIB3148-051-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3355471
NCBI GI
                   370
BLAST score
                   2.0e-35
E value
                   91
Match length
                   67
% identity
NCBI Description (AC004218) putative lysophospholipase [Arabidopsis
                   thaliana]
                   218576
Seq. No.
Seq. ID
                   LIB3148-051-Q1-K1-G11
Method
                   BLASTX
                   q4027891
NCBI GI
BLAST score
                   622
E value
                   5.0e-65
Match length
                   136
% identity
                   82
NCBI Description (AF049350) alpha-expansin precursor [Nicotiana tabacum]
                   218577
Seq. No.
                   LIB3148-051-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3927826
BLAST score
                   152
                   6.0e-10
E value
Match length
                   103
% identity
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
                   218578
Seq. No.
                   LIB3148-051-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2281115
BLAST score
                   139
                   1.0e-08
E value
```

% identity



```
NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis
                  thaliana]
                  218579
Seq. No.
                  LIB3148-051-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2661840
BLAST score
                  230
E value
                  4.0e-19
                  60
Match length
% identity
                  73
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                  218580
Seq. No.
                  LIB3148-051-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024126
BLAST score
                  597
E value
                  4.0e-62
Match length
                  137
                  85
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                  synthetase 1 [Catharanthus roseus]
Seq. No.
                  218581
                  LIB3148-051-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455276
BLAST score
                  219
E value
                  9.0e-18
Match length
                  64
% identity
                  61
NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis
                  thaliana]
                   218582
Seq. No.
Seq. ID
                  LIB3148-052-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                   g3123745
BLAST score
                   486
E value
                   3.0e-49
Match length
                  105
% identity
                   87
NCBI Description (AB013447) aluminum-induced [Brassica napus]
                  218583
Seq. No.
Seq. ID
                  LIB3148-052-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                   g3668077
BLAST score
                  145
E value
                   4.0e-09
Match length
                  63
```

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

E value

Match length

2.0e-24 57



```
218584
Seq. No.
                  LIB3148-052-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3599968
BLAST score
                  385
                  1.0e-37
E value
                  80
Match length
                  86
% identity
NCBI Description (AF032123) clp protease [Arabidopsis thaliana]
                  218585
Seq. No.
                  LIB3148-052-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3695021
                   522
BLAST score
                   2.0e-53
E value
                   113
Match length
                   85
% identity
NCBI Description (AF055849) hypothetical protein [Arabidopsis thaliana]
                   218586
Seq. No.
                   LIB3148-052-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g4415992
NCBI GI
BLAST score
                   621
                   5.0e-65
E value
                   120
Match length
% identity
NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]
                   218587
Seq. No.
                   LIB3148-052-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   q4567245
NCBI GI
                   392
BLAST score
E value
                   3.0e - 38
Match length
                   119
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                   218588
Seq. No.
                   LIB3148-052-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263785
BLAST score
                   335
E value
                   2.0e-31
Match length
                   114
                   57
% identity
NCBI Description (AC006068) putative Tiny protein [Arabidopsis thaliana]
                   218589
Seq. No.
                   LIB3148-052-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g231586
NCBI GI
                   Ž74
BLAST score
```

% identity

```
% identity
                   95
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
                   218590
Seq. No.
                   LIB3148-052-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g1350944
NCBI GI
                   392
BLAST score
                   3.0e-38
E value
Match length
                   80
                   97
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S17
                   218591
Seq. No.
                   LIB3148-052-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   g1531758
NCBI GI
                   408
BLAST score
                   6.0e-40
E value
                   112
Match length
                   70
% identity
NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
                   unknown protein [Arabidopsis thaliana]
                   218592
Seq. No.
                   LIB3148-052-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g3935167
NCBI GI
                   410
BLAST score
                   4.0e-40
E value
                   98
Match length
                   85
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
                   218593
Seq. No.
                   LIB3148-052-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g1617270
NCBI GI
BLAST score
                    569
                    7.0e-59
E value
                   123
Match length
                   80
% identity
NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]
                    218594
Seq. No.
                   LIB3148-052-Q1-K1-D4
Seq. ID
                    BLASTX
Method
                   q3264607
NCBI GI
BLAST score
                    227
                    1.0e-18
E value
                   47
Match length
```

30710

NCBI Description (AF061509) shaggy kinase homolog [Zea mays]

% identity



```
218595
Seq. No.
                  LIB3148-052-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  g3023195
NCBI GI
BLAST score
                  385
                  1.0e-37
E value
Match length
                  78
                  96
% identity
                  14-3-3-LIKE PROTEIN B (SGF14B) >gi_1575727 (U70534) SGF14B
NCBI Description
                  [Glycine max]
                  218596
Seq. No.
                  LIB3148-052-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g3892056
NCBI GI
BLAST score
                  327
                  1.0e-30
E value
Match length
                  79
                  80
% identity
NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
Seq. No.
                   218597
                   LIB3148-052-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   g3377797
NCBI GI
BLAST score
                   554
                   5.0e-57
E value
Match length
                   138
                   77
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   218598
Seq. No.
                   LIB3148-052-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g3367536
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
                   64
Match length
                   86
% identity
                   (AC004392) Contains similarity to symbiosis-related like
NCBI Description
                   protein F1N20.80 gi_2961343 from A. thaliana BAC
                   gb AL022140. EST gb_T04695 comes from this gene.
                   [Arabidopsis thaliana]
                   218599
Seq. No.
                   LIB3148-052-Q1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1922242
                   147
BLAST score
                   2.0e-09
E value
                   28
Match length
```



```
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
                  218600
Seq. No.
Seq. ID
                  LIB3148-052-Q1-K1-E3
Method
                  BLASTX
                  q4206195
NCBI GI
                  202
BLAST score
                  5.0e-16
E value
Match length
                  39
                  87
% identity
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
                  [Arabidopsis thaliana]
                  218601
Seq. No.
                  LIB3148-052-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129604
BLAST score
                  249
E value
                  3.0e-21
Match length
                  54
                  85
% identity
                  GTP-binding protein 1 - Arabidopsis thaliana
NCBI Description
                  >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -
                  Arabidopsis thaliana >gi_1184981 (U46924) ATGB1
                  [Arabidopsis thaliana]
                  218602
Seq. No.
Seq. ID
                  LIB3148-052-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  q3377797
BLAST score
                   431
                   9.0e-43
E value
Match length
                  117
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                   218603
Seq. No.
Seq. ID
                   LIB3148-052-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                   g4455298
BLAST score
                   162
E value
                   2.0e-11
```

Match length 4466 % identity

NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

218604 Seq. No.

Seq. ID LIB3148-052-Q1-K1-F10

BLASTX Method NCBI GI g3860321 BLAST score 501 E value 8.0e-51



```
137
Match length
                   68
% identity
                  (AJ012687) beta-galactosidase [Cicer arietinum]
NCBI Description
                  218605
Seq. No.
                  LIB3148-052-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g3641870
NCBI GI
                  261
BLAST score
                  1.0e-22
E value
                  112
Match length
                   50
% identity
                 (AJ011013) hypothetical protein [Cicer arietinum]
NCBI Description
                   218606
Seq. No.
                   LIB3148-052-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g3169883
NCBI GI
                   146
BLAST score
                   3.0e-09
E value
                   35
Match length
                   77
% identity
                  (AF033194) dehydroquinate dehydratase/shikimate:NADP
NCBI Description
                   oxidoreductase [Lycopersicon esculentum] >gi_3169888
                   (AF034411) dehydroquinate dehydratase/shikimate:NADP
                   oxidoreductase [Lycopersicon esculentum]
Seq. No.
                   218607
                   LIB3148-052-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3540199
NCBI GI
                   470
BLAST score
                   3.0e-47
E value
                   120
Match length
% identity
                  (AC004260) Putative monosaccharide transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   218608
Seq. No.
                   LIB3148-052-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325341
                   400
BLAST score
                   6.0e-39
E value
Match length
                   81
% identity
                   (AF128393) similar to the Drosophila DES-1 protein
NCBI Description
                   (GB:X94180) [Arabidopsis thaliana]
                   218609
Seq. No.
                   LIB3148-052-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3540199
BLAST score
                   219
```

4.0e-28

80

82

E value Match length

% identity



NCBI Description (AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No. 218610

Seq. ID LIB3148-052-Q1-K1-G7
Method BLASTX
NCBI GI g3122388
BLAST score 440
E value 1.0e-43

E value 1.0 Match length 95 % identity 23

NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40

repeat protein [Arabidopsis thaliana]

Seq. No. 218611

Seq. ID LIB3148-052-Q1-K1-H4

Method BLASTX
NCBI GI g2695925
BLAST score 324
E value 2.0e-30
Match length 85
% identity 74

NCBI Description (AJ222776) hypothetical protein [Hordeum vulgare]

Seq. No. 218612

Seq. ID LIB3148-052-Q1-K1-H9

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 218613

Seq. ID LIB3148-053-Q1-K1-A1

Method BLASTN
NCBI GI g167325
BLAST score 57
E value 3.0e-23
Match length 113
% identity 88

NCBI Description Gossypium hirsutum group 4 late embryogenesis-abundant

protein (Lea14-A) gene, complete cds

Seq. No. 218614

Seq. ID LIB3148-053-Q1-K1-A2

Method BLASTX
NCBI GI g1729971
BLAST score 316
E value 4.0e-29
Match length 79
% identity 72

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza

sativa]

Seq. ID

Method



```
218615
Seq. No.
Seq. ID
                  LIB3148-053-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2281633
BLAST score
                  336
                  2.0e-31
E value
                  141
Match length
% identity
                  55
                 (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                  [Arabidopsis thaliana]
                  218616
Seq. No.
                  LIB3148-053-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128228
BLAST score
                  190
                   2.0e-14
E value
                  38
Match length
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                   218617
Seq. No.
                  LIB3148-053-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                   q3395436
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
Match length
                  62
                   69
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   218618
Seq. No.
                   LIB3148-053-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g1130682
NCBI GI
BLAST score
                   314
                   5.0e-29
E value
                   71
Match length
                   83
% identity
NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
                   218619
Seq. No.
                   LIB3148-053-Q1-K1-B8
Seq. ID
Method
                   BLASTX
                   g2827704
NCBI GI
BLAST score
                   417
                   6.0e-41
E value
                   113
Match length
% identity
NCBI Description (AL021684) LRR-like protein [Arabidopsis thaliana]
Seq. No.
                   218620
```

30715

LIB3148-053-Q1-K1-C12

BLASTX



```
g1170745
NCBI GI
                  332
BLAST score
                  5.0e-31
E value
                  76
Match length
                  79
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326
NCBI Description
                   (M88321) Group 4 late embryogenesis-abundant protein
                   [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  218621
Seq. No.
                  LIB3148-053-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  q3461844
NCBI GI
                  146
BLAST score
                   2.0e-09
E value
                  77
Match length
                   43
% identity
NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]
                   218622
Seq. No.
                   LIB3148-053-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g3249084
NCBI GI
BLAST score
                   568
                   1.0e-58
E value
Match length
                   140
                   25
% identity
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
NCBI Description
                   gb X92750 from Mus musculus. ESTs gb_AA712687 and
                   gb_Z37223 come from this gene [Arabidopsis thaliana]
                   218623
Seq. No.
                   LIB3148-053-Q1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3702326
BLAST score
                   619
                   1.0e-64
E value
Match length
                   124
                   89
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                   218624
Seq. No.
                   LIB3148-053-Q1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3860277
BLAST score
                   464
                   1.0e-46
E value
                   124
Match length
 % identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
```

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

218625 Seq. No.

Seq. ID LIB3148-053-Q1-K1-E12

Method BLASTX

E value

Match length

6.0e-09

87



```
q2129772
NCBI GI
BLAST score
                   161
                   2.0e-11
E value
                   33
Match length
                   82
% identity
                   xyloglucan endotransglycosylase-related protein XTR-7 -
NCBI Description
                   Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
                   218626
Seq. No.
                   LIB3148-053-Q1-K1-E4
Seq. ID
Method
                   BLASTN
                   g12292
NCBI GI
                   270
BLAST score
                   1.0e-150
E value
                   381
Match length
                   93
% identity
NCBI Description Spinach chloroplast DNA homologous to ARS and ARC elements
                   upstream of rDNA operon
                   218627
Seq. No.
                   LIB3148-053-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   q4539003
~NCBI GI
                   202
BLAST score
                   9.0e-16
E value
                   106
Match length
                   24
% identity
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
                   218628
Seq. No.
                   LIB3148-053-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4469025
 BLAST score
                   166
 E value
                   1.0e-11
                   37
Match length
 % identity
                   81
 NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
 Seq. No.
                   218629
                   LIB3148-053-Q1-K1-E9
 Seq. ID
 Method
                   BLASTX
                   g3925703
 NCBI GI
                   629
 BLAST score
 E value
                   7.0e-66
                   139
 Match length
 % identity
 NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
 Seq. No.
                    218630
                   LIB3148-053-Q1-K1-F1
 Seq. ID
                   BLASTN
 Method
                    g2281081
 NCBI GI
 BLAST score
                   33
```



% identity Arabidopsis thaliana chromosome II BAC F18019 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 218631 Seq. No. LIB3148-053-Q1-K1-F10 Seq. ID BLASTX Method q4490728 NCBI GI BLAST score 287 9.0e-26 E value Match length 80 64 % identity NCBI Description (AL035709) putative protein [Arabidopsis thaliana] 218632 Seq. No. LIB3148-053-Q1-K1-F11 Seq. ID Method BLASTX q3309583 NCBI GI 585 BLAST score E value 1.0e-60 136 Match length 86 % identity (AF073830) fructose-6-phosphate NCBI Description 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum] 218633 Seq. No. LIB3148-053-Q1-K1-F5 Seq. ID BLASTX Method q4530585 NCBI GI 357 BLAST score E value 6.0e-34 85 Match length % identity NCBI Description (AF130978) B12D protein [Ipomoea batatas] 218634 Seq. No. Seq. ID LIB3148-053-Q1-K1-H11 BLASTX Method NCBI GI g1170568 BLAST score 203 E value 6.0e-16 Match length 42 95 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi_2147316_pir__S60302 D-myo-inositol-3-phosphate synthase (EC 5.5.1.4) - Spirodela polyrrhiza >gi 558648 emb CAA77751 (Z11693) D-myo-inositol-3-phosphate synthase [Spirodela polyrrhiza] Seq. No. 218635 LIB3148-053-Q1-K1-H2 Seq. ID Method BLASTX NCBI GI g169363 BLAST score 337 1.0e-31 E value

30718

66

88

Match length

% identity

Seq. ID Method



```
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]
                  218636
Seq. No.
                  LIB3148-053-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  q2673917
NCBI GI
                  538
BLAST score
                  4.0e-55
E value
                  126
Match length
                  76
% identity
                 (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                   218637
Seq. No.
                  LIB3148-053-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                   g4105798
NCBI GI
                   318
BLAST score
                   2.0e-29
E value
                   95
Match length
                   49
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
                   218638
Seq. No.
                   LIB3148-054-Q1-K1-A10
Seq. ID
                   BLASTX
Method
                   g2129496
NCBI GI
                   625
BLAST score
                   2.0e-65
E value
Match length
                   134
                   88
% identity
NCBI Description acetolactate synthase (EC 4.1.3.18) precursor (clone A19) -
                   upland cotton
                   218639
Seq. No.
                   LIB3148-054-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g2213425
NCBI GI
                   239
BLAST score
                   7.0e-32
E value
                   89
Match length
                   41
 % identity
NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]
                   218640
 Seq. No.
                   LIB3148-054-Q1-K1-A5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2213425
                   196
 BLAST score
                   4.0e-15
 E value
                   48
 Match length
                   40
 % identity
 NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]
                    218641
 Seq. No.
```

30719

LIB3148-054-Q1-K1-B11

BLASTX

Match length % identity

64



```
g2894612
NCBI GI
                  384
BLAST score
                  3.0e-37
E value
                  107
Match length
                  67
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                  218642
Seq. No.
                  LIB3148-054-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g2760326
NCBI GI
                  224
BLAST score
                  2.0e-18
E value
                  119
Match length
                   42
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                  218643
Seq. No.
                  LIB3148-054-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                   g1435021
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   98
Match length
                   44
% identity
NCBI Description (D26575) DNA-binding protein [Daucus carota]
Seq. No.
                   218644
                   LIB3148-054-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   g2894612
NCBI GI
                   637
BLAST score
                   9.0e-67
E value
                   139
Match length
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                   218645
Seq. No.
                   LIB3148-054-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g2129709
NCBI GI
BLAST score
                   268
                   1.0e-23
E value
                   105
Match length
                   50
 % identity
                   reverse transcriptase - Arabidopsis thaliana
NCBI Description
                   retrotransposon Tall-1 >gi_976278 (L47193) reverse
                   transcriptase [Arabidopsis thaliana]
                   218646
 Seq. No.
                   LIB3148-054-Q1-K1-D4
 Seq. ID
Method
                   BLASTX
                   g4204575
 NCBI GI
                   418
 BLAST score
                   4.0e-41
 E value
                   129
```



```
(AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
NCBI Description
                      218647
Seq. No.
                      LIB3148-054-Q1-K1-D5
Seq. ID
                      BLASTX
Method
                      q4150963
NCBI GI
                      276
BLAST score
                      7.0e-32
E value
                      106
Match length
                      68
% identity
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]
                      218648
Seq. No.
                      LIB3148-054-Q1-K1-D8
Seq. ID
                      BLASTX
Method
                      q417103
NCBI GI
                      524
BLAST score
                      1.0e-53
E value
                      122
Match length
                      87
% identity
NCBI Description HISTONE H3.2, MINOR >gi_282871 pir _S24346 histone
                      H3.3-like protein - Arabidopsis thaliana
                      >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                       (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
                      histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
                      [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)
                       histone H3 variant H3.3 [Lycopersicon esculentum]
                       >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
                       >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
                       tabacum] >gi_{388}5890 (AF093633) histone H3 [Oryza sativa]
                       >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                       coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
                       H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1_
                       (AL035708) Histon H3 [Arabidopsis thaliana]
                       218649
Seq. No.
Seq. ID
                       LIB3148-054-Q1-K1-E7
                       BLASTX
Method
NCBI GI
                       g1172995
                       182
BLAST score
                       2.0e-13
E value
Match length
                       58
```

% identity 60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir S52084 ribosomal NCBI Description protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

218650 Seq. No.

LIB3148-054-Q1-K1-E9 Seq. ID

Method BLASTX

Match length

% identity

79



```
g4204575
NCBI GI
                  248
BLAST score
                  1.0e-27
E value
Match length
                  98
                  68
% identity
NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
                  218651
Seq. No.
                  LIB3148-054-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g1399450
NCBI GI
                  693
BLAST score
                  2.0e-73
E value
                  135
Match length
                  97
% identity
NCBI Description (U47660) beta-tubulin 2 [Lupinus albus]
                  218652
Seq. No.
                  LIB3148-054-Q1-K1-F3
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  218653
Seq. No.
                  LIB3148-054-Q1-K1-F4
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   218654
Seq. No.
                   LIB3148-054-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   q4469011
NCBI GI
BLAST score
                   624
                   3.0e-65
E value
Match length
                   133
% identity
NCBI Description (AL035602) carbohydrate kinase-like protein [Arabidopsis
                   thaliana]
 Seq. No.
                   218655
                   LIB3148-054-Q1-K1-G12
 Seq. ID
Method
                   BLASTX
                   g1351408
NCBI GI
                   472
BLAST score
                   1.0e-47
E value
                   114
```

30722

NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)



>gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi 633185 emb CAA87720 (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No. 218656 LIB3148-054-Q1-K1-G2 Seq. ID BLASTX Method g2909783 NCBI GI BLAST score 141 9.0e-09 E value 40 Match length 62 % identity

(AF020289) MgATP-energized glutathione S-conjugate pump NCBI Description

[Arabidopsis thaliana]

Seq. No. 218657

LIB3148-054-Q1-K1-G9 Seq. ID

BLASTX Method q2055273 NCBI GI BLAST score 602 1.0e-62 E value 125 Match length 91 % identity

NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No. 218658

LIB3148-054-Q1-K1-H1 Seq. ID

BLASTX Method g3024434 NCBI GI 388 BLAST score E value 1.0e-37 76 Match length 100 % identity

26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description

PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_(D88663) Tat binding protein 1 [Brassica rapa]

218659 Seq. No.

LIB3148-054-Q1-K1-H10 Seq. ID

Method BLASTX NCBI GI g2492519 727 BLAST score 2.0e-77 E value Match length 139 100 % identity

26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT NCBI Description

7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase

subunit [Spinacia oleracea]

Seq. No. 218660

Seq. ID LIB3148-054-Q1-K1-H2

Method BLASTX NCBI GI g3341688 BLAST score 412 2.0e-40 E value Match length 138



```
% identity
                  (AC003672) putative casein kinase II beta subunit
NCBI Description
                  [Arabidopsis thaliana]
                  218661
Seq. No.
                  LIB3148-054-Q1-K1-H3
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
                  36
BLAST score
                  3.0e-11
E value
                  36
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  218662
Seq. No.
                  LIB3148-054-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g4455208
NCBI GI
                  572
BLAST score
                   3.0e-59
E value
                  133
Match length
                   77
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   218663
Seq. No.
                  LIB3148-054-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   q4490737
NCBI GI
BLAST score
                   264
                   5.0e-23
E value
Match length
                   64
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                   218664
Seq. No.
Seq. ID
                   LIB3148-055-Q1-K1-A10
Method
                   BLASTX
                   g2160182
NCBI GI
                   472
BLAST score
                   2.0e-47
E value
                   118
Match length
% identity
                  (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   218665
Seq. No.
                   LIB3148-055-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512685
                   558
BLAST score
                   1.0e-57
E value
Match length
                   131
                   79
 % identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

>gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
hypothetical protein [Arabidopsis thaliana]

Method

NCBI GI BLAST score



```
218666
Seq. No.
                  LIB3148-055-Q1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1477428
                  534
BLAST score
                  9.0e-55
E value
                  120
Match length
                  88
% identity
                 (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
                  218667
Seq. No.
                  LIB3148-055-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g3877951
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
                   128
Match length
                   27
% identity
                  (Z81555) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
                   218668
Seq. No.
                   LIB3148-055-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g1931641
NCBI GI
                   274
BLAST score
                   3.0e-24
E value
Match length
                   129
                   53
% identity
NCBI Description (U95973) unknown protein [Arabidopsis thaliana]
                   218669
Seq. No.
                   LIB3148-055-Q1-K1-A8
Seq. ID
                   BLASTX
Method
                   g3551031
NCBI GI
                   571
BLAST score
                   4.0e-59
E value
                   128
Match length
                   88
% identity
NCBI Description (AB011467) chalcone synthase [Hydrangea macrophylla]
                   218670
Seq. No.
                   LIB3148-055-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g2564944
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
Match length
                   113
 % identity
                   (AF029349) ornithine decarboxylase [Lycopersicon
 NCBI Description
                   esculentum]
 Seq. No.
                   218671
                   LIB3148-055-Q1-K1-B3
 Seq. ID
                   BLASTX
```

30725

g3668087



```
3.0e-16
E value
                   98
Match length
                   31
% identity
                  (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   218672
Seq. No.
                   LIB3148-055-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   q3880282
NCBI GI
BLAST score
                   237
                   7.0e-20
E value
                   95
Match length
                   30
% identity
                   (Z82059) similar to ABC transporters (2 domains); cDNA EST
NCBI Description
                   EMBL: D73856 comes from this gene; cDNA EST EMBL: D73975
                   comes from this gene; cDNA EST EMBL: C09722 comes from this
                   gene; cDNA EST yk428c4.5 comes from this gene; cDNA ES...
                   >gi_3881299_emb_CAA21772_ (AL032665) similar to ABC
transporters (2 domains); cDNA EST EMBL:D73856 comes from
                   this gene; cDNA EST EMBL: D73975 comes from this gene; cDNA
                   EST EMBL: C09722 comes from this gene; cDNA EST yk428c4.5
                   comes from this gene; cDNA
                   218673
Seq. No.
                   LIB3148-055-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4530585
                   181
BLAST score
                   1.0e-13
E value
                   58
Match length
                    57
% identity
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
                    218674
Seq. No.
                    LIB3148-055-Q1-K1-C1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2623881
                    192
BLAST score
                    7.0e-15
E value
                    37
Match length
                    97
% identity
NCBI Description (AF031318) catalase [Raphanus sativus]
                    218675
Seq. No.
                    LIB3148-055-Q1-K1-C10
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3482910
BLAST score
                    297
E value
                    3.0e-40
Match length
                    109
                    64
 % identity
```

NCBI Description (AC003970) Similar to rice water stress induced protein gi 537404 [Arabidopsis thaliana]

218676 Seq. No.

LIB3148-055-Q1-K1-C4 Seq. ID

BLASTX Method

Seq. ID

Method

NCBI GI



```
q285286
NCBI GI
                  262
BLAST score
                  7.0e-23
E value
Match length
                  100
                  49
% identity
                 flavonol 4'-sulfotransferase - Flaveria chloraefolia
NCBI Description
                  218677
Seq. No.
                  LIB3148-055-Q1-K1-C5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q995906
BLAST score
                  34
                  1.0e-09
E value
                  110
Match length
% identity
                  83
NCBI Description Gossypium hirsutum nonspecific lipid transfer protein
                  precursor mRNA, complete cds
                   218678
Seq. No.
                  LIB3148-055-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   q3123264
NCBI GI
BLAST score
                   161
E value
                   1.0e-11
                   42
Match length
                   74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   218679
Seq. No.
                   LIB3148-055-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2829751
BLAST score
                   215
                   3.0e-17
E value
Match length
                   114
% identity
                   39
                   MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)
NCBI Description
                   >gi 1850559 (U88035) macrophage migration inhibitory factor
                   [Brugia malayi] >gi 2190976 (AF002699) macrophage migration
                   inhibitory factor [Brugia malayi]
                   218680
Seq. No.
                   LIB3148-055-Q1-K1-D10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q436031
BLAST score
                   54
                   1.0e-21
E value
                   122
Match length
                   86
 % identity
                   Nicotiana tabacum (TSC40-4) 60S ribosomal protein L34 mRNA,
NCBI Description
                   complete cds
                   218681
 Seq. No.
```

30727

LIB3148-055-Q1-K1-D11

BLASTX

g2104957



```
403
BLAST score
                   2.0e-39
E value
                  112
Match length
                   68
% identity
                  (U96924) immunophilin [Arabidopsis thaliana]
NCBI Description
                   218682
Seq. No.
                  LIB3148-055-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                   g4008159
NCBI GI
                   628
BLAST score
                   8.0e-66
E value
                   125
Match length
                   90
% identity
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
                   218683
Seq. No.
                   LIB3148-055-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   q4099092
NCBI GI
                   387
BLAST score
                   1.0e-37
E value
                   111
Match length
                   69
% identity
NCBI Description - (U83179) unknown [Arabidopsis thaliana]
                   218684
Seq. No.
                   LIB3148-055-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   q3790587
NCBI GI
                   181
BLAST score
                   6.0e-17
E value
Match length
                   115
% identity
                   48
                  (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                   thaliana]
                   218685
Seq. No.
                   LIB3148-055-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2738248
NCBI GI
BLAST score
                   466
E value
                   7.0e-47
                   105
Match length
                   84
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   218686
Seq. No.
                   LIB3148-055-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3386614
                   488
BLAST score
                   2.0e-49
E value
```

30728

(AC004665) putative transcription factor SF3 [Arabidopsis

130

39

Match length

NCBI Description

% identity



thaliana]

```
218687
Seq. No.
Seq. ID
                  LIB3148-055-Q1-K1-F10
Method
                  BLASTX
                   g2281102
NCBI GI
                   274
BLAST score
                   2.0e-24
E value
                   111
Match length
                   61
% identity
                  (AC002333) SF16 isolog [Arabidopsis thaliana]
NCBI Description
                   218688
Seq. No.
                   LIB3148-055-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   q4325282
NCBI GI
                   324
BLAST score
                   4.0e-30
E value
                   121
Match length
                   54
% identity
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   218689
Seq. No.
                   LIB3148-055-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g548770
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
                   45
Match length
                   76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]
Seq. No.
                   218690
                   LIB3148-055-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   q3182981
NCBI GI
                   435
BLAST score
                   3.0e-43
E value
                   102
Match length
                   79
% identity
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
                    (D86494) diminuto [Pisum sativum]
Seq. No.
                   218691
                   LIB3148-055-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                    q3915096
NCBI GI
                    530
BLAST score
E value
                    2.0e-54
Match length
                   116
                    86
 % identity
 NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
```

4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)



>gi 1574976 (U47293) trans-cinnamate 4-hydroxylase [Populus tremuloides]

218692 Seq. No. LIB3148-055-Q1-K1-F7 Seq. ID BLASTX Method NCBI GI g3719211 580 BLAST score 4.0e-60 E value Match length 134 85 % identity

NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

218693 Seq. No.

LIB3148-055-Q1-K1-F8 Seq. ID

BLASTN Method q3702734 NCBI GI 42 BLAST score 2.0e-14E value 62 Match length 92 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNB8, complete sequence [Arabidopsis thaliana]

218694 Seq. No.

LIB3148-055-Q1-K1-G10 Seq. ID

Method BLASTX q4539455 NCBI GI 287 BLAST score 5.0e-26 E value 74 Match length

73 % identity

NCBI Description (AL049500) T5C23.70 [Arabidopsis thaliana]

218695 Seq. No.

LIB3148-055-Q1-K1-G12 Seq. ID

Method . BLASTX -q1707939 NCBI GI 696 BLAST score 1.0e-73 E value 138 Match length % identity

GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT NCBI Description

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi_1076256 pir_ S51943

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small

chain B1 precursor - beet (fragment)

>gi 556622 emb CAA55515_ (X78899) glucose-1-phosphate

adenylyltransferase [Beta vulgaris]

Seq. No. 218696

LIB3148-055-Q1-K1-G3 Seq. ID

BLASTX Method q4558552 NCBI GI 546 BLAST score 3.0e-56 E value



```
Match length
                  127
                  42
% identity
                  (AC007138) putative P-glycoprotein-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  218697
Seq. No.
                  LIB3148-055-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g2832691
NCBI GI
                  187
BLAST score
                  5.0e-14
E value
                  80
Match length
                  45
% identity
                  (AL021713) polygalacturonase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  218698
Seq. No.
                  LIB3148-055-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g4090257
NCBI GI
                  461
BLAST score
                   4.0e-46
E value
                  91
Match length
                   96
% identity
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
                   218699
Seq. No.
                   LIB3148-056-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g2262118
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   40
Match length
                   85
% identity
NCBI Description (AC002343) cell division protein isolog [Arabidopsis
                   thaliana]
                   218700
Seq. No.
                   LIB3148-056-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   q1710530
NCBI GI
BLAST score
                   610
                   1.0e-63
E value
                   122
Match length
                   89
% identity
                   60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi 1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                   218701
Seq. No.
                   LIB3148-056-Q1-K1-A3
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2914706
BLAST score 160
E value 6.0e-11
Match length 60



% identity

```
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
                  218702
Seq. No.
                  LIB3148-056-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q2213600
NCBI GI
                  454
BLAST score
                  2.0e-45
E value
Match length
                  136
% identity
                  62
                 (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
                  218703
Seq. No.
                  LIB3148-056-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  g602076
NCBI GI
                  682
BLAST score
                   4.0e-72
E value
                  136
Match length
                   23
% identity
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                  218704
Seq. No.
                  LIB3148-056-Q1-K1-B11
Seq. ID
                  BLASTN
Method
NCBI GI
                   q3821780
                   36
BLAST score
                   5.0e-11
E value
                   37
Match length
                   61
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   218705
Seq. No.
                   LIB3148-056-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3334299
BLAST score
                   664
E value
                   5.0e-70
Match length
                   136
% identity
                   93
                   PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX ALPHA SUBUNIT) >gi 2315211_emb_CAA74725_ (Y14339)
                   proteasome alpha subunit [Lycopersicon esculentum]
Seq. No.
                   218706
                   LIB3148-056-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3882321
BLAST score
                   143
E value
                   7.0e-09
                   102
Match length
                   37
% identity
NCBI Description (AB018343) KIAA0800 protein [Homo sapiens]
Seq. No.
                   218707
Seq. ID
                   LIB3148-056-Q1-K1-B9
```

Seq. ID Method



```
BLASTX
Method
                   g3335060
NCBI GI
                   428
BLAST score
                   2.0e-42
E value
Match length
                   105
                   90
% identity
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
NCBI Description
                   thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
                   218708
Seq. No.
                   LIB3148-056-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   q4103324
NCBI GI
BLAST score
                   662
                   1.0e-69
E value
Match length
                   135
                   92
% identity
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   218709
Seq. No.
                   LIB3148-056-Q1-K1-C11
Seq. ID
                   BLASTN
Method
                   g3510339
NCBI GI
                    34
BLAST score
                    1.0e-09
E value
                   157
Match length
                    83
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K3K7, complete sequence [Arabidopsis thaliana]
                    218710
Seq. No.
                    LIB3148-056-Q1-K1-C6
Seq. ID
                    BLASTX
Method
                    g322750
NCBI GI
BLAST score
                    459
                    6.0e-46
E value
Match length
                    88
                    99
% identity
                    ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                    >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                    sylvestris]
                    218711
Seq. No.
                    LIB3148-056-Q1-K1-D1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4469003
BLAST score
                    149
                    1.0e-09
E value
                    67
Match length
% identity
                    45
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                    218712
```

30733

LIB3148-056-Q1-K1-D5

BLASTX



```
g3193292
NCBI GI
                   504
BLAST score
                   3.0e-51
E value
                  135
Match length
                   73
% identity
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   218713
Seq. No.
                  LIB3148-056-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                   g2655420
NCBI GI
                   579
BLAST score
                   6.0e-60
E value
Match length
                   129
                   91
% identity
                  (AF035414) heat shock cognate protein HSC70 [Brassica
NCBI Description
                   napus]
                   218714
Seq. No.
                   LIB3148-056-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g2258315
NCBI GI
                   186
BLAST score
                   6.0e-14
E value
                   76
Match length
                   50
% identity
                   (AF004878) resistance complex protein I2C-1 [Lycopersicon
NCBI Description
                   esculentum]
                   218715
Seq. No.
                   LIB3148-056-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2668505
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
Match length
                   87
                   46
% identity
                   (U61837) putative cyclin G1 interacting protein [Homo
NCBI Description
                   sapiens]
                   218716
Seq. No.
                   LIB3148-056-Q1-K1-F3
Seq. ID
Method
                   BLASTN
                   q2337888
NCBI GI
BLAST score
                   42
E value
                   2.0e-14
Match length
                   78
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14J16,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   218717
Seq. No.
```

LIB3148-056-Q1-K1-F4 Seq. ID

Method BLASTX NCBI GI g480450

NCBI GI

BLAST score



```
465
BLAST score
                  9.0e-47
E value
Match length
                  115
                  77
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  218718
Seq. No.
                  LIB3148-056-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3452263
BLAST score
                  472
E value
                  2.0e-47
Match length
                  102
% identity
                  85
                  (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  218719
                  LIB3148-056-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  372
E value
                  1.0e-35
Match length
                  136
% identity
                  52
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi_2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                  218720
Seg. ID
                  LIB3148-056-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q2317762
BLAST score
                  218
                  1.0e-17
E value
                  46
Match length
% identity
NCBI Description (AF013804) Wilm's tumor supressor homolog [Pinus taeda]
                  218721
Seq. No.
Seq. ID
                  LIB3148-056-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q2944446
BLAST score
                  332
E value
                  4.0e-31
Match length
                  72
% identity
NCBI Description
                  (AF050756) cysteine endopeptidase precursor [Ricinus
                  communis]
Seq. No.
                  218722
                  LIB3148-056-Q1-K1-G3
Seq. ID
Method
                  BLASTX
```

g2293566



```
9.0e-18
E value
                  41
Match length
                  98
% identity
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                  218723
Seq. No.
                  LIB3148-056-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  q4567282
NCBI GI
                  443
BLAST score
                  4.0e-44
E value
                  131
Match length
                  69
% identity
                  (AC006841) putative DNAJ protein [Arabidopsis thaliana]
NCBI Description
                  218724
Seq. No.
                  LIB3148-056-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  q4580575
NCBI GI
                  284
BLAST score
                  2.0e - 35
E value
Match length
                  123
                  65
% identity
NCBI Description (AF082176) auxin response factor 9 [Arabidopsis thaliana]
                  218725
Seq. No.
                  LIB3148-056-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g1710530
NCBI GI
                  250
BLAST score
                   1.0e-35
E value
Match length
                   111
                   65
% identity
                  60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                   218726
Seq. No.
                   LIB3148-056-Q1-K1-H8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4098126
                   176
BLAST score
                   2.0e-94
E value
                   250
Match length
% identity
                   100
NCBI Description Gossypium hirsutum sucrose synthase mRNA, partial cds
Seq. No.
                   218727
                   LIB3148-057-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3522933
                   535
BLAST score
                   7.0e-55
E value
                   128
Match length
% identity
NCBI Description (AC004411) putative anion exchange protein 3 [Arabidopsis
```



thaliana]

```
Seq. No.
                   218728
Seq. ID
                  LIB3148-057-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                   g2558943
BLAST score
                   118
E value
                   3.0e-60
Match length
                   118
% identity
                   100
NCBI Description Gossypium hirsutum histone 3 mRNA, complete cds
Seq. No.
                   218729
Seq. ID
                  LIB3148-057-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                   g2244956
BLAST score
                   347
E value
                   9.0e-33
Match length
                   129
% identity
                   57
NCBI Description (Z97340) strong similarity to pectinesterase [Arabidopsis
                   thaliana]
                   218730
Seq. No.
Seq. ID
                   LIB3148-057-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   q2760326
BLAST score
                   145
E value
                   4.0e-09
Match length
                   60
% identity
                   50
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.
                   218731
Seq. ID
                   LIB3148-057-Q1-K1-B9
Method
                  BLASTN
NCBI GI
                   g2245073
BLAST score
                   33
E value
                   5.0e-09
Match length
                   65
% identity
                   88
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   218732
Seq. ID
                   LIB3148-057-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                   g1076609
BLAST score
                   179
                   3.0e-13
E value
Match length
                   53
                   62
% identity
```

Seq. No. 218733

Seq. ID LIB3148-057-Q1-K1-C8

NCBI Description NTL1 protein - curled-leaved tobacco

Method BLASTX



```
NCBI GI
                  g417154
                   512
BLAST score
                  4.0e-52
E value
Match length
                  125
                  82
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   218734
Seq. No.
                  LIB3148-057-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                   g3150415
NCBI GI
                   379
BLAST score
                   2.0e-36
E value
Match length
                   82
                   32
% identity
                  (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   218735
Seq. No.
                   LIB3148-057-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g2760839
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
                   68
Match length
                   43
% identity
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]
                   218736
Seq. No.
                   LIB3148-057-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262149
BLAST score
                   329
                   9.0e-31
E value
                   87
Match length
                   64
 % identity
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                   218737
 Seq. No.
                   LIB3148-057-Q1-K1-D11
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q3688123
 BLAST score
                   363
 E value
                   1.0e-34
 Match length
                   87
                   77
 % identity
                   (AJ006293) granule-bound starch synthase [Antirrhinum
 NCBI Description
                   majus]
```

30738

218738

BLASTX

LIB3148-057-Q1-K1-D12

Seq. No.

Seq. ID

Method

% identity



```
g4406775
NCBI GI
                  240
BLAST score
                  3.0e-20
E value
                  116
Match length
                  45
% identity
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                  218739
Seq. No.
                  LIB3148-057-Q1-K1-D2
Seq. ID
                  BLASTN
Method
                  g170455
NCBI GI
                  44
BLAST score
                  2.0e-15
E value
                  80
Match length
                  89
% identity
NCBI Description Tomato heat shock cognate protein 80 gene, 3' end
                  218740
Seq. No.
                  LIB3148-057-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                   g1843527
NCBI GI
                   528
BLAST score
                   4.0e-54
E value
                   112
Match length
                   52
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
                   218741
Seq. No.
                   LIB3148-057-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g3915866
NCBI GI
BLAST score
                   276
                   1.0e-24
E value
                   81
Match length
                   65
% identity
                   GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                   >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                   synthetase [Lupinus luteus]
                   218742
Seq. No.
                   LIB3148-057-Q1-K1-D9
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
                   36
BLAST score
                   9.0e-11
E value
                   48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   218743
 Seq. No.
 Seq. ID
                   LIB3148-057-Q1-K1-E12
Method
                   BLASTX
                   g3879111
 NCBI GI
                   172
 BLAST score
                   3.0e-12
 E value
                   96
 Match length
```



(Z81577) predicted using Genefinder; Similarity to Human NCBI Description tricarboxylate transport protein (SW:P53007); cDNA EST yk197f1.5 comes from this gene; cDNA EST yk313e6.3 comes from this gene; cDNA EST yk313e6.5 comes from this gene [C 218744 Seq. No. LIB3148-057-Q1-K1-E2 Seq. ID Method BLASTX g2129767 NCBI GI BLAST score 400 2.0e-43 E value Match length 132 % identity 65 vacuolar processing enzyme (EC 3.4.22.-) isozyme beta NCBI Description precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana] 218745 Seq. No. LIB3148-057-Q1-K1-E6 Seq. ID Method BLASTX q1346432 NCBI GI BLAST score 454 E value 2.0e-45 Match length 134 62 % identity LEGUMAIN PRECURSOR (ASPARAGINYL ENDOPEPTIDASE) NCBI Description >qi 1076483 pir JX0344 legumain (EC 3.4.22.34) precursor jack bean >gi 499294 dbj_BAA06596_ (D31787) asparaginyl endopeptidase (Legumain) [Canavalia ensiformis] 218746 Seq. No. LIB3148-057-Q1-K1-F10 Seq. ID BLASTX Method NCBI GI g2832625 208 BLAST score 9.0e-17 E value 63 Match length 60 % identity NCBI Description (AL021711) putative protein [Arabidopsis thaliana] Seq. No. 218747 LIB3148-057-Q1-K1-F11 Seq. ID Method BLASTX

g2500380 NCBI GI BLAST score 521 3.0e-53E value 95 Match length 100 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal protein RL44 - upland cotton $\overline{>}$ gi_1553 $\overline{1}$ 29 $\overline{(U}$ 64677) ribosomal

protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

218748 Seq. No.

LIB3148-057-Q1-K1-F12 Seq. ID

Method BLASTX



```
q462195
NCBI GI
BLAST score
                   441
                   7.0e-44
E value
                   93
Match length
                   92
 % identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi 3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
                   218749
 Seq. No.
                   LIB3148-057-Q1-K1-F3
 Seq. ID
                   BLASTN
 Method
                   g2924257
 NCBI GI
                   44
 BLAST score
                   2.0e-15
 E value
                   85
 Match length
                   44
 % identity
 NCBI Description Tobacco chloroplast genome DNA
                   218750
 Seq. No.
                   LIB3148-057-Q1-K1-F4
 Seq. ID
                   BLASTX
 Method
                   g2760326
 NCBI GI
                   166
 BLAST score
                    1.0e-11
 E value
                    95
 Match length
                    40
 % identity
 NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                    218751
 Seq. No.
                    LIB3148-057-Q1-K1-F5
 Seq. ID
                    BLASTX
 Method
                    g3202024
 NCBI GI
                    391
 BLAST score
 E value
                    4.0e-38
                    80
 Match length
                    90
 % identity
                   (AF069315) thylakoid-bound L-ascorbate peroxidase precursor
 NCBI Description
                    [Mesembryanthemum crystallinum]
                    218752
 Seq. No.
                    LIB3148-057-Q1-K1-F6
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q3126969
 BLAST score
                    190
 E value
                    2.0e-14
 Match length
                    95
                    47
 % identity
 NCBI Description (AF061808) chalcone isomerase [Elaeagnus umbellata]
                    218753
 Seq. No.
                    LIB3148-057-Q1-K1-F7
 Seq. ID
                    BLASTX
 Method
```

g134025

438

NCBI GI

BLAST score



E value 2.0e-43 Match length 93 % identity 90

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8

ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal

protein S8 [Nicotiana tabacum]

Seq. No. 218754

Seq. ID LIB3148-057-Q1-K1-F8

Method BLASTX
NCBI GI g2244832
BLAST score 141
E value 1.0e-08
Match length 54
% identity 57

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 218755

Seq. ID LIB3148-057-Q1-K1-G12

Method BLASTX
NCBI GI g4206122
BLAST score 233
E value 2.0e-19
Match length 65
% identity 72

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 218756

Seq. ID LIB3148-057-Q1-K1-G3

Method BLASTX
NCBI GI g3805845
BLAST score 551
E value 1.0e-56
Match length 138
% identity 74

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 218757

Seq. ID LIB3148-057-Q1-K1-G6

Method BLASTX
NCBI GI g2340166
BLAST score 286
E value 1.0e-25
Match length 82
% identity 61

NCBI Description (AF008124) glutathione S-conjugate transporting ATPase

[Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug

resistance-associated protein homolog [Arabidopsis

thaliana]

Seq. No. 218758

Seq. ID LIB3148-057-Q1-K1-G7

Method BLASTX NCBI GI g3478700



```
263
BLAST score
                   6.0e-23
E value
                  61
Match length
                  85
% identity
                  (AF034387) AFT protein [Arabidopsis thaliana]
NCBI Description
                  218759
Seq. No.
                  LIB3148-057-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                   g2894593
NCBI GI
                   152
BLAST score
                   6.0e-10
E value
                   37
Match length
                   76
% identity
NCBI Description (AL021889) hypothetical protein [Arabidopsis thaliana]
                   218760
Seq. No.
                   LIB3148-057-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   q294845
NCBI GI
                   289
BLAST score
                   5.0e-26
E value
Match length
                   119
                   52
% identity
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                   H65-7052
Seq. No.
                   218761
                   LIB3148-057-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g4539452
NCBI GI
                   420
BLAST score
                   2.0e-41
E value
                   111
Match length
                   42
% identity
NCBI Description (AL049500) putative phosphoribosylanthranilate transferase
                   [Arabidopsis thaliana]
                   218762
Seq. No.
                   LIB3148-057-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   q404688
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
                   104
Match length
                   39
 % identity
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]
                   218763
 Seq. No.
                   LIB3148-057-Q1-K1-H7
 Seq. ID
                   BLASTX
Method
                   q4138592
 NCBI GI
BLAST score
                   294
                   1.0e-26
E value
                   80
Match length
                    61
 % identity
 NCBI Description (AJ005840) thioredoxin M [Triticum aestivum]
```

Method

BLASTX



```
218764
Seq. No.
                  LIB3148-058-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g2760830
NCBI GI
                  463
BLAST score
                  2.0e-46
E value
                  99
Match length
                  81
% identity
                  (ACO03105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  218765
Seq. No.
                  LIB3148-058-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                   g3341697
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   73
Match length
                   62
% identity
                  (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   218766
Seq. No.
                   LIB3148-058-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   q3643610
NCBI GI
                   139
BLAST score
E value
                   5.0e-09
Match length
                   32
                   78
% identity
                  (AC005395) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   218767
Seq. No.
                   LIB3148-058-Q1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4049401
BLAST score
                   205
                   4.0e-16
E value
                   60
Match length
                   63
% identity
                   (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                   thaliana]
                   218768
Seq. No.
                   LIB3148-058-Q1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2564237
BLAST score
                   163
                   9.0e-12
E value
                   42
Match length
% identity
NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]
                   218769
Seq. No.
                   LIB3148-058-Q1-K1-B5
Seq. ID
```

Match length

NCBI Description

% identity

126

44



```
g585165
NCBI GI
BLAST score
                   458
                   5.0e-46
E value
                   96
Match length
                   90
% identity
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato
                   >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
                   1-dehydrogenase [Solanum tuberosum]
                   218770
Seq. No.
                   LIB3148-058-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g1737492
NCBI GI
                   333
BLAST score
                   4.0e - 31
E value
                   131
Match length
                   58
% identity
                  (U81318) poly(A)-binding protein [Triticum aestivum]
NCBI Description
                   218771
Seq. No.
                   LIB3148-058-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1708313
NCBI GI
BLAST score
                   230
E value
                   4.0e-19
                   65
Match length
                   80
% identity
NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                   thaliana]
                   218772
Seq. No.
Seq. ID
                   LIB3148-058-Q1-K1-C12
Method
                   BLASTX
                   q4455223
NCBI GI
                   509
BLAST score
                   8.0e-52
E value
Match length
                   131
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   218773
Seq. No.
Seq. ID
                   LIB3148-058-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   g3860274
BLAST score
                   271
                    6.0e-24
E value
```

~

protein [Arabidopsis thaliana]

(AC005824) unknown protein [Arabidopsis thaliana]

>qi 4314397 gb AAD15607 (AC006232) putative zinc finger



```
218774
Seq. No.
                  LIB3148-058-Q1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455300
BLAST score
                  174
                  1.0e-12
E value
                  63
Match length
                  54
% identity
                  (AL035528) putative pectate lyase All (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                  218775
Seq. No.
                  LIB3148-058-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  g4115381
NCBI GI
                  146
BLAST score
                   2.0e-09
E value
                  77
Match length
                   40
% identity
NCBI Description (AC005967) putative limonene cyclase [Arabidopsis thaliana]
Seq. No.
                  218776
                  LIB3148-058-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g100525
NCBI GI
                   560
BLAST score
E value
                   8.0e-58
                   117
Match length
                   23
% identity
                  ubiquitin precursor UbB2 - common sunflower (fragment)
NCBI Description
                   >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein
                   [Helianthus annuus]
                   218777
Seq. No.
                   LIB3148-058-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3450842
BLAST score
                   205
                   4.0e-16
E value
Match length
                   117
                   39
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   218778
Seq. ID
                   LIB3148-058-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   q3298548
BLAST score
                   565
E value
                   2.0e-58
Match length
                   122
% identity
                   87
                   (AC004681) putative spliceosomal protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 218779

Seq. ID LIB3148-058-Q1-K1-E1



```
Method BLASTX
NCBI GI g3914002
BLAST score 332
E value 3.0e-31
Match length 101
% identity 66
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279
(AF033862) Lon protease [Arabidopsis thaliana]
Seq. No. 218780
```

Seq. No. 218780 Seq. ID LIB3148-058-Q1-K1-E12

Method BLASTX
NCBI GI g1076746
BLAST score 631
E value 4.0e-66
Match length 129
% identity 98

NCBI Description heat shock protein 70 - rice (fragment)

>gi 763160_emb_CAA47948_ (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 218781

Seq. ID LIB3148-058-Q1-K1-E4

Method BLASTX
NCBI GI g4220524
BLAST score 304
E value 9.0e-28
Match length 100
% identity 58

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 218782

Seq. ID LIB3148-058-Q1-K1-E8

Method BLASTX
NCBI GI g2674203
BLAST score 383
E value 5.0e-37
Match length 133
% identity 64

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

Seq. No. 218783

Seq. ID LIB3148-058-Q1-K1-E9

Method BLASTX
NCBI GI g141435
BLAST score 189
E value 3.0e-14
Match length 101
% identity 38

NCBI Description DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_98360_pir_E37854

folate biosynthesis protein 1 (sul 3 region) - Bacillus subtilis >gi 143411 (M34053) ORF1 [Bacillus subtilis] >gi 467467_dbj_BAA05313_ (D26185) unknown [Bacillus

subtilis] >gi 2632345 emb CAB11854 (Z99104) dihydroneopterin aldolase [Bacillus subtilis]



Seq. No. 218784

Seq. ID LIB3148-058-Q1-K1-F10

Method BLASTX
NCBI GI g120669
BLAST score 502
E value 6.0e-51
Match length 101
% identity 93

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora

>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 218785

Seq. ID LIB3148-058-Q1-K1-F11

Method BLASTX
NCBI GI g3377795
BLAST score 197
E value 3.0e-15
Match length 104
% identity 42

NCBI Description (AF075597) contains similarity to pectinesterases

[Arabidopsis thaliana]

Seq. No. 218786

Seq. ID LIB3148-058-Q1-K1-F5

Method BLASTX
NCBI GI g102290
BLAST score 167
E value 1.0e-11
Match length 32
% identity 100

NCBI Description histone H4.2 - slime mold (Physarum polycephalum)

>gi 1183935 emb CAA33239 (X15141) histone H42 [Physarum

polycephalum]

Seq. No. 218787

Seq. ID LIB3148-058-Q1-K1-F9

Method BLASTX
NCBI GI g1184774
BLAST score 352
E value 1.0e-33
Match length 71
% identity 93

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 218788

Seq. ID LIB3148-058-Q1-K1-G10

Method BLASTX
NCBI GI g2668505
BLAST score 175
E'value 1.0e-12
Match length 87
% identity 46

NCBI Description (U61837) putative cyclin G1 interacting protein [Homo



sapiens]

218789 Seq. No. LIB3148-058-Q1-K1-G11 Seq. ID BLASTX Method NCBI GI q3152605 BLAST score 422 1.0e-41 E value 93 Match length 84 % identity (AC004482) hypothetical protein [Arabidopsis thaliana] NCBI Description 218790 Seq. No. LIB3148-058-Q1-K1-G2 Seq. ID BLASTX Method NCBI GI g3924613 BLAST score 312 1.0e-28 E value 128 Match length 48 % identity (AF069442) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein [Arabidopsis thaliana] 218791 Seq. No. LIB3148-058-Q1-K1-G3 Seq. ID BLASTX Method g2894611 NCBI GI 186 BLAST score 7.0e-14E value 108 Match length 45 % identity NCBI Description (AL021889) putative protein [Arabidopsis thaliana] 218792 Seq. No. LIB3148-058-Q1-K1-G5 Seq. ID Method BLASTX NCBI GI q4204804 BLAST score 448 E value 1.0e-44 123 Match length % identity 67 NCBI Description (U52520) cyclin [Pisum sativum] 218793 Seq. No. LIB3148-058-Q1-K1-H10 Seq. ID Method BLASTX NCBI GI q3024386 BLAST score 547 3.0e-56 E value Match length 139 73 % identity

POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) NCBI Description

>gi_2129500_pir__S52006 polygalacturonase - upland cotton >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]

Seq. No. 218794



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· · LIB3148-058-Q1-K1-H12
Seq. ID
Method
                   BLASTX
                   q4538965
NCBI GI
BLAST score
                   146
E value
                   3.0e-09
                   50
Match length
                   54
% identity
                  (AL049488) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   218795
Seq. No.
                   LIB3148-058-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   g2244775
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
Match length
                   65
                   58
% identity
                  (Z97335) salt-inducible protein homolog [Arabidopsis
NCBI Description
                   thaliana]
                   218796
Seq. No.
                   LIB3148-059-Q1-K1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3493171
BLAST score
                   49
                   1.0e-18
E value
Match length
                   85
                   89
% identity
NCBI Description Gossypium hirsutum fiber annexin mRNA, complete cds
                   218797
Seq. No.
                   LIB3148-059-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q585960
                   211
BLAST score
E value
                   7.0e-17
Match length
                   43
% identity
                   93
                   PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
NCBI Description
                   >gi 433665 emb_CAA81412 (Z26753) Sec61 beta-subunit
                   homolog [Arabidopsis thaliana]
                   218798
Seq. No.
                   LIB3148-059-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129649
BLAST score
                   239
E value
                   3.0e-20
Match length
                   60
 % identity
NCBI Description myb-related protein 5 - Arabidopsis thaliana >gi_1218000
                   (U26935) myb-related protein Atmyb5 [Arabidopsis thaliana]
                   >gi 1587244 prf 2206352A Atmyb5 gene [Arabidopsis
                   thaliana]
```

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LIB3148-059-Q1-K1-A6

218799

Seq. No.

Seq. ID



```
Method
                  BLASTX
                  g1362150
NCBI GI
                  189
BLAST score
                  2.0e-14
E value
Match length
                  38
                  97
% identity
                  hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                  >gi 726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.
                  218800
                  LIB3148-059-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q586339
BLAST score
                  365
                  6.0e-35
E value
Match length
                  114
                  57
% identity
                 PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098
NCBI Description
                  probable AMP-binding protein - yeast (Saccharomyces
                  cerevisiae) >gi 536615 emb CAA85185_ (Z36091) ORF YBR222c
                   [Saccharomyces cerevisiae]
                  218801
Seq. No.
                  LIB3148-059-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1620986
BLAST score
                  179
E value
                  4.0e-13
Match length
                  40
                   90
% identity
                  (Y08858) 40S ribosomal protein S17 [Nicotiana
NCBI Description
                  plumbaginifolia]
                  218802
Seq. No.
                  LIB3148-059-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4490297
BLAST score
                   431
E value
                   1.0e-42
Match length
                   127
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   218803
                   LIB3148-059-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3901014
BLAST score
                   234
E value
                   1.0e-19
                  55
Match length
                   76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
```

Seq. ID LIB3148-059-Q1-K1-C10

218804

Method BLASTX

Seq. No.



```
g2281090
NCBI GI
                  313
BLAST score
                  7.0e-29
E value
Match length
                  122
                  51
% identity
                 (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  218805
Seq. No.
                  LIB3148-059-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  163
                  3.0e-11
E value
Match length
                  43
% identity
                  67
                  (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                  hirsutum]
                  218806
Seq. No.
                  LIB3148-059-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056489
BLAST score
                  169
                   4.0e-12
E value
                  35
Match length
                  83
% identity
NCBI Description (AC005896) putative white protein [Arabidopsis thaliana]
                  218807
Seq. No.
                  LIB3148-059-Q1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1439631
BLAST score
                  409
                   4.0e-40
E value
Match length
                  121
                   66 -
% identity
NCBI Description
                  (U64598) similar to helicases of the SNF2/RAD54 family.
                   Does not contain the bromodomain. [Caenorhabditis elegans]
                   218808
Seq. No.
```

LIB3148-059-Q1-K1-D1 Seq. ID

Method BLASTX NCBI GI q3024020 BLAST score 636 E value 1.0e-66 Match length 126 % identity 95

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

218809 Seq. No.

LIB3148-059-Q1-K1-D11 Seq. ID

Method BLASTX NCBI GI g228404 BLAST score 518 E value 7.0e-53

NCBI Description



```
114
Match length
                  82
% identity
NCBI Description alpha amylase [Vigna radiata]
                  218810
Seq. No.
                  LIB3148-059-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g294062
                  152
BLAST score
                   6.0e-10
E value
                  109
Match length
                   34
% identity
NCBI Description (L06469) major latex protein [Papaver somniferum]
                  218811
Seq. No.
                  LIB3148-059-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3169182
NCBI GI
                   223
BLAST score
                  2.0e-18
E value
                   43
Match length
                   88
% identity
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
                   218812
Seq. No.
                   LIB3148-059-Q1-K1-D6
Seq. ID
                   BLASTX
Method
                   g2961353
NCBI GI
                   506
BLAST score
                   2.0e-51
E value
Match length
                   131
% identity
                  (AL022140) pectate lyase like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   218813
Seq. ID
                   LIB3148-059-Q1-K1-D7
                   BLASTX
Method
NCBI GI
                   g1711507
BLAST score
                   211
E value
                   7.0e-17
Match length
                   108
                   45
% identity
                   SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19)
NCBI Description
                   >gi 624221 (U19030) signal recognition particle 19 kDa
                   protein subunit SRP19 [Oryza sativa]
Seq. No.
                   218814
                   LIB3148-059-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512125
                   273
BLAST score
E value
                   3.0e-24
                   51
Match length
                   100
% identity
```

30753

[Phalaenopsis sp. 'KCbutterfly']

(AF133340) putative chlorophyll a/b-binding protein

Match length

% identity



```
218815
Seq. No.
                  LIB3148-059-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3023858
BLAST score
                  567
                  1.0e-58
E value
                  131
Match length
                  36
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 1256608 (U44850) G protein beta subunit
                  [Glycine max]
                  218816
Seq. No.
                  LIB3148-059-Q1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2688829
BLAST score
                  43
                  5.0e-15
E value
                  75
Match length
                  89
% identity
NCBI Description Prunus armeniaca putative sugar transporter mRNA, complete
Seq. No.
                  218817
                  LIB3148-059-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g1730635
NCBI GI
                  150
BLAST score
                   1.0e-09
E value
Match length
                   71
                   44
% identity
                  HYPOTHETICAL 40.7 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION
NCBI Description
                   >gi_2132777_pir__S60917 probable membrane protein YNL264c -
                   yeast (Saccharomyces cerevisiae) >gi_1045245_emb_CAA63233_
                   (X92494) ORF N0815 [Saccharomyces cerevisiae]
                   >gi_1302321_emb_CAA96171_ (Z71540) ORF YNL264c
                   [Saccharomyces cerevisiae]
Seq. No.
                   218818
Seq. ID
                   LIB3148-059-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2244734
BLAST score
                   665
E value
                   4.0e-70
Match length
                   130
% identity
                   99
NCBI Description (D88414) actin [Gossypium hirsutum]
                   218819
Seq. No.
Seq. ID
                   LIB3148-059-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g2293288
BLAST score
                   150
                   1.0e-09
E valúe
```



(AF008220) YtcB [Bacillus subtilis] NCBI Description >qi 2635571 emb CAB15065 (Z99119) similar to NDP-sugar epimerase [Bacillus subtilis] Seq. No. 218820 LIB3148-059-Q1-K1-G11 Seq. ID Method BLASTX NCBI GI g1495251 BLAST score 526 E value 8.0e-54 Match length 130 % identity 75 NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

218821 Seq. No.

LIB3148-059-Q1-K1-G3 Seq. ID

Method BLASTX NCBI GI g1173187 BLAST score 478 E value 4.0e-48 Match length 96 98 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

218822 Seq. No.

LIB3148-059-Q1-K1-G4 Seq. ID

BLASTN Method NCBI GI g167366 BLAST score 247 E value 1.0e-136 Match length 351 94 % identity

NCBI Description Gossypium hirsutum peroxidase mRNA, complete cds

Seq. No. 218823

LIB3148-059-Q1-K1-H1 Seq. ID

Method BLASTX NCBI GI q445612 519 BLAST score E value 5.0e-53 109 Match length 92 % identity

NCBI Description ribosomal protein S19 [Solanum tuberosum]

218824 Seq. No.

LIB3148-059-Q1-K1-H2 Seq. ID

BLASTX Method NCBI GI g3367593 399 BLAST score E value 6.0e - 39Match length 128 53 % identity

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

>gi 3805841 emb CAA21461 (AL031986) putative protein



[Arabidopsis thaliana]

```
218825
Seq. No.
                  LIB3148-059-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g485512
NCBI GI
                  331
BLAST score
                  6.0e-31
E value
                  99
Match length
                  64
% identity
NCBI Description salt-associated protein csaA - sweet orange
                  218826
Seq. No.
                  LIB3148-059-Q1-K1-H8
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  33
BLAST score
                  6.0e-09
E value
                  48
Match length
                  51
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  218827
Seq. No.
                  LIB3149-001-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g1350930
NCBI GI
                  575
BLAST score
                  2.0e-59
E value
                  116
Match length
                  97
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S13
                   218828
Seq. No.
                  LIB3149-001-P1-K1-A11
Seq. ID
                   BLASTX
Method
                   q3738092
NCBI GI
BLAST score
                   492
                   1.0e-49
E value
                   113
Match length
                   85
% identity
NCBI Description (AC005617) similar to glyoxysomal malate dehydrogenase
                   [Arabidopsis thaliana]
                   218829
 Seq. No.
                   LIB3149-001-P1-K1-A2
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g1172556
 BLAST score
                   300
 E value
                   3.0e-27
                   68
 Match length
                   82
 % identity
 NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                    (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 36) >gi 629729_pir__S46925 porin II, 36K - potato
                   >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato
                   mitochondrion >gi 515360 emb CAA56600 (X80387) 36kDA porin
                   II [Solanum tuberosum]
```

% identity



```
218830
Seq. No.
                  LIB3149-001-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377509
BLAST score
                  617
E value
                  2.0e-64
Match length
                  140
% identity
                  87
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]
                  218831
Seq. No.
                  LIB3149-001-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335378
BLAST score
                  352
E value
                  2.0e-33
Match length
                  86
                  73
% identity
NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis
                  thaliana]
Seq. No.
                  218832
                  LIB3149-001-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3128192
BLAST score
                  312
E value
                  1.0e-28
Match length
                  67
% identity
                  79
NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]
                  218833
Seq. No.
                  LIB3149-001-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170936
BLAST score
                  145
E value
                  2.0e-09
                  24
Match length
                  100
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 1084406 pir __S46538 methionine adenosyltransferase (EC
                   2.5.1.6) - tomato >gi_429104_emb_CAA80865_ (Z24741)
                   S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  218834
Seq. No.
Seq. ID
                  LIB3149-001-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2511691
BLAST score
                  256
                  1.0e-31
E value
Match length
                  106
```

NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]



```
Seq. No.
                  218835
                  LIB3149-001-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g3033375
NCBI GI
BLAST score
                  272
                  5.0e-24
E value
Match length
                  118
                  47
% identity
NCBI Description
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
Seq. No.
                  218836
                  LIB3149-001-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g3850108
NCBI GI
BLAST score
                  296
E value
                  9.0e-27
Match length
                  143
                   44
% identity
                  (AL033388) putative calcium-transporting atpase
NCBI Description
                   [Schizosaccharomyces pombe]
                  218837
Seq. No.
                  LIB3149-001-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133940
BLAST score
                  345
                  2.0e-32
E value
Match length
                  89
                  76
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A
                   ribosomal protein S3a - African clawed frog
                   >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a
                   [Xenopus laevis]
Seq. No.
                   218838
Seq. ID
                  LIB3149-001-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  q3868723
BLAST score
                   35
E value
                   3.0e-10
Match length
                  75
% identity
                   87
NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete
                   sequence [Arabidopsis thaliana]
Seq. No.
                   218839
Seq. ID
                  LIB3149-001-P1-K1-C4
Method
                  BLASTX
                   g2827550
NCBI GI
BLAST score
                  233
```

E value 2.0e-19 Match length 140 % identity 28

NCBI Description (AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana]



```
Seq. No.
                  218840
                  LIB3149-001-P1-K1-C5
Seq. ID
Method
                  BLASTX
                  q3880606
NCBI GI
                  145
BLAST score
                  4.0e-09
E value
                  32
Match length
                   91
% identity
                  (Z82081) similar to Core histones H2A, H2B, H3 and H4
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                  218841
                  LIB3149-001-P1-K1-C9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3868723
BLAST score
                   35
                   4.0e-10
E value
                  75
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome V map 60.5 cM, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
Seq. No.
                   218842
                  LIB3149-001-P1-K1-D1
Seq. ID
                   BLASTX
Method
                   g730456
NCBI GI
                   123
BLAST score
E value
                   1.0e-08
                   91
Match length
                   47
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   218843
Seq. No.
                   LIB3149-001-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2088652
BLAST score
                   540
E value
                   2.0e-55
                   152
Match length
% identity
                  (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2351376 (U54561) translation
                   initiation factor eIF2 p47 subunit homolog [Arabidopsis
                   thaliana]
                   218844
Seq. No.
Seq. ID
                   LIB3149-001-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q2511594
BLAST score
                   454
E value
                   2.0e-45
Match length
                   110
% identity
                   79
                  (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
```

precursor, beta subunit [Arabidopsis thaliana]
>gi 2827525 emb CAA16533 (AL021633) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit

BLAST score

E value

656

6.0e-69



[Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

```
218845
Seq. No.
                   LIB3149-001-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3881724
BLAST score
                   254
                   7.0e-22
E value
Match length
                   82
                   56
% identity
                   (Z69385) Similarity to Yeast JTA107 protein (PIR Acc. No.
NCBI Description
                   S55137); cDNA EST yk290e3.3 comes from this gene; cDNA EST
                   yk290e3.5 comes from this gene [Caenorhabditis elegans]
                   218846
Seq. No.
                   LIB3149-001-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g586004
NCBI GI
BLAST score
                   557
E value
                   2.0e-57
Match length
                   113
                   89
% identity
                   SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato
NCBI Description
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
                   (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
                   superoxide dismutase [Ipomoea batatas]
                   218847
Seq. No.
Seq. ID
                   LIB3149-001-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g1709761
BLAST score
                   626
E value
                   2.0e-65
Match length
                   126
% identity
                   97
                   PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 27 KD SUBUNIT) >gi 1262146 emb_CAA65660_ (X96974)
                   proteasome subunit [Spinacia oleracea]
Seq. No.
                   218848
                   LIB3149-001-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244792
BLAST score
                   245
E value
                   8.0e-21
Match length
                   64
% identity
                   75
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]
Seq. No.
                   218849
Seq. ID
                   LIB3149-001-P1-K1-E10
                   BLASTX
Method
NCBI GI
                   g1730171
```



Match length 148 84 % identity GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI) NCBI Description (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_1370066_emb_CAA61574_ (X89394) glucose-6-phosphate isomerase [Clarkia williamsonii] 218850 Seq. No. Seq. ID LIB3149-001-P1-K1-E11 Method BLASTX NCBI GI q2588816 BLAST score 209 E value 5.0e-17 83 Match length 52 % identity NCBI Description (D88926) cytosolic phosphoglucose isomerase [Dioscorea tokoro] >gi_2588820_dbj_BAA23183_ (D88928) cytosolic phosphoglucose isomerase [Dioscorea tokoro] 218851 Seq. No. LIB3149-001-P1-K1-E12 Seq. ID BLASTX Method NCBI GI g2651307 BLAST score 631 E value 5.0e-66 144 Match length % identity 86 (AC002336) putative uroporphyinogen decarboxylase NCBI Description [Arabidopsis thaliana] Seq. No. 218852 LIB3149-001-P1-K1-E2 Seq. ID Method BLASTX q4139493 NCBI GI BLAST score 300 E value 7.0e-28 Match length 60 97 % identity NCBI Description Rub1 Seq. No. 218853 LIB3149-001-P1-K1-E4 Seq. ID Method BLASTX NCBI GI g1703380 BLAST score 280 E value 6.0e-25 Match length 65 % identity ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760) NCBI Description ADP-ribosylation factor [Oryza sativa] Seq. No. 218854

LIB3149-001-P1-K1-E7 Seq. ID

Method BLASTX NCBI GI g1729980 BLAST score 586 E value 8.0e-61



Match length 122 % identity NCBI Description

THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana $>gi_536825$ (L34693) thaumatin-like protein [Arabidopsis thaliana]

>gi 1094863 prf 2106421A thaumatin-like protein

[Arabidopsis thaliana]

218855 Seq. No.

LIB3149-001-P1-K1-F10 Seq. ID

Method BLASTX NCBI GI g2511598 BLAST score 164 2.0e-11 E value 42 Match length 71 % identity

(Y13696) multicatalytic endopeptidase complex, proteasome NCBI Description

component, beta subunit [Arabidopsis thaliana]

218856 Seq. No.

Seq. ID LIB3149-001-P1-K1-F11

Method BLASTX g1843527 NCBI GI BLAST score 762 E value 2.0e-81 Match length 153 % identity 43

NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 218857

Seq. ID LIB3149-001-P1-K1-F3

Method BLASTX NCBI GI q499693 BLAST score 357 E value 6.0e - 34Match length 83 % identity

NCBI Description (L32095) cyclophilin [Vicia faba]

Seq. No. 218858

Seq. ID LIB3149-001-P1-K1-F4

Method BLASTX NCBI GI g2982299 BLAST score 200 E value 1.0e-15 Match length 76 % identity

(AF051234) transcription factor BTF3 homolog [Picea NCBI Description

mariana]

218859 Seq. No.

Seq. ID LIB3149-001-P1-K1-F5

Method BLASTX NCBI GI g1173234 BLAST score 352 E value 2.0e-33 77 Match length



% identity 40S RIBOSOMAL PROTEIN S25 >qi 481909 pir S40089 ribosomal NCBI Description protein S25 - tomato >gi 435679 emb CAA54132 (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi_1584836_prf__2123431A ribosomal protein S25 [Lycopersicon esculentum] 218860 Seq. No. LIB3149-001-P1-K1-F9 Seq. ID Method BLASTX g2511598 NCBI GI BLAST score 217 E value 9.0e-18 47 Match length 83 % identity NCBI Description (Y13696) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] 218861 Seq. No. Seq. ID LIB3149-001-P1-K1-G1 Method BLASTN NCBI GI g2687434 BLAST score 304 1.0e-170 E value Match length 360 96 % identity NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence 218862 Seq. No. Seq. ID LIB3149-001-P1-K1-G11 Method BLASTX NCBI GI q3024126 BLAST score 424 9.0e-42 E value Match length 99 % identity 85 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus] 218863 Seq. No. Seq. ID LIB3149-001-P1-K1-G12 Method BLASTX NCBI GI q2511594 BLAST score 527 E value 7.0e-54Match length 124 % identity

NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome

precursor, beta subunit [Arabidopsis thaliana]

>gi 2827525 emb CAA16533 (AL021633) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S

proteasome subunit PBA1 [Arabidopsis thaliana]



```
Seq. No.
                  218864
                  LIB3149-001-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  q3717946
NCBI GI
                  186
BLAST score
                  7.0e-14
E value
                  53
Match length
                  72
% identity
                 (AJ005901) vag1 [Arabidopsis thaliana]
NCBI Description
                  218865
Seq. No.
                  LIB3149-001-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  g123684
NCBI GI
BLAST score
                  539
                  3.0e-55
E value
                  139
Match length
                  74
% identity
                 HEAT SHOCK FACTOR PROTEIN HSF24 (HEAT SHOCK TRANSCRIPTION
NCBI Description
                  FACTOR 24) (HSTF 24) (HEAT STRESS TRANSCRIPTION FACTOR)
                  >gi_100267_pir__S12361 heat shock transcription factor
                  HSF24 - Peruvian tomato >gi_19488_emb_CAA39034_ (X55347)
                  heat stress transcription factor [Lycopersicon peruvianum]
                  218866
Seq. No.
                  LIB3149-001-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1222552
BLAST score
                  341
                  1.0e-32
E value
                  79
Match length
                  78
% identity
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
                  218867
Seq. No.
                  LIB3149-001-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g2911071
NCBI GI
BLAST score
                   246
                   7.0e-21
E value
                  79
Match length
                   59
% identity
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]
                   218868
Seq. No.
                   LIB3149-001-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   g2253442
NCBI GI
                   178
BLAST score
E value
                   3.0e-13
                   60
Match length
                   53
% identity
NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]
```

Seq. No. 218869

Seq. ID LIB3149-001-P1-K1-H5

Method BLASTX

Method

NCBI GI BLAST score BLASTN g4406805

50



```
q1709651
NCBI GI
BLAST score
                  307
E value
                  3.0e-28
Match length
                  114
% identity
                  60
                  PLASTOCYANIN A PRECURSOR >gi 2117431_pir__S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
Seq. No.
                  218870
                  LIB3149-001-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982289
BLAST score
                  402
E value
                  3.0e-39
Match length
                  82
% identity
                  94
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]
                  218871
Seq. No.
Seq. ID
                  LIB3149-001-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g730557
BLAST score
                  267
E value
                  7.0e-24
Match length
                  53
% identity
                  96
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal
                 protein L34 - garden pea >gi 498908 (U10047) ribosomal
                  protein L34 homolog [Pisum sativum]
                  218872
Seq. No.
                  LIB3149-002-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982303
BLAST score
                  175
                  7.0e-13
E value
Match length
                  44
                  77
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                  218873
Seq. ID
                  LIB3149-002-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4454097
BLAST score
                  364
E value
                  9.0e-35
                  127
Match length
% identity
                  61
NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]
Seq. No.
                  218874
Seq. ID
                  LIB3149-002-P1-K1-C11
```



3.0e-19 E value Match length 85 % identity 72 NCBI Description Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana] 218875 Seq. No. LIB3149-002-P1-K1-F11 Seq. ID Method BLASTX NCBI GI q3122703 BLAST score 481 1.0e-48 E value Match length 115 83 % identity 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal NCBI Description protein L23a [Fritillaria agrestis] 218876 Seq. No. LIB3149-002-P1-K1-F9 Seq. ID Method BLASTX NCBI GI g2583108 BLAST score 373 8.0e-36 E value 108 Match length % identity 68 (AC002387) putative surface protein [Arabidopsis thaliana] NCBI Description 218877 Seq. No. LIB3149-002-P1-K2-A3 Seq. ID Method BLASTX NCBI GI g481236 187 BLAST score 6.0e-14 E value Match length 63 63 % identity NCBI Description hypothetical protein - Madagascar periwinkle >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide [Catharanthus roseus] 218878 Seq. No. Seq. ID LIB3149-002-P1-K2-A5 Method BLASTX NCBI GI g2982303 BLAST score 278 E value 1.0e-24 Match length 63 % identity 81 NCBI Description (AF051236) hypothetical protein [Picea mariana] 218879 Seq. No. Seq. ID LIB3149-002-P1-K2-B11 Method BLASTX

Method BLASTX
NCBI GI g125887
BLAST score 226
E value 1.0e-18
Match length 118
% identity 37



NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>gi_82092_pir__S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 218880

Seq. ID LIB3149-002-P1-K2-B6

Method BLASTX
NCBI GI g4027895
BLAST score 166
E value 1.0e-11
Match length 43
% identity 74

NCBI Description (AF049352) alpha-expansin precursor [Nicotiana tabacum]

Seq. No. 218881

Seq. ID LIB3149-002-P1-K2-C10

Method BLASTX
NCBI GI g2459429
BLAST score 471
E value 2.0e-47
Match length 124
% identity 70

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 218882

Seq. ID LIB3149-002-P1-K2-C3

Method BLASTX
NCBI GI g4126473
BLAST score 430
E value 2.0e-42
Match length 86
% identity 94

NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium

hirsutum]

Seq. No. 218883

Seq. ID LIB3149-002-P1-K2-C4

Method BLASTX
NCBI GI g1084461
BLAST score 363
E value 1.0e-34
Match length 89
% identity 73

NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 218884

Seq. ID LIB3149-002-P1-K2-C6

Method BLASTX
NCBI GI 94406816
BLAST score 189
E value 3.0e-14
Match length 38
% identity 92

NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 218885

E value

Match length

8.0e-55

131



```
LIB3149-002-P1-K2-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4314389
BLAST score
                  379
E value
                  1.0e-36
Match length
                  102
                  72
% identity
                  (AC006232) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  218886
Seq. No.
                  LIB3149-002-P1-K2-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982303
BLAST score
                  565
E value
                  2.0e-58
Match length
                  128
                  79
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                  218887
                  LIB3149-002-P1-K2-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1084461
BLAST score
                  190
E value
                  2.0e-14
                  46
Match length
                  72
% identity
NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  218888
Seq. ID
                  LIB3149-002-P1-K2-E10
Method
                  BLASTX
NCBI GI
                  q2258469
BLAST score
                  326
E value
                  1.0e-30
Match length
                  81
                  75
% identity
NCBI Description (AF009179) replication protein A1 [Oryza sativa]
Seq. No.
                  218889
Seq. ID
                  LIB3149-002-P1-K2-E2
Method
                  BLASTX
NCBI GI
                  g1732365
BLAST score
                  258
E value
                  3.0e-22
                  73
Match length
                  67
% identity
NCBI Description (U80271) proline rich protein [Malus domestica]
Seq. No.
                  218890
Seq. ID
                  LIB3149-002-P1-K2-E4
Method
                  BLASTX
NCBI GI
                  g2258469
BLAST score
                  535
```

NCBI Description



```
% identity
                  (AF009179) replication protein Al [Oryza sativa]
NCBI Description
                  218891
Seq. No.
                  LIB3149-002-P1-K2-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1888357
BLAST score
                  629
E value
                  8.0e-66
Match length
                  146
                  79
% identity
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  218892
                  LIB3149-002-P1-K2-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006818
BLAST score
                   266
                  2.0e-23
E value
Match length
                  62
                  84
% identity
NCBI Description
                  (AC005970) putative translation initiation factor eIF-2B,
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                   218893
                  LIB3149-002-P1-K2-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1402888
BLAST score
                   312
                   1.0e-28
E value
Match length
                   104
                   63
% identity
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                   218894
                   LIB3149-002-P1-K2-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1710587
BLAST score
                   486
E value
                   3.0e-49
Match length
                   106
% identity
                   93
                   60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic
NCBI Description
                   ribosomal protein PO [Glycine max]
                   218895
Seq. No.
Seq. ID
                   LIB3149-002-P1-K2-F5
Method
                   BLASTX
NCBI GI
                   g1888357
BLAST score
                   411
E value
                   2.0e-40
Match length
                   110
                   73
% identity
```

(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi 1890154 emb CAA72432_ (Y11767) alpha-mannosidase



precursor [Arabidopsís thaliana]

```
Seq. No.
                   218896
                   LIB3149-002-P1-K2-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122703
BLAST score
                   343
                   2.0e-32
E value
                   110
Match length
                   65
% identity
                  60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
NCBI Description
                   protein L23a [Fritillaria agrestis]
                   218897
Seq. No.
                   LIB3149-002-P1-K2-F8
Seq. ID
                   BLASTX
Method
                   q2829896
NCBI GI
                   208
BLAST score
                   1.0e-16
E value
                   68
Match length
                   56
% identity
                  (AC002311) highly similar to auxin-regulated protein GH3,
NCBI Description
                   gp X60033_18591 [Arabidopsis thaliana]
Seq. No.
                   218898
                   LIB3149-002-P1-K2-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1730171
                   425.
BLAST score
                   5.0e-42
E value
Match length
                   106
                   78
% identity
NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI)
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi_1370066_emb_CAA61574_ (X89394) glucose-6-phosphate isomerase [Clarkia williamsonii]
                   218899
Seq. No.
                   LIB3149-002-P1-K2-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2583108
BLAST score
                   286
E value
                   1.0e-25
Match length
                   80
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                   218900
Seq. ID
                   LIB3149-002-P1-K2-G12
Method
                   BLASTX
NCBI GI
                   g3914722
BLAST score
                   166
E value
                   1.0e-11
Match length
                   45
% identity
                   67
```

NCBI Description 60S RIBOSOMAL PROTEIN L29



```
218901
Seq. No.
                  LIB3149-002-P1-K2-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4008159
BLAST score
                  448
                  1.0e-44
E value
                  121
Match length
                  71
% identity
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
                  218902
Seq. No.
                  LIB3149-002-P1-K2-G8
Seq. ID
Method
                  BLASTX
                  g2224731
NCBI GI
BLAST score
                   215
E value
                   2.0e-17
                   86
Match length
                   53
% identity
NCBI Description (AB004932) Aux22d [Vigna radiata]
                   218903
Seq. No.
                  LIB3149-002-P1-K2-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4337189
BLAST score
                   247
                   4.0e-21
E value
Match length
                   69
                   71
% identity
                  (AC006403) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   218904
Seq. No.
                   LIB3149-002-P1-K2-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2454182
BLAST score
                   244
E value
                   5.0e-21
Match length
                   50
                   92
% identity
                  (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
                   218905
Seq. No.
                   LIB3149-002-P1-K2-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4234768
BLAST score
                   207
E value
                   1.0e-16
Match length
                   60
% identity
NCBI Description (AF069468) sterol-C5-desaturase [Arabidopsis thaliana]
                   218906
Seq. No.
                   LIB3149-003-P1-K1-A1
Seq. ID
```

30771

BLASTX

247

g2738998

Method NCBI GI

BLAST score



```
E value
                  3.0e-21
Match length
                  57
                  75
% identity
NCBI Description
                 (AF022458) CYP98A2p [Glycine max]
                  218907
Seq. No.
                  LIB3149-003-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q303750
BLAST score
                  442
E value
                  4.0e-44
Match length
                  85
% identity
                  100
                  (D12548) GTP-binding protein [Pisum sativum]
NCBI Description
                  >gi_738940_prf__2001457H GTP-binding protein [Pisum
                  sativuml
                  218908
Seq. No.
                  LIB3149-003-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1815759
BLAST score
                  148
E value
                  9.0e-10
Match length
                  53
% identity
                  55
NCBI Description (U85499) pollen-specific protein [Phalaris coerulescens]
                  218909
Seq. No.
                  LIB3149-003-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3600030
BLAST score
                  155
E value
                  3.0e-10
Match length
                  134
% identity
                  34
NCBI Description
                  (AF080119) contains similarity to ankyrin repeats (Pfam:
                  ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis
                  thaliana]
Seq. No.
                  218910
Seq. ID
                  LIB3149-003-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3355468
BLAST score
                  283
E value
                  1.0e-25
Match length
                  68
% identity
                  90
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 218911

Seq. ID LIB3149-003-P1-K1-A9

Method BLASTX NCBI GI g3868758 BLAST score 342 E value 2.0e-32 Match length 77



```
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                   218912
                   LIB3149-003-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g123656
BLAST score
                   504
E value
                   5.0e-51
Match length
                   137
% identity
                   80
                  CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED
NCBI Description
                   PROTEIN >gi_285407_pir__A42582 heat shock protein SCE70 -
                   spinach > gi_21338\_emb\_\overline{CAA}43711\_ \ (X61491) \ 70 \ kDa \ heat \ shock
                   protein [Spinacia oleracea]
                   218913
Seq. No.
Seq. ID
                   LIB3149-003-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q3080371
BLAST score
                   295
                   4.0e-27
E value
Match length
                   79
                   66
% identity
                  (AL022580) putative pectinacetylesterase protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   218914
                   LIB3149-003-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3687243
BLAST score
                   245
E value
                   8.0e-21
Match length
                   61
                   79
% identity
NCBI Description
                   (AC005169) putative ribosomal protein [Arabidopsis
                   thaliana]
Seq. No.
                   218915
                   LIB3149-003-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g169459
                   125
BLAST score
E value
                   6.0e-10
                   70
Match length
% identity
                   47
NCBI Description
                  (M18538) pop3 peptide [Populus balsamifera subsp.
                   trichocarpa X Populus deltoides]
                   218916
Seq. No.
Seq. ID
                   LIB3149-003-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3687243
BLAST score
                   245
E value
                   8.0e-21
Match length
                   61
% identity
                   79
```

Seq. No.

218922



```
NCBI Description (AC005169) putative ribosomal protein [Arabidopsis
                  thaliana]
                  218917
Seq. No.
                  LIB3149-003-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g1523800
NCBI GI
                  322
BLAST score
                  7.0e-30
E value
                  79
Match length
                  76
% identity
                  (Y07694) MAP kinase kinase alpha protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  218918
Seq. No.
                  LIB3149-003-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g170920
NCBI GI
BLAST score
                  136
                  1.0e-08
E value
                  29
Match length
                  79
% identity
                  (M62396) ribosomal protein L41 [Candida maltosa]
NCBI Description
                  218919
Seq. No.
                  LIB3149-003-P1-K1-D1
Seq. ID
                  BLASTN
Method
                  g11805
NCBI GI
                  75
BLAST score
                   6.0e - 34
E value
                  259
Match length
                  85
% identity
NCBI Description Intron in tobacco chloroplast gene rps16 for ribosomal
                  protein S16
                   218920
Seq. No.
Seq. ID
                  LIB3149-003-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   q4106388
BLAST score
                   154
                   3.0e-10
E value
Match length
                   65
% identity
                   48
NCBI Description (AF074849) unknown [Arabidopsis thaliana]
Seq. No.
                   218921
Seq. ID
                   LIB3149-003-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q4263711
BLAST score
                   219
E value
                   8.0e-18
Match length
                   53
% identity
                  (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
```

NCBI Description



```
LIB3149-003-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539350
                   261
BLAST score
                   7.0e-23
E value
                  76
Match length
                   61
% identity
                  (AL035539) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  218923
Seq. No.
                  LIB3149-003-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  g1710780
NCBI GI
BLAST score
                   326
                   2.0e-30
E value
                   98
Match length
                   66
% identity
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb_CAA65433_
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   218924
Seq. No.
                  LIB3149-003-P1-K1-D9
Seq. ID
                   BLASTX
Method
                   g4038035
NCBI GI
                   182
BLAST score
E value
                   2.0e-13
                   70
Match length
                   47
% identity
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   218925
Seq. No.
                   LIB3149-003-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129915
BLAST score
                   345
                   1.0e-32
E value
                   103
Match length
                   60
% identity
                   ferredoxin precursor - sweet orange
NCBI Description
                   >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
                   218926
Seq. No.
                   LIB3149-003-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3834309
BLAST score
                   355
E value
                   9.0e - 34
Match length
                   125
% identity
```

(AC005679) Strong similarity to glycoprotein EP1 gb_L16983

Daucus carota and a member of S locus glycoprotein family

PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]



```
218927
Seq. No.
                  LIB3149-003-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885328
BLAST score
                  177
                  4.0e-13
E value
                  88
Match length
                   47
% identity
                   (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  218928
Seq. No.
                  LIB3149-003-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  g3738320
NCBI GI
BLAST score
                   215
                   3.0e-17
E value
                  126
Match length
% identity
                   33
                  (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                   218929
Seq. No.
                  LIB3149-003-P1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4455208
BLAST score
                   481
                   2.0e-48
E value
                   136
Match length
                   71
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   218930
Seq. No.
                   LIB3149-003-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3819164
BLAST score
                   273
                   3.0e-24
E value
                   59
Match length
% identity
                   95
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                   max]
                   218931
Seq. No.
                   LIB3149-003-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2961372
BLAST score
                   549
E value
                   1.0e-56
Match length
                   110
                   91
% identity
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                   thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
```

Seq. No. 218932

Seq. ID LIB3149-003-P1-K1-F9

protein L2 [Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  g2218152
BLAST score
                   200
                  1.0e-15
E value
Match length
                   63
                   63
% identity
                   (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                  unguiculata]
Seq. No.
                   218933
                  LIB3149-003-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g425194
BLAST score
                   343
E value
                   2.0e-32
Match length
                  104
                   68
% identity
                   (L26243) heat shock protein [Spinacia oleracea] >gi 2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                   oleracea]
                   218934
Seq. No.
                  LIB3149-003-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3892055
BLAST score
                   135
E value
                   1.0e-08
Match length
                   39
                   77
% identity
NCBI Description
                  (AC002330) putative transport protein [Arabidopsis
                   thaliana]
                   218935
Seq. No.
Seq. ID
                   LIB3149-003-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   q3687251
BLAST score
                   441
E value
                   6.0e-44
Match length
                   109
                   79
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                   218936
Seq. ID
                   LIB3149-003-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g1616616
BLAST score
                   561
E value
                   5.0e-58
Match length
                   110
% identity
                   98
                  (Y08424) small GTP-binding protein [Nicotiana
NCBI Description
                   plumbaginifolia]
```

Seq. No. 218937

Seq. ID LIB3149-003-P1-K1-H12

Method BLASTX NCBI GI g3334321



```
BLAST score
                   206
                   8.0e-17
E value
Match length
                   45
% identity
                   89
NCBI Description
                  GTP-BINDING PROTEIN SAR1A >qi 2108345 (U55035) small
                  GTP-binding protein Bsarla [Brassica rapa]
                   218938
Seq. No.
Seq. ID
                  LIB3149-003-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q1563741
BLAST score
                  55
E value
                   1.0e-22
Match length
                  67
% identity
                  96
NCBI Description N.plumbaginifolia mRNA for GTP-binding protein, partial
                  218939
Seq. No.
                  LIB3149-003-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512688
BLAST score
                  224
E value
                  2.0e-18
Match length
                  65
                   77
% identity
NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]
                  218940
Seq. No.
Seq. ID
                  LIB3149-004-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1083739
BLAST score
                  426
E value
                   5.0e-42
Match length
                  114
% identity
                   68
NCBI Description
                  nucleolar protein Nopp140, hepatic - rat
                   >gi_1093316_prf__2103261A nuclear protein NAP57 [Rattus
                  norvegicus]
                   218941
Seq. No.
Seq. ID
                  LIB3149-004-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g4574208
BLAST score
                  411
E value
                  3.0e-40
Match length
                  83
% identity
                  100
NCBI Description (AF093108) histone H3 [Tortula ruralis]
                  218942
Seq. No.
Seq. ID
                  LIB3149-004-P1-K1-A7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4097579
BLAST score 268
E value 1.0e-23
Match length 119
% identity 62

E value

Match length

% identity

6.0e-10

67 45



```
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
Seq. No.
                  218943
Seq. ID
                  LIB3149-004-P1-K1-B10
Method
                  BLASTX
NCBI GI
                   g1706323
BLAST score
                   382
E value
                   7.0e-37
Match length
                  125
% identity
                   60
NCBI Description
                  ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__$64704
                   ornithine decarboxylase (EC 4.1.1.17) - jimsonweed
                  >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase
                   [Datura stramonium]
Seq. No.
                   218944
                  LIB3149-004-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4510363
BLAST score
                   480
E value
                   2.0e-48
Match length
                   94
                   90
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                   218945
Seq. ID
                  LIB3149-004-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1370166
BLAST score
                   698
E value
                   6.0e-74
Match length
                   138
                   97
% identity
NCBI Description (Z73932) RAB1C [Lotus japonicus]
Seq. No.
                   218946
Seq. ID
                  LIB3149-004-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q418854
BLAST score
                   435
E value
                   2.0e-43
Match length
                   94
% identity
                   16
NCBI Description
                  ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
                   (X64344) polyubiquitin [Petroselinum crispum]
                   >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
Seq. No.
                   218947
Seq. ID
                  LIB3149-004-P1-K1-C12
Method
                  BLASTX
NCBI GI
                   g2829899
BLAST score
                   152
```



```
(AC002311) similar to ripening-induced protein,
NCBI Description
                  gp_AJ001449_2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
                  218948
Seq. No.
                  LIB3149-004-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g2344892
NCBI GI
BLAST score
                  237
                  5.0e-20
E value
                  47
Match length
                  96
% identity
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]
                  218949
Seq. No.
                  LIB3149-004-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g1173223
NCBI GI
BLAST score
                  235
                  6.0e-20
E value
                  77
Match length
                  47
% identity
                 40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal
NCBI Description
                  protein S11 [Glycine max]
Seq. No.
                  218950
Seq. ID
                  LIB3149-004-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q3913633
BLAST score
                  414
                  1.0e-40
E value
Match length
                  127
                  68
% identity
NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                 - 218951
                  LIB3149-004-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133867
BLAST score
                  166
E value
                  1.0e-11
Match length
                  48
                  67
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                  protein S11 - maize >gi_22470_emb \overline{CAA39438} (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                   218952
                  LIB3149-004-P1-K1-D8
Seq. ID
Method
                  BLASTX
```

NCBI GI q4263519 BLAST score 251 E value 4.0e-22 Match length 67 73 % identity

NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis

NCBI GI



thaliana]

218953 Seq. No. Seq. ID LIB3149-004-P1-K1-E1 Method BLASTX NCBI GI q135860 BLAST score 567 1.0e-58 E value Match length 136 % identity 78 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi 445129 prf 1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana] Seq. No. 218954 LIB3149-004-P1-K1-E10 Seq. ID Method BLASTX g2130052 NCBI GI BLAST score 595 E value 8.0e-62 Match length 144 % identity 80 xylose isomerase (EC 5.3.1.5) - barley NCBI Description >gi 1296809 emb CAA64545 (X95257) xylose isomerase [Hordeum vulgare] 218955 Seq. No. Seq. ID LIB3149-004-P1-K1-E2 Method BLASTX NCBI GI q4263519 BLAST score 453 E value 3.0e-45 Match length 93 % identity 91 (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis NCBI Description thaliana] Seq. No. 218956 Seq. ID LIB3149-004-P1-K1-E3 Method BLASTX NCBI GI g2688824 BLAST score 269 E value 1.0e-23 73 Match length 79 % identity NCBI Description (U93273) putative auxin-repressed protein [Prunus armeniaca] 218957 Seq. No. Seq. ID LIB3149-004-P1-K1-F10 Method BLASTX

30781

g1729971



```
BLAST score
                  266
E value
                   3.0e-23
Match length
                  100
% identity
                  53
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                  218958
Seq. No.
Seq. ID
                  LIB3149-004-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3834310
BLAST score
                  201
E value
                  8.0e-16
Match length
                  48
                  83
% identity
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                  gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122
                  come from this gene. [Arabidopsis thaliana]
                  218959
Seq. No.
Seq. ID
                  LIB3149-004-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1657617
BLAST score
                  161
                  5.0e-11
E value
                  74
Match length
% identity
                  51
NCBI Description
                  (U72503) G2p [Arabidopsis thaliana] >gi 3068707 (AF049236)
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
                  218960
Seq. No.
Seq. ID
                  LIB3149-004-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g4102600
BLAST score
                  187
E value
                  7.0e-17
Match length
                  82
% identity
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                   218961
Seq. ID
                  LIB3149-004-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2244749
BLAST score
                  586
```

E value 8.0e-61

Match length 131 86 % identity

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.

218962

Seq. ID

LIB3149-004-P1-K1-G11

Method

BLASTX



NCBI GI g3334346
BLAST score 516
E value 1.0e-52
Match length 106
% identity 92
NCBI Description PROTEIN 991 2852

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG

>gi_2852445_dbj_BAA24697_ (AB003378) SUI1 homolog [Salix

bakko]

Seq. No. 218963

Seq. ID LIB3149-004-P1-K1-G5

Method BLASTX
NCBI GI g2905893
BLAST score 443
E value 4.0e-44
Match length 110
% identity 78

NCBI Description (U66424) fimbrin-like protein [Arabidopsis thaliana]

Seq. No. 218964

Seq. ID LIB3149-004-P1-K1-H11

Method BLASTX
NCBI GI g2459440
BLAST score 310
E value 2.0e-28
Match length 103
% identity 63

NCBI Description (AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 218965

Seq. ID LIB3149-004-P1-K1-H12

Method BLASTX
NCBI GI g4454263
BLAST score 150
E value 1.0e-09
Match length 94
% identity 39

NCBI Description (Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens]

Seq. No. 218966

Seq. ID LIB3149-004-P1-K1-H2

Method BLASTN
NCBI GI g2688829
BLAST score 44
E value 2.0e-15
Match length 116
% identity 84

NCBI Description Prunus armeniaca putative sugar transporter mRNA, complete

cds

Seq. No. 218967

Seq. ID LIB3149-004-P1-K1-H4

Method BLASTX
NCBI GI g2253442
BLAST score 206
E value 3.0e-16
Match length 56



% identity NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca] 218968 Seq. No. LIB3149-004-P1-K1-H6 Seq. ID Method BLASTX NCBI GI g2062167 BLAST score 494 E value 5.0e-50 Match length 137 68 % identity NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana] 218969 Seq. No. Seq. ID LIB3149-004-P1-K1-H8 Method BLASTX NCBI GI q3046696 BLAST score 529 E value 4.0e-54132 Match length 70 % identity NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana] 218970 Seq. No. Seq. ID LIB3149-005-Q1-K2-A2 Method BLASTX NCBI GI q2879811 BLAST score 227 7.0e-19E value Match length 45 % identity 87 NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus] Seq. No. 218971 Seq. ID LIB3149-005-Q1-K2-B4 Method BLASTX NCBI GI q4056551 BLAST score 312 E value 8.0e-29 Match length 97 58 % identity (AL034583) putative elongation initation factor subunit NCBI Description [Schizosaccharomyces pombe] Seq. No. 218972 Seq. ID LIB3149-005-Q1-K2-B5 BLASTX Method

Method BLASTX
NCBI GI g1848237
BLAST score 136
E value 6.0e-17
Match length 82
% identity 55

NCBI Description (U57320) blue copper-binding protein II [Arabidopsis

thaliana]

Seq. No. 218973



```
LIB3149-005-Q1-K2-B6
Seq. ID
Method
                  BLASTX
                  g1871577
NCBI GI
                  226
BLAST score
                  1.0e-18
E value
                  115
Match length
% identity
                  43
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  218974
Seq. No.
                  LIB3149-005-Q1-K2-C3
Seq. ID
Method
                  BLASTX
                  q3063396
NCBI GI
                  530
BLAST score
E value
                  3.0e-54
Match length
                  118
% identity
                  84
NCBI Description (AB012947) vcCyP [Vicia faba]
                  218975
Seq. No.
                  LIB3149-005-Q1-K2-D4
Seq. ID
                  BLASTN
Method
                  g2570118
NCBI GI
                  43
BLAST score
                  5.0e-15
E value
                  83
Match length
                  88
% identity
NCBI Description S.latifolia mRNA, clone CCLS
                  218976
Seq. No.
                  LIB3149-005-Q1-K2-E1
Seq. ID
Method
                  BLASTX
                  g3152591
NCBI GI
                  401
BLAST score
                  4.0e-39
E value
                  132
Match length
% identity
                  29
                  (AC002986) Similar to hypothetical protein gb Z97336 from
NCBI Description
                  A. thaliana. This gene is probably cut off. [Arabidopsis
                  thaliana]
Seq. No.
                  218977
                  LIB3149-005-Q1-K2-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1362086
BLAST score
                  617
E value
                  2.0e-64
Match length
                  133
% identity
                  87
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919_pir__S65957
```

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 886471 emb CAA58474 (X83499) methionine synthase

[Catharanthus roseus]



Seq. No. 218978 LIB3149-005-Q1-K2-E8 Seq. ID Method BLASTN g3821780 NCBI GI BLAST score 36 6.0e-11 E value Match length 48 % identity 67 Xenopus laevis cDNA clone 27A6-1 NCBI Description 218979 Seq. No. Seq. ID LIB3149-005-Q1-K2-F10 Method BLASTX NCBI GI g2129772 BLAST score 137 E value 1.0e-25 Match length 96 % identity 59 xyloglucan endotransglycosylase-related protein XTR-7 -NCBI Description Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] Seq. No. 218980 LIB3149-005-Q1-K2-F4 Seq. ID Method BLASTX NCBI GI g3928083 BLAST score 564 E value 3.0e-58 Match length 134 75 % identity NCBI Description (AC005770) unknown protein [Arabidopsis thaliana] 218981 Seq. No. LIB3149-005-Q1-K2-F7 Seq. ID Method BLASTX NCBI GI g3036816 BLAST score 252 E value 1.0e-21 113 Match length % identity 45 NCBI Description (AL022373) myosin-like protein [Arabidopsis thaliana] 218982 Seq. No. LIB3149-005-Q1-K2-F8 Seq. ID Method BLASTX g3757514 NCBI GI 553 BLAST score E value 6.0e-57 121 Match length % identity 88 (AC005167) putative plasma membrane intrinsic protein NCBI Description [Arabidopsis thaliana]

218983 Seq. No.

LIB3149-005-Q1-K2-G2 Seq. ID

Method BLASTX NCBI GI g4090533



```
BLAST score
                  6.0e-44
E value
                  133
Match length
% identity
                  68
NCBI Description (U68215) ACC oxidase [Carica papaya]
                  218984
Seq. No.
                  LIB3149-005-Q1-K2-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g445612
BLAST score
                  252
E value
                  1.0e-21
Match length
                  93
                  62
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                  218985
Seq. No.
                  LIB3149-005-Q1-K2-H12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g35329
BLAST score
                  44
E value
                  1.0e-15
Match length
                  96
                  86
% identity
NCBI Description
                  H.sapiens mRNA for procarboxypeptidase A1
                  >gi 1254688 gb G19989 G19989 sWSS41 Eric D. Green Homo
                  sapiens STS genomic, sequence tagged site [Homo sapiens]
                  >gi_4502996_ref_NM_001868.1_CPA1_ Homo sapiens
                  carboxypeptidase A1 (pancreatic) (CPA1) mRNA
Seq. No.
                  218986
                  LIB3149-005-Q1-K2-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432835
BLAST score
                  275
E value
                  2.0e-24
Match length
                  93
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  218987
Seq. ID
                  LIB3149-006-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4510363
BLAST score
                  385
E value
                  2.0e-37
Match length
                  83
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  218988
Seq. ID
                  LIB3149-006-Q1-K1-A2
```

Method BLASTX NCBI GI g541546 BLAST score 496 E value 2.0e-50



Match length 113 % identity 18

NCBI Description ubiquitin precursor - Volvox carteri

>gi 395295 emb CAA52290 (X74214) polyubiquitin [Volvox

carteri]

Seq. No. 218989

Seq. ID LIB3149-006-Q1-K1-A4

Method BLASTX
NCBI GI g3786011
BLAST score 377
E value 2.0e-36
Match length 112
% identity 83

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 218990

Seq. ID LIB3149-006-Q1-K1-A5

Method BLASTX
NCBI GI g4457221
BLAST score 188
E value 2.0e-14
Match length 88
% identity 53

NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum

chinense]

Seq. No. 218991

Seq. ID LIB3149-006-Q1-K1-A9

Method BLASTX
NCBI GI g4263712
BLAST score 159
E value 2.0e-17
Match length 64
% identity 73

NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis

thaliana]

Seq: No. 218992

Seq. ID LIB3149-006-Q1-K1-B1

Method BLASTX
NCBI GI g1172597
BLAST score 178
E value 3.0e-13
Match length 45
% identity 76

NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir__JS0731

wound-inducible basic protein - kidney bean >gi 169365

(L00625) basic protein [Phaseolus vulgaris]

>gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein

[Phaseolus vulgaris]

Seq. No. 218993

Seq. ID LIB3149-006-Q1-K1-B3

Method BLASTX NCBI GI g3201477

```
BLAST score
                   410
                   3.0e-40
E value
                   110
Match length
% identity
                   71
                   (AJ006021) putative PRL1 associated protein [Arabidopsis
NCBI Description
                   thaliana]
                   218994
Seq. No.
Seq. ID
                   LIB3149-006-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   q417719
```

BLAST score 401 E value 3.0e-39 Match length 96 % identity 86 NCBI Description 40S RIB

NCBI Description 40S RIBOSOMAL PROTEIN S3 >gi_2144763_pir__R3HUS3 ribosomal

protein S3 - human >gi_233042_bbs_42659 (S42658) S3 ribosomal protein [human, colon, Peptide, 243 aa] [Homo sapiens] >gi_555941 (U14990) ribosomal protein S3 [Homo sapiens] >gi_555943 (U14991) ribosomal protein S3 [Homo sapiens] >gi_555945 (U14992) ribosomal protein S3 [Homo

sapiens]

Seq. No. 218995

Seq. ID LIB3149-006-Q1-K1-D1

Method BLASTX
NCBI GI g1619300
BLAST score 457
E value 7.0e-46
Match length 109
% identity 83

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 218996

Seq. ID LIB3149-006-Q1-K1-D2

Method BLASTX
NCBI GI g2811029
BLAST score 385
E value 2.0e-37
Match length 93
% identity 77

NCBI Description ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)

(ACETYLORNITHINE TRANSAMINASE) (AOTA)

>gi_1944511_emb_CAA69936_ (Y08680) acetylornithine

aminotransferase [Alnus glutinosa]

Seq. No. 218997

Seq. ID LIB3149-006-Q1-K1-D7

Method BLASTX
NCBI GI 93402683
BLAST score 266
E value 2.0e-23
Match length 111
% identity 55

NCBI Description (AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No. 218998



Seq. ID LIB3149-006-Q1-K1-E2

BLASTX Method g3023512 NCBI GI BLAST score 164 E value 2.0e-11 Match length 79 44 % identity

NCBI Description PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT

PRECURSOR (ENDOPEPTIDASE CLP) >gi_2134793_pir__S68421 ATP-dependent Clp proteinase (EC 3.4.21.92) chain P homolog

- human >gi 963048 emb CAA90705 (Z50853) CLPP [Homo

sapiens]

218999 Seq. No.

LIB3149-006-Q1-K1-E6 Seq. ID

Method BLASTX g3193293 NCBI GI BLAST score 340 4.0e-32 E value 93 Match length 74 % identity

(AF069298) contains a short region of similarity to another NCBI Description

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

219000 Seq. No.

Seq. ID LIB3149-006-Q1-K1-E7

Method BLASTX NCBI GI q2961372 BLAST score 521 E value 2.0e-53 Match length 104 92 % identity

(AL022141) putative ribosomal protein L8 [Arabidopsis NCBI Description

thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal

protein L2 [Arabidopsis thaliana]

219001 Seq. No.

Seq. ID LIB3149-006-Q1-K1-F1

Method BLASTX NCBI GI g3947448 BLAST score 191 E value 1.0e-14 Match length 97 % identity 40

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA

EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 219002

Seq. ID LIB3149-006-Q1-K1-F11



```
BLASTX
Method
                  g3851636
NCBI GI
BLAST score
                   422
                   1.0e-41
E value
                  102
Match length
% identity
                   78
                  (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   219003
Seq. No.
                  LIB3149-006-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   g2062167
NCBI GI
BLAST score
                   364
                   7.0e-35
E value
                   96
Match length
                   70
% identity
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   219004
Seq. No.
                   LIB3149-006-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   g2245131
NCBI GI
                   227
BLAST score
                   7.0e-19
E value
Match length
                   70
% identity
                   69
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
                   219005
Seq. No.
                   LIB3149-006-Q1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204859
BLAST score
                   112
E value
                   2.0e-12
Match length
                   54
                   76
% identity
NCBI Description (U55859) heat shock protein 80 [Triticum aestivum]
Seq. No.
                   219006
                   LIB3149-006-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1771780
BLAST score
                   144
E value
                   3.0e-09
Match length
                   24
% identity
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
Seq. No.
                   219007
Seq. ID
                   LIB3149-006-Q1-K1-G8
```

Method BLASTX
NCBI GI g1399757
BLAST score 160
E value 6.0e-11
Match length 112



% identity 33 (U57969) membrane fusion protein MexC [Pseudomonas NCBI Description aeruginosa] 219008 Seq. No. LIB3149-006-Q1-K1-H11 Seq. ID BLASTX Method NCBI GI g464847 206 BLAST score 8.0e-17 E value 47 Match length 85 % identity TUBULIN ALPHA CHAIN >gi 397913 emb CAA80497_ (Z22877) NCBI Description tubulin [Euglena gracilis] 219009 Seq. No. LIB3149-006-Q1-K1-H5 Seq. ID Method BLASTX NCBI GI g2431769 BLAST score 241 E value 1.0e-20 59 Match length % identity 80 (U62752) acidic ribosomal protein Pla [Zea mays] NCBI Description 219010 Seq. No. Seq. ID LIB3149-006-Q1-K1-H7 Method BLASTX NCBI GI q218157 BLAST score 476 5.0e-48E value Match length 111 86 % identity NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa] 219011 Seq. No. Seq. ID LIB3149-007-Q1-K1-A12 Method BLASTX NCBI GI q1850546 BLAST score 355 E value 2.0e-37 Match length 110 % identity (U88045) syntaxin related protein AtVam3p [Arabidopsis NCBI Description thaliana] Seq. No. 219012 Seq. ID LIB3149-007-Q1-K1-A5 Method BLASTX NCBI GI q2244792 BLAST score 610 E value 1.0e-63 Match length 131 % identity 83 NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 219013



```
LIB3149-007-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1843525
BLAST score
                   352
E value
                   5.0e-65
                  145
Match length
                  89
% identity
                  (U73746) annexin [Gossypium hirsutum]
NCBI Description
                  219014
Seq. No.
                  LIB3149-007-Q1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3650032
BLAST score
                  233
                  2.0e-19
E value
Match length
                  63
                  62
% identity
                  (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   219015
                  LIB3149-007-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706551
BLAST score
                  282
                   3.0e-25
E value
Match length
                  84
% identity
                   60
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                   1,3-glucanase [Triticum aestivum]
                   219016
Seq. No.
                  LIB3149-007-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                   g100347
NCBI GI
BLAST score
                   386
E value
                   2.0e-37
Match length
                   101
                   71
% identity
                  monosaccharide transport protein MST1 - common tobacco
NCBI Description
                   >gi 19885 emb CAA47324 (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
Seq. No.
                   219017
Seq. ID
                  LIB3149-007-Q1-K1-B12
Method
                  BLASTX
                   g2495365
NCBI GI
BLAST score
                   398
E value
                   1.0e-38
Match length
                  114
% identity
                   75
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
NCBI Description
```

No. 219018

Seq. No.

30793

heat shock protein HSP81-2 [Arabidopsis thaliana]



```
Seq. ID
                   LIB3149-007-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1808656
BLAST score
                   498
                   2.0e-50
E value
Match length
                   115
% identity
                   83
NCBI Description
                  (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]
Seq. No.
                   219019
Seq. ID
                   LIB3149-007-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2832664
BLAST score
                   157
E value
                   1.0e-10
Match length
                   66
% identity
                   45
NCBI Description
                   (AL021710) pollen-specific protein - like [Arabidopsis
                   thaliana]
Seq. No.
                   219020
Seq. ID
                   LIB3149-007-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g728882
BLAST score
                   547
E value
                   3.0e-56
Match length
                   115
% identity
                   90
NCBI Description
                  ADP-RIBOSYLATION FACTOR 3 >gi 541846 pir S41938
                   ADP-ribosylation factor 3 - Arabidopsis thaliana
                   >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3
                   [Arabidopsis thaliana]
                   219021
Seq. No.
                  LIB3149-007-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI .
                   g2104681
BLAST score
                  150
E value
                   1.0e-09
Match length
                   39
                   77
% identity
NCBI Description (X97907) transcription factor [Vicia faba]
                  219022
Seq. No.
Seq. ID
                  LIB3149-007-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                   g3912917 -
BLAST score
                  104
E value
                   2.0e-09
Match length
                  54
                   70
% identity
NCBI Description
                  (AF001308) putative NAK-like ser/thr protein kinase
                   [Arabidopsis thaliana]
```

Seq. No. 219023

Seq. ID LIB3149-007-Q1-K1-F6

Method BLASTX



```
NCBI GI
                  g4468050
BLAST score
                  218
                  1.0e-17
E value
Match length
                  130
% identity
                  35
                  (X87099) S-adenosyl-L-methionine:caffeic acid
NCBI Description
                  3-O-methyltransferase [Vanilla planifolia]
                  219024
Seq. No.
                  LIB3149-007-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4191788
BLAST score
                  215
                  2.0e-17
E value
                  104
Match length
                  43
% identity
NCBI Description
                  (AC005917) putative 1-aminocyclopropane-1-carboxylate
                  oxidase [Arabidopsis thaliana]
                  219025
Seq. No.
                  LIB3149-007-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g2335099
NCBI GI
BLAST score
                  468
                  6.0e-47
E value
Match length
                  137
                  64
% identity
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
                  219026
Seq. No.
                  LIB3149-007-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549063
                  359
BLAST score
                  3.0e - 34
E value
                  111
Match length
% identity
                  65
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                  219027
                  LIB3149-007-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  g4206122
NCBI GI
BLAST score
                  674
                                                                        . M. ..
E value
                  4.0e-71
Match length
                  142
% identity
```

(AF097667) protein phosphatase 2C homolog [Mesembryanthemum NCBI Description

crystallinum]

219028 Seq. No.

Seq. ID LIB3149-007-Q1-K1-H3

Method BLASTX NCBI GI g3212879

Method

NCBI GI BLAST score BLASTX q730645

201



```
BLAST score
                   278
                    7.0e-25
 E value
 Match length
                   89
                   62
 % identity
                   (AC004005) putative ribosomal protein L7 [Arabidopsis
 NCBI Description
                   thaliana]
                   219029
 Seq. No.
                   LIB3149-007-Q1-K1-H6
 Seq. ID
 Method
                   BLASTX
                   g1351279
 NCBI GI
 BLAST score
                   264
                   3.0e-23
 E value
                   72
 Match length
 % identity
                   71
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 NCBI Description
                   >gi 602590 emb CAA58230 (X83227) triosephosphate isomerase
                    [Petunia x hybrida]
                    219030
 Seq. No.
                   LIB3149-008-Q1-K1-A11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g2129496
 BLAST score
                    584
                    6.0e-62
_E value
 Match length
                    124
                    95
 % identity
                    acetolactate synthase (EC 4.1.3.18) precursor (clone A19) -
 NCBI Description
                    upland cotton
                    219031
 Seq. No.
                    LIB3149-008-Q1-K1-A12
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g3821280
                    350
 BLAST score
                    2.0e-33
 E value
                    86
 Match length
                    76
 % identity
                    (AJ009952) asparagine synthetase type II [Phaseolus
 NCBI Description
                    vulgaris]
                    219032
 Seq. No.
                    LIB3149-008-Q1-K1-A7
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1362093
                    173
 BLAST score
                    6.0e-13
 E value
 Match length
                    38
                    87
 % identity
                    hypothetical protein (clone TPP15) - tomato (fragment)
 NCBI Description
                    >gi_924632 (U20595) unknown [Solanum lycopersicum]
                    219033
 Seq. No.
                    LIB3149-008-Q1-K1-B10
 Seq. ID
```



```
E value
                  8.0e-16
Match length
                  66
                  65
% identity
                  40S RIBOSOMAL PROTEIN S15 > gi 629556 pir S43412 ribosomal
NCBI Description
                  protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                  [Arabidopsis thaliana] >gi 1903366 gb AAB70449 (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                  gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
                  219034
Seq. No.
                  LIB3149-008-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334113
BLAST score
                  323
                  2.0e-30
E value
Match length
                  66
                  94
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
NCBI Description
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  219035
                  LIB3149-008-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g232031
NCBI GI
BLAST score
                  209
E value
                  1.0e-16
Match length
                  67
                  57
% identity
                 ELONGATION FACTOR 1 BETA' >gi 322851_pir__S29224
NCBI Description
                  translation elongation factor eEF-1 beta chain - rice
                   >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   219036
Seq. No.
                  LIB3149-008-Q1-K1-B8
Seq. ID
Method
                   BLASTX
                  g1883034
NCBI GI
BLAST score
                  154
                   4.0e-11
E value
                   48
Match length
                   81
% identity
NCBI Description (X91510) histone H4 [Diadromus pulchellus]
                   219037
Seq. No.
                   LIB3149-008-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   g1220196
NCBI GI
BLAST score
                   290
                   3.0e-26
E value
                   103
Match length
```

Seq. No. 219038

% identity

NCBI Description

(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]



```
LIB3149-008-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  g2760606
NCBI GI
BLAST score
                  262
                  6.0e-23
E value
                  80
Match length
                  66
% identity
                  (AB001568) phospholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Arabidopsis thaliana] >gi 3004869
                   (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                  thaliana] >gi 4539451 emb CAB39931.1 (AL049500)
                  phospholipid hydroperoxide glutathione peroxidase
                   [Arabidopsis thaliana]
Seq. No.
                  219039
                  LIB3149-008-Q1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82263
BLAST score
                  626
                  2.0e-65
E value
Match length
                  141
                  87
% identity
NCBI Description
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                  cl precursor (clone pC(1)3II) - potato
                  219040
Seq. No.
                  LIB3149-008-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3242077
BLAST score
                  332
                  4.0e-31
E value
                  88
Match length
                  70
% identity
NCBI Description (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
                  219041
Seq. No.
                  LIB3149-008-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4580398
BLAST score
                   346
                   2.0e-37
E value
Match length
                  105
                   74
% identity
                  (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                  thaliana]
                   219042
Seq. No.
Seq. ID
                  LIB3149-008-Q1-K1-D4
Method
                  BLASTX
                  g1345787
NCBI GI
BLAST score
                  468
E value
                   4.0e-47
```

Match length 97 % identity 89

NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)

>gi_567937_dbj_BAA05641_ (D26594) chalcone synthase

[Camellia sinensis]

```
Seq. No.
                  219043
Seq. ID
                  LIB3149-008-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g123684
BLAST score
                  254
E value
                  5.0e-22
Match length
                  109
% identity
                  58
NCBI Description HEAT SHOCK FACTOR PROTEIN HSF24 (HEAT SHOCK TRANSCRIPTION
                  FACTOR 24) (HSTF 24) (HEAT STRESS TRANSCRIPTION FACTOR)
                  >gi_100267_pir__S12361 heat shock transcription factor
                  HSF24 - Peruvian tomato >gi_19488_emb_CAA39034_ (X55347)
                  heat stress transcription factor [Lycopersicon peruvianum]
                  219044
Seq. No.
Seq. ID
                  LIB3149-008-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3877725
BLAST score
                  169
E value
                  5.0e-12
Match length
                  96
% identity
                  41
NCBI Description (Z70781) F57A8.2 [Caenorhabditis elegans]
Seq. No.
                  219045
Seq. ID
                  LIB3149-008-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2583123
BLAST score
                  155
E value
                  2.0e-10
Match length
                  44
% identity
                  59
NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                  219046
Seq. ID
                  LIB3149-008-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4127456
BLAST score
                  163
E value
                  2.0e-11
Match length
                  93
% identity
                  45
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]
                  219047
Seq. No.
```

Seq. ID LIB3149-008-Q1-K1-F5

Method BLASTX NCBI GI g3023419 BLAST score 255 E value 2.0e-22 Match length 73 67 % identity

CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA NCBI Description

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)

>gi 1934859 emb CAA72911 (Y12228) caffeoyl-CoA



O-methyltransferase [Eucalyptus gunnii]

```
219048
Seq. No.
                  LIB3149-008-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  g421960
NCBI GI
BLAST score
                  261
                   9.0e-23
E value
Match length
                  118
% identity
                   48
NCBI Description small nuclear ribonucleoprotein U2B'' - potato >gi 169589
                   (M72892) spliceosomal protein [Solanum tuberosum]
                  219049
Seq. No.
                  LIB3149-008-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3717946
BLAST score
                  177
                   5.0e-13
E value
Match length
                  75
                  51
% identity
NCBI Description (AJ005901) vag1 [Arabidopsis thaliana]
                  219050
Seq. No.
                  LIB3149-008-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q345829
                  456
BLAST score
E value
                  1.0e-45
Match length
                  125
% identity
                   65
NCBI Description ubiquitin carrier protein E2 - human
Seq. No.
                  219051
Seq. ID
                  LIB3149-008-Q1-K1-H5
Method
                  BLASTX
                  g3142301
NCBI GI
BLAST score
                  144
E value
                   5.0e-09
Match length
                  53
% identity
                   57
                  (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb M76710 from Xenopus
                   laevis, and beta transducin from S. cerevisiae gb_Q05946.
                   ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,
                   gb_H3630
Seq. No.
                   219052
Seq. ID
                  LIB3149-013-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                   g2502085
BLAST score
                  470
E value
                   3.0e-47
Match length
                  127
% identity
                   55
NCBI Description
                  (AF022925) adenosine triphosphatase; c-subunit of V-ATPase
```

30800

[Vigna radiata]

Seq. ID

Method

```
219053
 Seq. No.
                   LIB3149-013-Q1-K1-A11
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q2924257
                   39
 BLAST score
                   1.0e-12
 E value
 Match length
                   119
 % identity
                   42
 NCBI Description Tobacco chloroplast genome DNA
 Seq. No.
                   219054
                   LIB3149-013-Q1-K1-A2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q4098129
 BLAST score
                   242
 E value
                   2.0e-20
 Match length
                   49
                   96
 % identity
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                   219055
 Seq. No.
                   LIB3149-013-Q1-K1-A4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1709990
 BLAST score
                   227
 E value
                   9.0e-19
 Match length
                   47
                   89
% identity
 NCBI Description 60S RIBOSOMAL PROTEIN L35A
                   219056
 Seq. No.
                   LIB3149-013-Q1-K1-A8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1169228
 BLAST score
                   236
 E value
                   7.0e-20
 Match length
                   55
                   85
 % identity
                   RNA HELICASE-LIKE PROTEIN DB10 >gi 1084413 pir S42639
 NCBI Description
                   helicase-like protein - Wood tobacco
                   >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein
                   DB10 [Nicotiana sylvestris]
                   219057
 Seq. No.
 Seq. ID
                   LIB3149-013-Q1-K1-B11
 Method
                   BLASTX
 NCBI GI
                   q1906830
 BLAST score
                   499
 E value
                   1.0e-50
 Match length
                   103
 % identity
                    91
 NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]
 Seq. No.
                    219058
```

30801

LIB3149-013-Q1-K1-B7

BLASTX

Method

NCBI GI

BLASTX

g3915826



```
NCBI GI
                   q1717952
BLAST score
                   515
                   1.0e-52
E value
Match length
                  114
                  89
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 4
NCBI Description
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN 4) (RISP4) >gi 530054
                   (L16812) Rieske iron-sulfur protein [Nicotiana tabacum]
                  219059
Seq. No.
Seq. ID
                  LIB3149-013-Q1-K1-B9
                  BLASTX
Method
NCBI GI
                   q4539405
                   474
BLAST score
E value
                   1.0e-47
Match length
                  118
                   78
% identity
NCBI Description (AL049524) putative ribosomal protein L9, cytosolic
                   [Arabidopsis thaliana]
                   219060
Seq. No.
                  LIB3149-013-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                 g129245
                   172
BLAST score
E value
                   2.0e-12
                   111
Match length
                   41
% identity
NCBI Description ORGAN SPECIFIC PROTEIN P4 >gi_72317_pir__KNPMP4 protein P4
                   - garden pea >gi_295829_emb_CAA3594\overline{3}_ (\overline{X5}1594) P4 protein
                   [Pisum sativum]
                   219061
Seq. No.
Seq. ID
                   LIB3149-013-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   q3493172
BLAST score
                   514
E value
                   2.0e-52
Match length
                   103
                   97
% identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                   219062
                   LIB3149-013-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760362
BLAST score
                   436
                   3.0e-43
E value
Match length
                   101
% identity
                   84
                  (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
                   219063
Seq. No.
                   LIB3149-013-Q1-K1-C5
Seq. ID
```



```
BLAST score
                   223
E value
                   8.0e-19
                  57
Match length
% identity
                   72
NCBI Description
                 60S RIBOSOMAL PROTEIN L5
                  219064
Seq. No.
                  LIB3149-013-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3493172
BLAST score
                   525
E value
                  1.0e-53
Match length
                   113
```

91

(U89609) fiber annexin [Gossypium hirsutum] NCBI Description

219065 Seq. No. LIB3149-013-Q1-K1-D1 Seq. ID Method BLASTX NCBI GI q1346526 BLAST score 478 E value 2.0e-48

94 Match length % identity 96

% identity

S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

> >gi 1076533 pir S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559

(L36681) S-adenosylmethionine synthase [Pisum sativum]

Seq. No. 219066

LIB3149-013-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI g2708532 484 BLAST score E value 6.0e-49Match length 122 % identity 26

NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]

219067 Seq. No.

LIB3149-013-Q1-K1-D3 Seq. ID

Method BLASTX NCBI GI q2914700 BLAST score 622 E value 4.0e-65 Match length 129 % identity 96

(AC003974) tRNA-processing protein SEN3-like [Arabidopsis NCBI Description

thaliana]

Seq. No. 219068

Seq. ID LIB3149-013-Q1-K1-D6

Method BLASTX NCBI GI q1871577 BLAST score 290



```
E value
                  4.0e-26
Match length
                  92
% identity
                  57
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
                  219069
Seq. No.
                  LIB3149-013-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915031
BLAST score
                  542
E value
                  1.0e-55
Match length
                  114
% identity
                  94
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                   (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                  219070
Seq. No.
Seq. ID
                  LIB3149-013-Q1-K1-D8
Method
                  BLASTX
                  g2218152
NCBI GI
BLAST score
                  642
E value
                  2.0e-67
Match length
                  125
% identity
                  93
NCBI Description (AF005279) type IIIa membrane protein cp-wap13 [Vigna
                  unguiculata]
                  219071
Seq. No.
Seq. ID
                  LIB3149-013-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4158232
BLAST score
                  383
E value
                  2.0e-45
Match length
                  119
% identity
NCBI Description (Y18626) reversibly glycosylated polypeptide [Triticum
                  aestivum]
Seq. No.
                  219072
                  LIB3149-013-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193316
BLAST score
                  339
E value
                  7.0e-32
Match length
                  90
                  72
% identity
```

NCBI Description (AF069299) contains similarity to nucleotide sugar

epimerases [Arabidopsis thaliana]

Seq. No. 219073

Seq. ID LIB3149-013-Q1-K1-E11

Method BLASTX NCBI GI g2982299 BLAST score 168 E value 7.0e-12



47

% identity

```
69
Match length
                   54
% identity
NCBI Description
                   (AF051234) transcription factor BTF3 homolog [Picea
                  mariana]
                  219074
Seq. No.
                  LIB3149-013-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244798
BLAST score
                  134
                   4.0e-17
E value
Match length
                  108
                   47
% identity
                 (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  219075
Seq. No.
                  LIB3149-013-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3881381
BLAST score
                   272
                   4.0e-24
E value
Match length
                  106
                   51
% identity
                  (Z68270) Similarity to Yeast Man(0)-alpha-mannosidase
NCBI Description
                   (SW:MNS1 YEAST); cDNA EST EMBL:D71247 comes from this gene;
                   cDNA EST EMBL: D73896 comes from this gene [Caenorhabditis
                   elegans]
                   219076
Seq. No.
                  LIB3149-013-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  g1800281
NCBI GI
BLAST score
                   586
E value
                   6.0e-61
Match length
                  119
                   19
% identity
NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]
                   219077
Seq. No.
                   LIB3149-013-Q1-K1-E9
Seq. ID
Method
                   BLASTX
                   g2369714
NCBI GI
BLAST score
                   257
E value
                   3.0e-22
Match length
                   58
% identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   219078
Seq. ID
                   LIB3149-013-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   q417256
BLAST score
                   157
E value
                   1.0e-10
Match length
                   87
```

30805

NCBI Description LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)

NCBI Description

thaliana]



```
219079
Seq. No.
                   LIB3149-013-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   g3242785
NCBI GI
BLAST score
                   446
E value
                   2.0e-44
Match length
                   128
                   73
% identity
NCBI Description
                   (AF055355) respiratory burst oxidase protein C [Arabidopsis
                   thaliana]
Seq. No.
                   219080
                   LIB3149-013-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3355468
BLAST score
                   345
                   1.0e-32
E value
                   97
Match length
                   73
% identity
NCBI Description
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
                   thaliana]
                   219081
Seq. No.
                   LIB3149-013-Q1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346771
BLAST score
                   328
E value
                   1.0e-30
Match length
                   79
                   80
% identity
                   PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
NCBI Description
                   >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase
                   (PCK1) - Urochloa panicoides >gi_607752 (U09241)
                   phosphoenolpyruvate carboxykinase [Urochloa panicoides]
Seq. No.
                   219082
Seq. ID
                   LIB3149-013-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3122673
BLAST score
                   550
E value
                   1.0e-56
Match length
                   112
                   89
% identity
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   219083
Seq. ID
                   LIB3149-013-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2829923
BLAST score
                   438
E value
                   2.0e-43
Match length
                   100
% identity
                   44
```

30806

(AC002291) Similar to uridylyl transferases [Arabidopsis

Method

BLASTX



```
219084
Seq. No.
                  LIB3149-013-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g2739004
NCBI GI
                  361
BLAST score
                  2.0e-34
E value
                  126
Match length
                  57
% identity
                 (AF022461) CYP82Clp [Glycine max]
NCBI Description
Seq. No.
                  219085
                  LIB3149-013-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g2739004
NCBI GI
BLAST score
                  235
                  8.0e-20
E value
                  89
Match length
                  55
% identity
NCBI Description (AF022461) CYP82C1p [Glycine max]
                  219086
Seq. No.
                  LIB3149-013-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g2829923
NCBI GI
                  161
BLAST score
                  1.0e-11
E value
Match length
                  35
                  89
% identity
NCBI Description (AC002291) Similar to uridylyl transferases [Arabidopsis
                  thaliana]
                  219087
Seq. No.
                  LIB3149-013-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g2829923
NCBI GI
BLAST score
                  287
                  6.0e-26
E value
                  81
Match length
                  73
% identity
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                  thaliana]
                   219088
Seq. No.
                  LIB3149-013-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3901012
BLAST score
                   521
E value
                   7.0e-55
                   114
Match length
                   88
% identity
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   219089
Seq. No.
                   LIB3149-013-Q1-K1-G10
Seq. ID
```

E value

Match length

5.0e-39 82



```
NCBI GI
                  g2244970
BLAST score
                  461
                  3.0e-46
E value
Match length
                  126
% identity
                   67
NCBI Description
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
                  >gi 2326365 emb CAA74765 (Y14423) putative cell wall
                  protein [Arabidopsis thaliana]
                  219090
Seq. No.
                  LIB3149-013-Q1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4115377
BLAST score
                  531
                  2.0e-54
E value
Match length
                  111
% identity
                  88
                 (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  219091
Seq. No.
                  LIB3149-013-Q1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2058273
BLAST score
                   469
                   4.0e-47
E value
Match length
                   100
                   90
% identity
NCBI Description (D83527) YK426 [Oryza sativa]
                  219092
Seq. No.
                   LIB3149-013-Q1-K1-G8
Seq. ID
                   BLASTX
Method
                   g4008159
NCBI GI
BLAST score
                   613
                   5.0e-64
E value
                   123
Match length
% identity
                   90
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
                   219093
Seq. No.
                  LIB3149-013-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g4510428
NCBI GI
BLAST score
                   161
                   4.0e-24
E value
                   86
Match length
                   67
% identity
NCBI Description
                  (AC006929) putative argonaute protein [Arabidopsis
                   thaliana]
                   219094
Seq. No.
                   LIB3149-013-Q1-K1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1553128
                   82
BLAST score
```



```
% identity
                  Gossypium hirsutum ribosomal protein L44 isoform a (RL44),
NCBI Description
                  complete cds
Seq. No.
                  219095
                  LIB3149-013-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706319
BLAST score
                  419
E value
                  3.0e-41
Match length
                  130
                  60
% identity
                  HISTIDINE DECARBOXYLASE (HDC) (TOM92)
NCBI Description
                  >gi 481829 pir__S39554 histidine decarboxylase (EC
                  4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900)
                  histidine decarboxylase [Lycopersicon esculentum]
                  219096
Seq. No.
                  LIB3149-014-Q1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4325369
BLAST score
                  136
                  1.0e-08
E value
                  23
Match length
                  91
% identity
                 (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
NCBI Description
                  219097
Seq. No.
                  LIB3149-014-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q445613
                  503
BLAST score
E value
                  3.0e-51
                  118
Match length
                  75
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                  219098
Seq. No.
                  LIB3149-014-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244898
BLAST score
                  296
E value
                  7.0e-27
Match length
                  116
                   50
% identity
                  (Z97338) strong similarity to protein phosphatase 2A
NCBI Description
                  regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.
                   219099
                  LIB3149-014-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3169182
```

Method BLASTX
NCBI GI g3169182
BLAST score 167
E value 4.0e-12
Match length 35
% identity 83

NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

```
219100
Seq. No.
                  LIB3149-014-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539305
BLAST score
                   182
                   1.0e-13
E value
                   59
Match length
                   59
% identity
NCBI Description (AL049480) putative protein [Arabidopsis thaliana]
                  219101
Seq. No.
                  LIB3149-014-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                   g1679794
NCBI GI
BLAST score
                   238
E value
                   4.0e-20
                  101
Match length
% identity
                   47
NCBI Description (U77627) Allele: hi2 [Danio rerio]
Seq. No.
                   219102
                  LIB3149-014-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4519507
BLAST score
                   137
                   1.0e-08
E value
                   31
Match length
                   84
% identity
NCBI Description (D88434) protein abundantly expressed during apple fruit
                   development [Malus domestica]
                   219103
Seq. No.
                   LIB3149-014-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   410
E value
                   3.0e-40
                   119
Match length
% identity
                   69
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   219104
Seq. No.
                   LIB3149-014-Q1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1666173
BLAST score
                   285
E value
                   9.0e-26
Match length
                   65
% identity
NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]
Seq. No.
                   219105
                   LIB3149-014-Q1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g134025
BLAST score
                   269
```

NCBI GI

E value

BLAST score

g1762945

2.0e-30

326



```
E value
                   3.0e-24
Match length
                   67
% identity
                   78
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >qi 70913 pir R3NT8
                   ribosomal protein S8 - common tobacco chloroplast
                   >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8
[Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal
                   protein S8 [Nicotiana tabacum]
Seq. No.
                   219106
Seq. ID
                   LIB3149-014-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   q1710546
BLAST score
                   296
E value
                   2.0e-27
Match length
                   63
% identity
                   89
NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
                   ribosomal protein [Daucus carota]
Seq. No.
                   219107
Seq. ID
                   LIB3149-015-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1843527
BLAST score
                   483
E value
                   1.0e-48
Match length
                   124
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   219108
Seq. ID
                   LIB3149-015-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g730536
BLAST score
                   348
E value
                   6.0e-33
Match length
                   68
% identity
                   99
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal
                   protein subunit L17 [Nicotiana tabacum]
Seq. No.
                   219109
Seq. ID
                   LIB3149-015-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   g4508073
BLAST score
                   405
E value
                   1.0e-39
Match length
                   136
                   58
% identity
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
Seq. No.
                   219110
Seq. ID
                   LIB3149-015-Q1-K1-A6
Method
                   BLASTX
```



```
Match length
                  96
% identity
                  65
NCBI Description
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
                  tabacum]
                  219111
Seq. No.
                  LIB3149-015-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1563719
BLAST score
                  313
E value
                  1.0e-35
                  89
Match length
% identity
                  87
NCBI Description (Y08320) cyclophylin [Digitalis lanata]
                  219112
Seq. No.
                  LIB3149-015-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417745
BLAST score
                  629
E value
                  7.0e-66
Match length
                  127
% identity
                  96
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)
                  S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
Seq. No.
                  219113
                  LIB3149-015-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548852
BLAST score
                  361
E value
                  2.0e-34
Match length
                  82
% identity
                  80
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir S38357 ribosomal
                  protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  219114
Seq. ID
                  LIB3149-015-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                  g2497752
BLAST score
                  294
                  1.0e-26
E value
                  96
Match length
                  59
% identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                  >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                  [Prunus dulcis]
                  219115
Seq. No.
Seq. ID
                  LIB3149-015-Q1-K1-B6
```

Method BLASTX NCBI GI q322750 BLAST score 658 3.0e-69 E value

```
Match length
                   128
% identity
                   99
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
                   >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
                   219116
Seq. No.
Seq. ID
                   LIB3149-015-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q3482973
BLAST score
                   251
                   1.0e-21
E value
                   127
Match length
% identity
                   54
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
Seq. No.
                   219117
Seq. ID
                   LIB3149-015-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                   g4510425
BLAST score
                   506
E value
                   2.0e-51
                  128
Match length
% identity
                   76
NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]
                   219118
Seq. No.
                   LIB3149-015-Q1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2961300
BLAST score
                   244
E value
                   6.0e-21
Match length
                   64
% identity
                   80
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
Seq. No.
                   219119
                   LIB3149-015-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245394
BLAST score
                   289
                   5.0e-26
E value
Match length
                   107
                   52
% identity
NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]
```

Seq. ID LIB3149-015-Q1-K1-C3

Method BLASTX
NCBI GI g1915974
BLAST score 597
E value 4.0e-62
Match length 138
% identity 82

NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693

(U64818) fructokinase [Lycopersicon esculentum]

Seq. ID

Method



```
Seq. No.
                   219121
Seq. ID
                  LIB3149-015-Q1-K1-C5
Method
                  BLASTX
                  g3319882
NCBI GI
BLAST score
                   470
E value
                   3.0e-47
Match length
                   92
% identity
                   98
NCBI Description
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
                   219122
Seq. No.
Seq. ID
                  LIB3149-015-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                   q2398531
BLAST score
                   360
E value
                   3.0e - 34
Match length
                   130
% identity
                   64
NCBI Description (Y13726) Transcription factor [Arabidopsis thaliana]
                   219123
Seq. No.
                  LIB3149-015-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172587
BLAST score
                   166
                   1.0e-11
E value
Match length
                   95
                   42
% identity
                  POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)
NCBI Description
                   >gi_1076272_pir__S52629 catechol oxidase (EC 1.10.3.1)
                   precursor - grape >gi_510234_emb_CAA81798_ (Z27411)
                   polyphenol oxidase [Vitis vinifera]
Seq. No.
                   219124
Seq. ID
                   LIB3149-015-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g3212877
BLAST score
                   465
E value
                   1.0e-46
Match length
                   104
% identity
                   82
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
Seq. No.
                   219125
Seq. ID
                   LIB3149-015-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g3688170
BLAST score
                   414
E value
                   1.0e-40
Match length
                   123
% identity
                   68
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   219126
```

30814

LIB3149-015-Q1-K1-D7

BLASTX



```
g3695392
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
Match length
                   114
% identity
NCBI Description
                  (AF096371) No definition line found [Arabidopsis thaliana]
                  219127
Seq. No.
                  LIB3149-015-Q1-K1-D9
Seq. ID
Method
                  BLASTN
                  g1848205
NCBI GI
BLAST score
                   39
E value
                   1.0e-12
                   55
Match length
                   93
% identity
NCBI Description N.tabacum mRNA for 14-3-3-like protein (A)
                   219128
Seq. No.
                  LIB3149-015-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                   g3319882
NCBI GI
BLAST score
                   697
E value
                   8.0e-74
Match length
                  138
% identity
                   96
NCBI Description
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                   arietinum]
                   219129
Seq. No.
                  LIB3149-015-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g416730
BLAST score
                   393
E value
                   3.0e-38
Match length
                   104
% identity
                   67
NCBI Description
                  BETA-UREIDOPROPIONASE (BETA-ALANINE SYNTHASE)
                   (N-CARBAMOYL-BETA-ALANINE AMIDOHYDROLASE)
                   >gi_285064_pir__S27881 beta-alanine synthase - rat
                   >gi 203106 (M97662) beta-alanine synthase [Rattus
                   norvegicus]
Seq. No.
                   219130
Seq. ID
                   LIB3149-015-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                   g508304
BLAST score
                  151
E value
                   6.0e-10
                  40
Match length
                   72
% identity
NCBI Description
                  (L22305) corC [Medicago sativa]
Seq. No.
                   219131
Seq. ID
                  LIB3149-015-Q1-K1-F5
```

NCBI GI g2266994 BLAST score 426

BLASTX

Method



```
E value
                   5.0e-42
Match length
                   123
% identity
                   63
NCBI Description
                   (U77413) O-linked GlcNAc transferase [Homo sapiens]
                   >gi_4505499_ref_NP_003596.1_pOGT_ O-GlcNAc transferase
                   (uridine diphospho-N-acetylglucosamine:polypeptide
                   beta-N-acetylglucosaminyl transferase)
Seq. No.
                   219132
                  LIB3149-015-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2431767
BLAST score
                  177
E value
                   8.0e-13
Match length
                  107
% identity
                   38
NCBI Description (U62751) acidic ribosomal protein P3a [Zea mays]
Seq. No.
                  219133
Seq. ID
                  LIB3149-015-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g548852
BLAST score
                   361
E value
                  2.0e-34
Match length
                  82
                  80
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S21 >gi_481227 pir S38357 ribosomal
                  protein S21 - rice >gi_303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  219134
Seq. ID
                  LIB3149-015-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q2842480
BLAST score
                  383
E value
                   5.0e-37
Match length
                  93
% identity
                  48
                  (AL021749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  219135
Seq. ID
                  LIB3149-015-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1361979
BLAST score
                  544
E value
                  7.0e-56
Match length
                  113
```

% identity 93

serine O-acetyltransferase (EC 2.3.1.30) - watermelon NCBI Description

>gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase
[Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535)

serine acetyltransferase. [Citrullus lanatus] >gi_2337772_dbj_BAA21827_ (AB006530) serine

acetyltransferase [Citrullus lanatus]

Seq. No. 219136

BLAST score

E value

211

7.0e-17



```
Seq. ID
                  LIB3149-015-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3927831
BLAST score
                  399
                  7.0e-39
E value
Match length
                  105
                  75
% identity
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  219137
                  LIB3149-015-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1850546
BLAST score
                  263
                  6.0e-23
E value
Match length
                  87
% identity
                  64
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
                  thaliana]
                  219138
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-A1
Method
                  BLASTX
                  g3702323
NCBI GI
BLAST score
                  234
                  4.0e-20
E value
Match length
                  66
                  74
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  219139
Seq. No.
                  LIB3149-016-Q1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q167366
BLAST score
                  57
E value
                  3.0e-24
Match length
                  57
% identity
                  100
NCBI Description Gossypium hirsutum peroxidase mRNA, complete cds
Seq. No.
                  219140
                  LIB3149-016-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928095
BLAST score
                  537
E value
                  4.0e-55
Match length
                  123
% identity
                  81
NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  219141
Seq. ID
                  LIB3149-016-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3928095
```



Match length 103 % identity 48

NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No. 219142

Seq. ID LIB3149-016-Q1-K1-A7

Method BLASTX
NCBI GI g992706
BLAST score 558
E value 1.0e-57
Match length 109
% identity 92

NCBI Description (U33758) UBC13 [Arabidopsis thaliana]

Seq. No. 219143

Seq. ID LIB3149-016-Q1-K1-A9

Method BLASTX
NCBI GI g232031
BLAST score 221
E value 4.0e-18
Match length 105
% identity 45

NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224

translation elongation factor eEF-1 beta chain - rice >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta

[Oryza sativa]

Seq. No. 219144

Seq. ID LIB3149-016-Q1-K1-B10

Method BLASTX
NCBI GI 94454044
BLAST score 331
E value 5.0e-31
Match length 102
% identity 70

NCBI Description (AL035394) putative Ap2 domain protein [Arabidopsis

thaliana]

Seq. No. 219145

Seq. ID LIB3149-016-Q1-K1-B12

Method BLASTX
NCBI GI g1709761
BLAST score 410
E value 3.0e-40
Match length 110
% identity 73

NCBI Description PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX 27 KD SUBUNIT) >gi_1262146_emb_CAA65660_ (X96974)

proteasome subunit [Spinacia oleracea]

Seq. No. 219146

Seq. ID LIB3149-016-Q1-K1-B2

Method BLASTX
NCBI GI g1439609
BLAST score 591
E value 2.0e-61
Match length 118



```
% identity
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
                  219147
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-B9
                  BLASTX
Method
NCBI GI
                  g3123264
BLAST score
                  429
E value
                  2.0e-42
                  105
Match length
                  79
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  219148
                  LIB3149-016-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730463
BLAST score
                  286
E value
                  1.0e-25
                  99
Match length
                  57
% identity
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi 1420537 emb CAA99454 (Z75142) ORF YOR234c
                  [Saccharomyces cerevisiae]
                  219149
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-C4
                  BLASTX
Method
NCBI GI
                  g3928095
BLAST score
                  515
E value
                  2.0e-52
                  129
Match length
                  76
% identity
NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  219150
Seq. ID
                  LIB3149-016-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2454182
BLAST score
                  602
E value
                  1.0e-62
Match length
                  131
% identity
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
Seq. No.
                  219151
                  LIB3149-016-Q1-K1-C7
Seq. ID
```

Method BLASTX NCBI GI q136647 BLAST score 212 E value 4.0e-17



Match length % identity

UBIQUITIN-CONJUGATING ENZYME E2-20 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100813 pir A41547

ubiquitin-conjugating enzyme E2 - wheat

Seq. No. 219152

Seq. ID LIB3149-016-Q1-K1-D10

Method BLASTX NCBI GI g1170373 BLAST score 542 E value 9.0e-56 Match length 114 % identity 91

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir \$46302

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

Seq. No. 219153

Seq. ID LIB3149-016-Q1-K1-D5

Method BLASTX NCBI GI q629483 BLAST score 342 E value 3.0e - 32Match length 121 % identity 59

NCBI Description gene 1-Sc3 protein - European white birch

> >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula] >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 219154

Seq. ID LIB3149-016-Q1-K1-D6

Method BLASTX NCBI GI g2129754 BLAST score 213 4.0e-17 E value 47 Match length

% identity 89

NCBI Description translation elongation factor Tu precursor - Arabidopsis

thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial

elongation factor Tu [Arabidopsis thaliana]

Seq. No. 219155

Seq. ID LIB3149-016-Q1-K1-D9

Method BLASTX NCBI GI q4006827 BLAST score 209 E value 9.0e-17 47 Match length % identity

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 219156

Seq. ID LIB3149-016-Q1-K1-E1

BLASTX Method

% identity

74



```
q3096944
NCBI GI
BLAST score
                  108
E value
                  1.0e-08
Match length
                  79
                  46
% identity
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]
                  219157
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q4406756
BLAST score
                  511
                  4.0e-52
E value
Match length
                  125
% identity
                  80
NCBI Description (AC006836) putative integral membrane protein A3
                  [Arabidopsis thaliana]
                  219158
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q4567309
BLAST score
                  146
E value
                  3.0e-09
Match length
                  70
% identity
                  44
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
                  219159
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g532701
                  204
BLAST score
E value
                  5.0e-16
Match length
                  89
% identity
                  49
NCBI Description (U13179) similar to Atriplex nummularia chaperone ANJ1
                  protein, Swiss-Prot Accession Number JQ2142 [Glycine max]
                  219160
Seq. No.
                  LIB3149-016-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                  g1076722
NCBI GI
BLAST score
                  624
E value
                  3.0e-65
Match length
                  130
                  89
% identity
NCBI Description hypothetical protein - barley (fragment)
                  219161
Seq. No.
Seq. ID
                  LIB3149-016-Q1-K1-E6
                  BLASTX
Method
                  q4567260
NCBI GI
BLAST score
                  489
E value
                  2.0e-49
Match length
                  121
```



NCBI Description (AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

219162 Seq. No.

LIB3149-016-Q1-K1-E8 Seq. ID

Method BLASTX NCBI GI g2104681 BLAST score 286 E value 1.0e-25 Match length 124 % identity 56

(X97907) transcription factor [Vicia faba] NCBI Description

219163 Seq. No.

LIB3149-016-Q1-K1-F7 Seq. ID

BLASTX Method NCBI GI q2501353 BLAST score 108 1.0e-09 E value 57 Match length 52 % identity

NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300

transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase

[Craterostigma plantagineum]

Seq. No. 219164

LIB3149-016-Q1-K1-F8 Seq. ID

Method BLASTX g517500 NCBI GI BLAST score 263 E value 6.0e-23 Match length 85 64

% identity

NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa

protein [Zea mays] >gi_444338_prf__1906386A photosystem II

OE17 protein [Pisum sativum]

219165 Seq. No.

LIB3149-016-Q1-K1-G1 Seq. ID

Method BLASTX NCBI GI g2829899 BLAST score 270 E value 8.0e-24 Match length 112 % identity 45

NCBI Description (AC002311) similar to ripening-induced protein,

gp_AJ001449_2465015 and major#latex protein,

gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No. 219166

Seq. ID LIB3149-016-Q1-K1-G12

Method BLASTX NCBI GI g3096939 BLAST score 147 E value 2.0e-09 Match length 31



% identity (AL023094) putative protein [Arabidopsis thaliana] NCBI Description 219167 Seq. No. LIB3149-016-Q1-K1-G2 Seq. ID BLASTX Method NCBI GI q3064039 BLAST score 239 4.0e-20 E value 90 Match length 48 % identity (AF054445) major latex protein homolog [Mesembryanthemum NCBI Description crystallinum] 219168 Seq. No. LIB3149-016-Q1-K1-G4 Seq. ID BLASTX Method g132865 NCBI GI BLAST score 338 6.0e-32 E value Match length 92 77 % identity CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 (RIBOSOMAL PROTEIN NCBI Description CS-L4) >gi_71090_pir__R5SP2 ribosomal protein L2 - spinach chloroplast >gi_12303_emb_CAA25377_ (X00797) ribosomal protein L2 [Spinacia oleracea] 219169 Seq. No. LIB3149-016-Q1-K1-G5 Seq. ID Method BLASTX NCBI GI q132863 153 BLAST score 4.0e-15 E value 75 Match length % identity 66 NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi 12214 emb CAA46568 (X65615) ribosomal protein L2 [Sinapis alba] 219170 Seq. No. Seq. ID LIB3149-016-Q1-K1-G6 Method BLASTX NCBI GI g129248 BLAST score 176 E value 9.0e-13 Match length 100 % identity 22 ORGAN SPECIFIC PROTEIN S2 >gi 72318 pir KNPMS2 protein S2 NCBI Description - garden pea >gi_295831_emb_CAA3594 $\overline{4}$ _ ($\overline{X5}$ 1595) S2 protein [Pisum sativum]

Seq. No. 219171

Seq. ID LIB3149-016-Q1-K1-G7

Method BLASTX
NCBI GI g120669
BLAST score 425
E value 5.0e-42



Match length 85 % identity 92

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 219172

Seq. ID LIB3149-016-Q1-K1-H4

Method BLASTX
NCBI GI g2447107
BLAST score 402
E value 3.0e-39
Match length 133
% identity 57

NCBI Description (U42580) A638R [Paramecium bursaria Chlorella virus 1]

Seq. No. 219173

Seq. ID LIB3149-016-Q1-K1-H5

Method BLASTX
NCBI GI g2760834
BLAST score 373
E value 4.0e-36
Match length 88
% identity 81

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

Seq. No. 219174

Seq. ID LIB3149-016-Q1-K1-H7

Method BLASTX
NCBI GI g3269289
BLAST score 211
E value 7.0e-17
Match length 68
% identity 65

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 219175

Seq. ID LIB3149-016-Q1-K1-H9

Method BLASTX
NCBI GI g1171978
BLAST score 466
E value 7.0e-47
Match length 110
% identity 19

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi 304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 219176

Seq. ID LIB3149-017-Q1-K1-A1

Method BLASTX NCBI GI g1856971 BLAST score 453



```
E value
                   3.0e-45
                  95
Match length
                  92
% identity
                  (D26058) This gene is specifically expressed at the S phase
NCBI Description
                  during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
                  219177
Seq. No.
                  LIB3149-017-Q1-K1-A10
Seq. ID
Method
                  BLASTX
                   g2662377
NCBI GI
BLAST score
                   211
                  8.0e-17
E value
Match length
                   61
% identity
                   64
                  (D89063) oligosaccharyltransferase [Mus musculus]
NCBI Description
Seq. No.
                  219178
                  LIB3149-017-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g464849
BLAST score
                   594
E value
                   1.0e-61
Match length
                   139
                   86
% identity
                  TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20413 emb CAA47635 (X67162)
                   alpha-tubulin [Prunus dulcis]
                   219179
Seq. No.
                   LIB3149-017-Q1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2262172
BLAST score
                   292
                   2.0e-26
E value
                   131
Match length
% identity
                   52
NCBI Description
                  (AC002329) predicted protein of unknown function
                   [Arabidopsis thaliana]
                   219180
Seq. No.
Seq. ID
                   LIB3149-017-Q1-K1-A5
Method
                   BLASTX
                   g4567311
NCBI GI
                   152
BLAST score
                   6.0e-10
E value
                   63
Match length
                   52
% identity
                  (AC005956) putative protein kinase [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB3149-017-Q1-K1-A7

Method BLASTX
NCBI GI g4539405
BLAST score 412
E value 2.0e-40
Match length 119

```
% identity
                  69
                   (AL049524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
                  219182
Seq. No.
                  LIB3149-017-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245107
BLAST score
                  306
                  5.0e-28
E value
                  109
Match length
% identity
                  33
NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]
                  219183
Seq. No.
                  LIB3149-017-Q1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3269280
                  34
BLAST score
                  2.0e-09
E value
                  62
Match length
                  89
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
                  (ESSAII project)
                  219184
Seq. No.
                  LIB3149-017-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g547683
                  655
BLAST score
E value
                  6.0e-69
Match length
                  131
                  97
% identity
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
Seq. No.
                  219185
                  LIB3149-017-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417154
                  545
BLAST score
                  6.0e-56
E value
                  120
Match length
% identity
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
```

Seg. ID LIB3149-017-Q1-K1-B5

Method BLASTX NCBI GI g3927825 BLAST score 497 E value 2.0e-50



```
120
Match length
% identity
                  (AC005727) putative dTDP-qlucose 4-6-dehydratase
NCBI Description
                  [Arabidopsis thaliana]
                  219187
Seq. No.
                  LIB3149-017-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512679
BLAST score
                  234
E value
                  1.0e-19
Match length
                  65
% identity
                  72
NCBI Description (AC006931) putative 60S ribosomal protein L11B [Arabidopsis
                  thaliana]
                  219188
Seq. No.
                  LIB3149-017-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643607
BLAST score
                  222
E value
                  4.0e-18
Match length
                  55
                  75
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  219189
                  LIB3149-017-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927825
BLAST score
                  244
                  8.0e-21
E value
Match length
                  49
                  92
% identity
NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                  219190
Seq. ID
                  LIB3149-017-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  513
E value
                  3.0e-52
Match length
                  121
% identity
                  84
NCBI Description
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
```

Seq. ID LIB3149-017-Q1-K1-C2

Method BLASTX
NCBI GI g1632831
BLAST score 432
E value 9.0e-43
Match length 93



```
% identity
NCBI Description (Z49698) orf [Ricinus communis]
                  219192
Seq. No.
Seq. ID
                  LIB3149-017-Q1-K1-C5
Method
                  BLASTX
                  g296502
NCBI GI
BLAST score
                  219
                  8.0e-26
E value
Match length
                  91
                  65
% identity
NCBI Description (X69187) beta tubulin 3 [Anemia phyllitidis]
Seq. No.
                  219193
Seq. ID
                  LIB3149-017-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q461735
BLAST score
                  551
                  7.0e-57
E value
Match length
                  120
                  93
% identity
NCBI Description
                  MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
                  >gi_478785_pir__S29315 chaperonin 60 - cucurbit
                  >gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita
                  sp.]
Seq. No.
                  219194
                  LIB3149-017-Q1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2258469
BLAST score
                  526
                  6.0e-54
E value
Match length
                  112
% identity
                  86
NCBI Description (AF009179) replication protein A1 [Oryza sativa]
Seq. No.
                  219195
Seq. ID
                  LIB3149-017-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3874228
BLAST score
                  217
E value
                  1.0e-17
Match length
                  139
% identity
                  21
                  (Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST
NCBI Description
                  EMBL:D73546 comes from this gene; cDNA EST EMBL:D73669
                  comes from this gene; cDNA EST EMBL: D70979 comes from this
                  gene; cDNA EST EMBL:D71075 comes from this gene; cDNA E
Seq. No.
                  219196
```

Seq. ID LIB3149-017-01-K1-D2

Method BLASTN NCBI GI q2244991

BLAST score 34 E value 1.0e-09 Match length 106 % identity 83

219202



```
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  219197
Seq. No.
Seq. ID
                  LIB3149-017-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  616
                  2.0e-64
E value
Match length
                  130
                  95
% identity
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  219198
Seq. No.
Seq. ID
                  LIB3149-017-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1439609
BLAST score
                  205
                  3.0e-16
E value
                  53
Match length
% identity
                  74
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
                  219199
Seq. No.
                  LIB3149-017-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3901012
NCBI GI
BLAST score
                  682
                  5.0e-72
E value
Match length
                  139
% identity
                  83
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                  219200
Seq. ID
                  LIB3149-017-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2398829
BLAST score
                  493
E value
                   7.0e-50
Match length
                  125
                   47
% identity
                  (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   219201
Seq. ID
                   LIB3149-017-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2662375
BLAST score
                  291
E value
                   3.0e-26
Match length
                  132
% identity
NCBI Description (D89060) oligosaccharyltransferase [Homo sapiens]
```



```
LIB3149-017-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  q730583
NCBI GI
BLAST score
                  239
                  3.0e-20
E value
Match length
                  62
                  74
% identity
NCBI Description
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
                  219203
Seq. No.
Seq. ID
                  LIB3149-017-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q4468984
BLAST score
                  174
E value
                  1.0e-12
Match length
                  139
                  35
% identity
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                  219204
Seq. No.
                  LIB3149-017-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  g1362078
NCBI GI
BLAST score
                  483
E value
                  1.0e-48
                  135
Match length
                  66
% identity
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
NCBI Description
                   - common nasturtium >gi 311835 emb CAA48324 (X68254)
                  cellulase [Tropaeolum majus]
                  219205
Seq. No.
Seq. ID
                  LIB3149-017-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3953467
BLAST score
                   422
E value
                   1.0e-41
Match length
                  92
% identity
NCBI Description (AC002328) F20N2.12 [Arabidopsis thaliana]
                   219206
Seq. No.
Seq. ID
                   LIB3149-017-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   612
E value
                   6.0e-64
Match length
                  117
% identity
                   97
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   219207
                   LIB3149-017-Q1-K1-G7
Seq. ID
```

30830

BLASTX

g167367

Method NCBI GI

```
BLAST score
                  159
                  8.0e-11
E value
Match length
                  66
% identity
                  53
                 (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  219208
Seq. No.
                  LIB3149-017-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076675
BLAST score
                  170
                  2.0e-26
E value
Match length
                  71
                  79
% identity
                 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur
NCBI Description
                  protein - potato
                  219209
Seq. No.
                  LIB3149-017-Q1-K1-H11
Seq. ID
                  BLASTN
Method
                  g3236234
NCBI GI
BLAST score
                   42
                  2.0e-14
E value
                  90
Match length
                   87
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                   219210
Seq. No.
                   LIB3149-017-Q1-K1-H7
Seq. ID
Method
                   BLASTX
                   q3201541
NCBI GI
                   524
BLAST score
                   2.0e-53
E value
                   113
Match length
% identity
NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]
                   219211
Seq. No.
                   LIB3149-017-Q1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760834
BLAST score
                   496
E value
                   3.0e-50
Match length
                   140
```

72 % identity

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

Seq. No. 219212

LIB3149-018-Q1-K1-A1 Seq. ID

Method BLASTX NCBI GI g3080371 428 BLAST score 2.0e-42 E value Match length 122 % identity 63



```
(AL022580) putative pectinacetylesterase protein
NCBI Description
                  [Arabidopsis thaliana]
                  219213
Seq. No.
                  LIB3149-018-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q3702331
NCBI GI
BLAST score
                  221
E value
                  4.0e-18
Match length
                  115
                  47
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  219214
                  LIB3149-018-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  q3600036
NCBI GI
                  267
BLAST score
                  2.0e-23
E value
Match length
                  62
% identity
                  87
NCBI Description (AF080119) contains similarity to protein kinase domains
                  (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]
Seq. No.
                  219215
                  LIB3149-018-Q1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3617741°
BLAST score
                  440
E value
                  9.0e-44
Match length
                  125
% identity
                  67
                  (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  219216
Seq. ID
                  LIB3149-018-Q1-K1-A8
Method'
                  BLASTX
NCBI GI
                   g2961372
                                   ; -c
BLAST score
                  513
E value
                   3.0e-52
Match length
                  101
                   93
% identity
                  (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                   thaliana] >gi 3036817 emb CAA18507 (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                   219217
Seq. No.
                  LIB3149-018-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q124224
BLAST score
                   624
                   3.0e-65
E value
                  121
Match length
                   96
% identity
```

>gi 100345 pir S21060 translation initiation factor eIF-5A

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

Seq. ID Method

NCBI GI

BLAST score E value

Match length

% identity

Seq. No. Seq. ID

Method

NCBI GI

```
- common tobacco >gi_19887_emb_CAA45105_ (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                  219218
                  LIB3149-018-Q1-K1-B6
                  BLASTX
                  q1710546
                  159
                  3.0e-11
                  74
                  47
                  60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
NCBI Description
                  ribosomal protein [Daucus carota]
                  219219
                  LIB3149-018-Q1-K1-C2
                  BLASTX
                  g135406
                  429
```

BLAST score 2.0e-42E value Match length 82 98 % identity TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin NCBI Description alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

219220 Seq. No. LIB3149-018-Q1-K1-C3 Seq. ID BLASTN Method NCBI GI g21098 BLAST score 47 E value 3.0e-17 71 Match length 92 % identity

NCBI Description Tomato U1 small nuclear RNA gene U1.5

219221 Seq. No. Seq. ID LIB3149-018-Q1-K1-C7 Method BLASTX NCBI GI g585963 BLAST score 264 E value 4.0e-23 Match length 69 78 % identity

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 219222

Seq. ID LIB3149-018-Q1-K1-C8

Method BLASTX NCBI GI q3925703 BLAST score 651 E value 2.0e-68 Match length 138 % identity 91

NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]

E value

Match length

3.0e-22

54



Seq. No. 219223 Seq. ID LIB3149-018-Q1-K1-C9 Method BLASTX NCBI GI q1170567 BLAST score 673 5.0e-71E value Match length 135 96 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi 1085960 pir S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi] Seq. No. 219224 LIB3149-018-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI g484656 BLAST score 390 8.0e-38 E value Match length 139 57 % identity monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -NCBI Description cucumber >gi 452165 dbj BAA05408 (D26392) monodehydroascorbate reductase [Cucumis sativus] Seq. No. 219225 LIB3149-018-Q1-K1-D4 Seq. ID Method BLASTX NCBI GI q399046 BLAST score 287 8.0e-26 E value 73 Match length 78 % identity ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) NCBI Description >gi 99657 pir S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana] 219226 Seq. No. LIB3149-018-Q1-K1-D9 Seq. ID Method BLASTX g4006827 NCBI GI BLAST score 515 2.0e-52 E value Match length 132 % identity NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana] 219227 Seq. No. LIB3149-018-Q1-K1-E11 Seq. ID Method BLASTX NCBI GI q1620982 BLAST score 257



```
% identity
                   (Y08860) 40S ribosomal protein S5 [Nicotiana
NCBI Description
                   plumbaginifolia]
Seq. No.
                   219228
Seq. ID
                   LIB3149-018-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   q1843527
BLAST score
                   614
E value
                   4.0e-64
Match length
                   122
% identity
                   51
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   219229
Seq. ID
                  LIB3149-018-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1899175
BLAST score
                   467
E value
                   7.0e-47
Match length
                  106
% identity
                   56
NCBI Description (U90262) calcium-dependent calmodulin-independent protein
                  kinase CDPK [Cucurbita pepo]
Seq. No.
                  219230
                  LIB3149-018-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3747111
BLAST score
                  180
E value
                   3.0e-13
Match length
                  72
% identity
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
Seq. No.
                  219231
Seq. ID
                  LIB3149-018-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1705678
BLAST score
                  238
E value
                  5.0e-20
Match length
                  55
                  89
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                  PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                  valosin-containing protein [Glycine max]
Seq. No.
                  219232
Seq. ID
                  LIB3149-018-Q1-K1-F1
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  103
E value
                  1.0e-50
Match length
                  396
% identity
                  99
NCBI Description R.norvegicus gene encoding prolactin, exon 5
```

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene



: exon ${\tt v}$ and flanks

```
219233
Seq. No.
Seq. ID
                   LIB3149-018-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   q266945
                   543
BLAST score
                   9.0e-56
E value
                   124
Match length
                   87
% identity
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                   >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                   >gi 1279645 emb CAA65987 (X97322) ribosomal protein L9
                   [Pisum sativum]
                   219234
Seq. No.
                   LIB3149-018-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2146734
BLAST score
                   171
                   4.0e-12
E value
Match length
                   68
                   47
% identity
NCBI Description GAST1 protein homolog (clone GASA4) - Arabidopsis thaliana
Seq. No.
                   219235
                   LIB3149-018-Q1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3747050
BLAST score
                   424
E value
                   8.0e-42
                   106
Match length
                   76
% identity
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                   219236
                   LIB3149-018-Q1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120668
BLAST score
                   457
                   9.0e-46
E value
Match length
                   119
                   79
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_82399_pir_ A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
Seq. No.
                   219237
Seq. ID
                   LIB3149-018-Q1-K1-F5
```

BLASTX

g2500354 677

Method NCBI GI

BLAST score



```
2.0e-71
E value
Match length
                  137
                  93
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_
NCBI Description
                  (AB001891) QM family protein [Solanum melongena]
                  219238
Seq. No.
                  LIB3149-018-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g2764941
NCBI GI
                  398
BLAST score
                  9.0e-39
E value
                  94
Match length
                  71
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  219239
Seq. No.
                  LIB3149-018-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  g3582339
NCBI GI
BLAST score
                   451
                   6.0e-45
E value
                  112
Match length
                  72
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   219240
                  LIB3149-018-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                   g1170508
NCBI GI
BLAST score
                   513
                   3.0e-52
E value
                   102
Match length
                   98
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
                   >gi_2119931_pir__S60244 translation initiation factor
                   eIF-4A.8, anther-specific - common tobacco
                   >gi_475219_emb_CAA55639_ (X79004) translation initiation
                   factor (eIF-4A) [Nicotiana tabacum]
                   >gi_475221_emb_CAA55640_ (X79005) translation initiation
                   factor (eIF-4A) [Nicotiana tabacum]
                   219241
Seq. No.
                   LIB3149-018-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1709970
BLAST score
                   439
```

1.0e-43 E value Match length 120 73 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L10A

219242 Seq. No.

LIB3149-018-Q1-K1-G3 Seq. ID

Method BLASTX

E value

Match length

8.0e-40



```
NCBI GI
                  g434759
BLAST score
                  608
                  2.0e-63
E value
Match length
                  139
                  79
% identity
                  (D21163) similar to human elongation factor 2 mRNA (HSEF2).
NCBI Description
                  [Homo sapiens]
                  219243
Seq. No.
                  LIB3149-018-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g1709970
NCBI GI
                  449
BLAST score
                  9.0e-45
E value
                  121
Match length
                  74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                  219244
Seq. No.
                  LIB3149-018-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g3157934
NCBI GI
BLAST score
                  350
                  4.0e-33
E value
                  82
Match length
                  82
% identity
                  (AC002131) Similar to hypothetical protein F09E5.8
NCBI Description
                  qb U37429 from C. elegans. ESTs gb T42019 and gb_N97000
                  come from this gene. [Arabidopsis thaliana]
                  219245
Seq. No.
                  LIB3149-018-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                  g2407800
NCBI GI
                   334
BLAST score
                   3.0e - 31
E value
Match length
                  73
% identity
                   90
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
                   219246
Seq. No.
                  LIB3149-018-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g559005
BLAST score
                   347
                   9.0e - 33
E value
Match length
                   90
% identity
                   72
NCBI Description (U15933) ascorbate peroxidase [Nicotiana tabacum]
                   219247
Seq. No.
                   LIB3149-018-Q1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2677830
BLAST score
                   407
```



```
75
% identity
                 (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                  219248
Seq. No.
                  LIB3149-018-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2924520
                  556
BLAST score
                  2.0e-57
E value
                  121
Match length
% identity
                  85
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  219249
Seq. No.
                  LIB3149-018-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  g297381
NCBI GI
BLAST score
                  221
                   6.0e-18
E value
                  62
Match length
                   65
% identity
NCBI Description (X67421) extA [Arabidopsis thaliana]
                  219250
Seq. No.
                  LIB3149-019-Q1-K1-A1
Seq. ID
Method
                  BLASTX
                  g3098571
NCBI GI
                   224
BLAST score
                   2.0e-18
E value
                  117
Match length
                   40
% identity
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
                   219251
Seq. No.
                   LIB3149-019-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   q4006932
NCBI GI
BLAST score
                   160
                   7.0e-11
E value
                   117
Match length
                   38
% identity
                   (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit
NCBI Description
                   [Bos taurus]
                   219252
Seq. No.
Seq. ID
                   LIB3149-019-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   q3643610
BLAST score
                   151
E value
                   2.0e-10
Match length
                   33
% identity
                   (AC005395) putative serine/threonine protein kinase
```

NCBI Description

[Arabidopsis thaliana]

NCBI Description

thaliana]



```
LIB3149-019-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2384758
BLAST score
                   656
                   5.0e-69
E value
                   132
Match length
% identity
                  (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                   sativa]
                   219254
Seq. No.
Seq. ID
                   LIB3149-019-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2995943
BLAST score
                   148
                   1.0e-09
E value
                   74
Match length
                   49
% identity
                  (AF053560) cytochrome c oxidase subunit Vb precursor
NCBI Description
                   [Mesembryanthemum crystallinum]
                   219255
Seq. No.
                   LIB3149-019-Q1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3212610
BLAST score
                   130
                   8.0e-16
E value
                   96
Match length
                   51
% identity
                   Chain A, Sulfite Oxidase From Chicken Liver
NCBI Description
                   >gi 3212611 pdb 1SOX B Chain B, Sulfite Oxidase From
                   Chicken Liver
Seq. No.
                   219256
Seq. ID
                   LIB3149-019-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g231683
                   585
BLAST score
E value
                   1.0e-60
Match length
                   137
% identity
                   75
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir JN0597
                   calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                   [Arabidopsis thaliana]
Seq. No.
                   219257
                   LIB3149-019-Q1-K1-B6
Seq. ID
Method
                   BLASTX
                   g4185131
NCBI GI
BLAST score
                   272
                   5.0e-24
E value
Match length
                   134
                   51
% identity
                  (AC005724) putative zinc finger protein [Arabidopsis
```

```
219258
Seq. No.
Seq. ID
                  LIB3149-019-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4522012
BLAST score
                  484
                  8.0e-49
E value
                  131
Match length
% identity
                   67
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   219259
                  LIB3149-019-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3694872
BLAST score
                  515
E value
                  2.0e-52
Match length
                  120
                  81
% identity
NCBI Description (AF092547) profilin [Ricinus communis]
                   219260
Seq. No.
                  LIB3149-019-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2209091
BLAST score
                   159
E value
                   7.0e-16
Match length
                   68
                   42
% identity
NCBI Description (AF003089) ubiquitin [Tetrahymena vorax]
Seq. No.
                   219261
                   LIB3149-019-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885884
BLAST score
                   583
E value
                   2.0e-60
Match length
                   115
% identity
                   92
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
Seq. No.
                   219262
                   LIB3149-019-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454466
BLAST score
                   192
E value
                   1.0e-14
Match length
                   48
                   69
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
```

219263 Seq. No.

Seq. ID LIB3149-019-Q1-K1-D11

Method BLASTX NCBI GI g1362051 BLAST score 172 E value 5.0e-17 Match length 114

Seq. No.

219269



```
% identity
                  protein kinase 3 - soybean >gi_310582 (L19361) protein
NCBI Description
                  kinase 3 [Glycine max]
                  219264
Seq. No.
                  LIB3149-019-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g2244734
NCBI GI
                  704
BLAST score
                  1.0e-74
E value
                  138
Match length
% identity
                  99
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
                  219265
Seq. No.
Seq. ID
                  LIB3149-019-Q1-K1-D5
Method
                  BLASTX
                  g2244734
NCBI GI
                   305
BLAST score
                  5.0e-28
E value
                  104
Match length
                   62
% identity
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
                   219266
Seq. No.
                  LIB3149-019-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q100294
                   164
BLAST score
                   2.0e-11
E value
Match length
                   43
% identity
                   36
NCBI Description
                  ribonucleoprotein B, 29K - wood tobacco
                   >gi_14135_emb_CAA43428_ (X61114) 29kD B ribonucleoprotein
                   [Nicotiana sylvestris]
Seq. No.
                   219267
                   LIB3149-019-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   q1052973
NCBI GI
                   258
BLAST score
E value
                   2.0e-22
                   64
Match length
                   81
% identity
NCBI Description (U37838) fructokinase [Beta vulgaris]
Seq. No.
                   219268
Seq. ID
                   LIB3149-019-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                   q4164161
BLAST score
                   567
                   1.0e-58
E value
Match length
                   133
% identity
                  (AB015497) ethylene response sensor [Passiflora edulis]
NCBI Description
```

BLAST score

E value

447

2.0e-44



```
LIB3149-019-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2146732
BLAST score
                   431
E value
                   1.0e-42
Match length
                   131
                   33
% identity
NCBI Description
                  FK506-binding protein - Arabidopsis thaliana >gi_1373396
                   (U57838) rof1 [Arabidopsis thaliana]
Seq. No.
                   219270
Seq. ID
                  LIB3149-019-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q1881585
BLAST score
                   199
                   2.0e-15
E value
Match length
                   64
                   62
% identity
NCBI Description (U72489) remorin [Solanum tuberosum]
                   219271
Seq. No.
Seq. ID
                  LIB3149-019-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q2500376
BLAST score
                   380
E value
                   7.0e-37
Match length
                   92
                   80
% identity
                  60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494_
NCBI Description
                   (AC005508) 23552 [Arabidopsis thaliana]
                   219272
Seq. No.
                   LIB3149-019-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3047111
BLAST score
                   228
                   7.0e-19
E value
                   49
Match length
                   88
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                   219273
Seq. No.
                   LIB3149-019-Q1-K1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3269284
BLAST score
                   430
E value
                   1.0e-42
Match length
                   125
                   71
% identity
NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.
                   219274
Seq. ID
                   LIB3149-019-Q1-K1-F11
                   BLASTX
Method
NCBI GI
                   g3668097
```

BLAST score

E value Match length 149 9.0e-10

32



```
107
 Match length
                    82
 % identity
                    (AC004667) putative glycine cleavage system protein H
 NCBI Description
                    precursor [Arabidopsis thaliana]
                    219275
 Seq. No.
                    LIB3149-019-Q1-K1-F3
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q4336139
                    35
 BLAST score
                    3.0e-10
 E value
                    87
 Match length
                    85
 % identity
                    Arabidopsis thaliana serine/threonine protein phosphatase
 NCBI Description
                    2A 65 kDa A regulatory subunit alpha isoform gene, promoter
                    region
                    219276
 Seq. No.
                    LIB3149-019-Q1-K1-F6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3024122
                    260
 BLAST score
                    8.0e-23
 E value
                    79
 Match length
                    72
 % identity
                    S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
~ NCBI Description
                    ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                    (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                    219277
 Seq. No.
                    LIB3149-019-Q1-K1-F9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3785978
 BLAST score
                    455
 E value
                    2.0e-45
 Match length
                    106
  % identity
                    75
 NCBI Description
                   (AC005560) unknown protein [Arabidopsis thaliana]
                    219278
  Seq. No.
                    LIB3149-019-Q1-K1-G10
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    q4185515
  BLAST score
                    427
  E value
                     3.0e-42
 Match length
                    100
  % identity
                     78
                    (AF102824) actin depolymerizing factor 6 [Arabidopsis
  NCBI Description
                    thaliana]
  Seq. No.
                    219279
                    LIB3149-019-Q1-K1-G12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g548852
```



```
88
% identity
                   40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
NCBI Description
                   subunit ribosomal protein [Oryza sativa]
                   219280
Seq. No.
                   LIB3149-019-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g169459
NCBI GI
BLAST score
                   247
                   5.0e-21
E value
                   96
Match length
                   51
% identity
                   (M18538) pop3 peptide [Populus balsamifera subsp.
NCBI Description
                   trichocarpa X Populus deltoides]
                   219281
Seq. No.
                   LIB3149-019-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g2146746
NCBI GI
                   473
BLAST score
                   7.0e-48
E value
                   90
Match length
                   97
% identity
                   protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi 166819 (L05562) protein kinase [Arabidopsis thaliana]
Seq. No.
                    219282
                   LIB3149-019-Q1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                    q3297819
BLAST score
                    437
                    2.0e-43
E value
Match length
                    111
                    76
% identity
                   (AL031032) protein kinase - like protein [Arabidopsis
NCBI Description
                    thaliana]
                    219283
Seq. No.
                    LIB3149-019-Q1-K1-G7
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2656017
BLAST score
                    179
E value
                    4.0e-13
Match length
                    54
% identity
                    61
NCBI Description
                   (Z99292) vacuolar atp synthase subunit a
                    [Schizosaccharomyces pombe]
                    219284
Seq. No.
                    LIB3149-019-Q1-K1-H12
Seq. ID
Method
                    BLASTX
```

Method BLASTX
NCBI GI g3024127
BLAST score 548
E value 2.0e-56
Match length 108
% identity 96



S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1655578_emb CAA95857 (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus] 219285 Seq. No. LIB3149-019-Q1-K1-H3 Seq. ID BLASTX Method g1621268 NCBI GI BLAST score 150 1.0e-09 E value 135 Match length 30 % identity (Z81012) unknown [Ricinus communis] NCBI Description 219286 Seq. No. LIB3149-019-Q1-K1-H8 Seq. ID BLASTN Method g1015315 NCBI GI 44 BLAST score 1.0e-15 E value Match length 76 89. % identity Pisum sativum (clone PsRCI35-2) ribosomal protein L41 mRNA, NCBI Description complete cds 219287 Seq. No. LIB3149-020-Q1-K1-A1 Seq. ID BLASTX Method g2496731 NCBI GI 255 BLAST score E value 3.0e-28113 Match length 58 % identity NCBI Description HYPOTHETICAL 30.2 KD PROTEIN Y40V >gi_2182566 (AE000089) Y4oV [Rhizobium sp. NGR234] Seq. No. 219288 LIB3149-020-Q1-K1-A11 Seq. ID Method BLASTN NCBI GI q2687434 BLAST score 260 1.0e-144 E value 320 Match length 95 % identity NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence Seq. No. 219289 LIB3149-020-Q1-K1-A4 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g122007
BLAST score 332
E value 5.0e-31
Match length 90
% identity 74

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley



>gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No. 219290 Sea. ID LIB314

Seq. ID LIB3149-020-Q1-K1-A8

Method BLASTX
NCBI GI g1076740
BLAST score 116
E value 3.0e-13
Match length 106
% identity 36

NCBI Description chitinase (EC 3.2.1.14) - rice >gi_407472_emb_CAA40107_

(X56787) chitinase [Oryza sativa] >gi_500616_dbj_BAA03750_

(D16222) endochitinase [Oryza sativa]

>gi_742301_prf__2009354A chitinase [Oryza sativa]

Seq. No. 219291

Seq. ID LIB3149-020-Q1-K1-A9

Method BLASTX
NCBI GI 94335750
BLAST score 252
E value 1.0e-21
Match length 75
% identity 56

NCBI Description (AC006284) putative beta-1,3-endoglucanase [Arabidopsis

thaliana]

Seq. No. 219292

Seq. ID LIB3149-020-Q1-K1-B1

Method BLASTX
NCBI GI g730526
BLAST score 526
E value 8.0e-54
Match length 117
% identity 82

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
thaliana >gi_404166_emb_CAA53005 (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 219293

Seq. ID LIB3149-020-Q1-K1-B10

Method BLASTX
NCBI GI g2665890
BLAST score 297
E value 6.0e-27
Match length 73
% identity 77

NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x

ananassa]

Seq. No. 219294

Seq. ID LIB3149-020-Q1-K1-B12

Method BLASTX
NCBI GI g3873807
BLAST score 145
E value 4.0e-09

BLAST score

E value

237

3.0e-20



```
97
Match length
% identity
                   40
                  (Z49907) B0491.1 [Caenorhabditis elegans]
NCBI Description
                   219295
Seq. No.
Seq. ID
                  LIB3149-020-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g730526
                   329
BLAST score
                   7.0e-31
E value
Match length
                   105
                   65
% identity
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                   >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi_404166_{emb_CAA53005_{emb_CX}} (X75162) BBC1 protein
                   [Arabidopsis thaliana]
                   219296
Seq. No.
                  LIB3149-020-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g730449
BLAST score
                   582
E value
                   2.0e-60
Match length
                   122
                   86
% identity
                   60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
NCBI Description
                   >gi_480647_pir__S37132 ribosomal protein L13.A - rape
                   >gi 398918 emb CAA80341 (Z22618) cold induced protein
                   (BnC24A) [Brassica napus]
                   219297
Seq. No.
                   LIB3149-020-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236242
BLAST score
                   438
E value
                   2.0e-43
Match length
                   111
% identity
                   79
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   219298
                   LIB3149-020-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3860319
BLAST score
                   630
E value
                   6.0e-66
Match length
                   136
% identity
                   90
NCBI Description
                  (AJ012686) nucleolar protein [Cicer arietinum]
Seq. No.
                   219299
                   LIB3149-020-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3241945
```

BLAST score

E value

562

5.0e-58



```
Match length
                  82
                  50
% identity
                  (AC004625) unknown protein [Arabidopsis thaliana]
NCBI Description
                  219300
Seq. No.
                  LIB3149-020-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g113217
NCBI GI
                  111
BLAST score
                  5.0e-09
E value
                  43
Match length
% identity
                  59
                  ACTIN 1 >gi 100149 pir S07002 actin 1 - carrot
NCBI Description
Seq. No.
                  219301
Seq. ID
                  LIB3149-020-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  271
                  6.0e-24
E value
Match length
                  73
                  70
% identity
NCBI Description
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
                  219302
Seq. No.
Seq. ID
                  LIB3149-020-Q1-K1-D5
                  BLASTX
Method
NCBI GI
                  q2499945
BLAST score
                  386
                  2.0e-37
E value
                  97
Match length
                  76
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi_1076363_pir__S46440 orotate
                  phosphoribosyltransferase (EC 2.4.2.10) /
                  orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                  Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)
                  pyrE-F [Arabidopsis thaliana]
                  219303
Seq. No.
                  LIB3149-020-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g167367
NCBI GI
                  708
BLAST score
E value
                  4.0e-75
Match length
                  137
                  98
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  219304
Seq. No.
Seq. ID
                  LIB3149-020-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q730526
```

E value

Match length

1.0e-19



```
Match length
                  116
% identity
                  88
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                  >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
                  [Arabidopsis thaliana]
                  219305
Seq. No.
                  LIB3149-020-Q1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1657449
BLAST score
                  34
                  1.0e-09
E value
Match length
                  42
% identity
                  8
NCBI Description
                  Plasmodium falciparum merozoite surface protein 2 (MSP-2)
                  gene, partial cds
Seq. No.
                  219306
                  LIB3149-020-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  559
                  9.0e-58
E value
Match length
                  114
% identity
                  93
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  219307
                  LIB3149-020-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q100535
BLAST score
                  148
                  2.0e-09
E value
                  42
Match length
                  69
% identity
                  hypothetical protein - swollen duckweed
NCBI Description
                  >gi 1929057 emb_CAA32236_ (X14075) longest ORF (1) [Lemna
                  gibba]
                  219308
Seq. No.
                  LIB3149-020-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006877
BLAST score
                  350
E value
                  4.0e-33
Match length
                  133
% identity
                  37
NCBI Description
                  (Z99707) RNA-binding like protein [Arabidopsis thaliana]
                  219309
Seq. No.
Seq. ID
                  LIB3149-020-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                  g3449327
BLAST score
                  51
```

Match length

% identity

100

64



```
% identity
                   85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   219310
Seq. ID
                  LIB3149-020-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g4454484
BLAST score
                   266
E value
                   2.0e-23
Match length
                  118
                   53
% identity
NCBI Description
                  (AC006234) putative diacylglycerol kinase [Arabidopsis
                  thaliana]
Seq. No.
                  219311
Seq. ID
                  LIB3149-020-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4454484
BLAST score
                  556
E value
                  3.0e-57
Match length
                  134
% identity
                  81
NCBI Description
                  (AC006234) putative diacylglycerol kinase [Arabidopsis
                  thaliana]
Seq. No.
                  219312
Seq. ID
                  LIB3149-020-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g399937
BLAST score
                  165
E value
                  2.0e-11
Match length
                  57
% identity
                  51
                  17.4 KD CLASS I HEAT SHOCK PROTEIN >gi_82481_pir__JS0710
NCBI Description
                  heat shock protein, low molecular weight - rice
                  >gi_218251_dbj_BAA02160_ (D12635) 'low molecular weight
                  heat shock protein' [Oryza sativa]
Seq. No.
                  219313
Seq. ID
                  LIB3149-020-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3378491
BLAST score
                  381
E value
                  9.0e-37
Match length
                  135
% identity
                  54
NCBI Description
                  (AJ007578) pRIB5 protein [Ribes nigrum]
Seq. No.
                  219314
                  LIB3149-020-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q114682
BLAST score
                  298
E value
                  5.0e-27
```



```
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi 168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                  219315
                  LIB3149-020-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g3150415
NCBI GI
                  259
BLAST score
                  1.0e-36
E value
                  110
Match length
% identity
                  38
                  (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                  thaliana]
                  219316
Seq. No.
                  LIB3149-020-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4508068
BLAST score
                  225
                  2.0e-18
E value
Match length
                  96
                   53
% identity
                  (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219317
                  LIB3149-020-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3309170
                   351
BLAST score
                   3.0e-33
E value
                  136
Match length
                   54
% identity
                  (AF071314) COP9 complex subunit 4 [Mus musculus]
NCBI Description
                  219318
Seq. No.
                  LIB3149-020-Q1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3309170
BLAST score
                   351
                   3.0e-33
E value
                   136
Match length
                   54
% identity
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]
Seq. No.
                   219319
                  LIB3149-020-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2271477
BLAST score
                   662
                   1.0e-69
E value
Match length
                   137
```

30852

93

% identity

Method

BLASTX



```
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.
                  219320
Seq. ID
                  LIB3149-021-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  151
E value
                  8.0e-10
Match length
                  54
                  57
% identity
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  219321
Seq. No.
                  LIB3149-021-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3355465
BLAST score
                  612
E value
                  7.0e-64
                  138
Match length
                  83
% identity
NCBI Description
                  (AC004218) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
                  219322
Seq. No.
                  LIB3149-021-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2414570
BLAST score
                  295
E value
                  7.0e-27
Match length
                  83
                  63
% identity
NCBI Description
                  (Z99173) cysteine proteinase precursor [Nicotiana tabacum]
Seq. No.
                  219323
                  LIB3149-021-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q585963
BLAST score
                  262
                  8.0e-23
E value
Match length
                  69
                  78
% identity
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
                  219324
Seq. No.
Seq. ID
                  LIB3149-021-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2351580
BLAST score
                  678
E value
                  1.0e-71
Match length
                  140
% identity
                  91
NCBI Description
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
                  homolog [Prunus armeniaca]
Seq. No.
                  219325
Seq. ID
                  LIB3149-021-Q1-K1-A8
```

Seq. ID

Method

NCBI GI



```
NCBI GI
                   g1170746
BLAST score
                   491
E value
                   1.0e-49
Match length
                   122
% identity
                   75
NCBI Description
                   DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi_472850
                   (U08108) putative desiccation protectant protein, homolog
                   of Lea14, GenBank Accession Number M88321 [Glycine max]
Seq. No.
                   219326
Seq. ID
                   LIB3149-021-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   q2351580
BLAST score
                   380
E value
                   1.0e-36
Match length
                   118
% identity
                   65
NCBI Description
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
                   homolog [Prunus armeniaca]
Seq. No.
                   219327
Seq. ID
                   LIB3149-021-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3241945
BLAST score
                   327
E value
                   2.0e-30
Match length
                   121
                   51
% identity
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]
Seq. No.
                   219328
Seq. ID
                  LIB3149-021-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                   g125887
BLAST score
                  228
E value
                   8.0e-19
Match length
                   132
% identity
                   40
NCBI Description
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                   >gi_82092_pir__S04765 LAT52 protein precursor - tomato
                   >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                   esculentum]
Seq. No.
                  219329
Seq. ID
                  LIB3149-021-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2708532
BLAST score
                  397
E value
                  1.0e-38
Match length
                  142
% identity
                  37
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]
Seq. No.
                  219330
```

30854

LIB3149-021-Q1-K1-B6

BLASTX

g2708532

% identity

82



```
BLAST score
                   286
                   4.0e-30
E value
Match length
                   134
% identity
                   36
NCBI Description
                  (AF029351) putative RNA binding protein [Nicotiana tabacum]
Seq. No.
                   219331
Seq. ID
                  LIB3149-021-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g2129604
BLAST score
                   376
E value
                   3.0e-36
Match length
                   93
% identity
                   81
NCBI Description
                  GTP-binding protein 1 - Arabidopsis thaliana
                   >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -
                  Arabidopsis thaliana >gi 1184981 (U46924) ATGB1
                   [Arabidopsis thaliana]
Seq. No.
                  219332
Seq. ID
                  LIB3149-021-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2582665
BLAST score
                  330
E value
                  8.0e-31
Match length
                  104
% identity
                   63
NCBI Description
                  (Z82983) thi [Citrus sinensis]
                  219333
Seq. No.
Seq. ID
                  LIB3149-021-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2270994
BLAST score
                  364
E value
                   9.0e-35
Match length
                  131
% identity
                   52
NCBI Description
                  (AF004809) Ca+2-binding EF hand protein [Glycine max]
Seq. No.
                  219334
Seq. ID
                  LIB3149-021-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3747050
BLAST score
                  432
E value
                  9.0e-43
Match length
                  95
% identity
                  86
                  (AF093540) ribosomal protein L26 [Zea mays]
NCBI Description
Seq. No.
                  219335
Seq. ID
                  LIB3149-021-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q3747050
BLAST score
                  392
E value
                  4.0e-38
Match length
                  92
```

Seq. ID

```
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                   219336
Seq. ID
                   LIB3149-021-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g3986695
BLAST score
                   168
E value
                   2.0e-12
Match length
                   51
% identity
                   71
NCBI Description
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
Seq. No.
                   219337
Seq. ID
                   LIB3149-021-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g2414624
BLAST score
                   154
E value
                   9.0e-11
Match length
                   44
% identity
                   66
NCBI Description
                  (Z99259) ATP synthase subunit [Schizosaccharomyces pombe]
Seq. No.
                   219338
Seq. ID
                   LIB3149-021-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g1408471
BLAST score
                   521
E value
                   4.0e-53
Match length
                   117
% identity
                   81
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
Seq. No.
                   219339
Seq. ID
                   LIB3149-021-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g1754795
BLAST score
                   699
E value
                   5.0e-74
Match length
                   139
% identity
                   89
NCBI Description
                  (U59477) omega-3 fatty acid desaturase [Perilla frutescens]
Seq. No.
                   219340
Seq. ID
                  LIB3149-021-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                   g585241
BLAST score
                   237
E value
                   7.0e-20
Match length
                   61
% identity
                   77
NCBI Description
                  HISTONE H1 >gi 629668 pir S45662 histone H1 - tomato
                  >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]
Seq. No.
```

30856

LIB3149-021-Q1-K1-D6

```
Method
                     BLASTX
  NCBI GI
                    g1514643
  BLAST score
                     151
  E value
                     3.0e-10
  Match length
                    54
  % identity
                    57
  NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
  Seq. No.
                    219342
  Seq. ID
                    LIB3149-021-Q1-K1-D7
  Method
                    BLASTX
  NCBI GI
                    g4510345
  BLAST score
                    345
  E value
                    6.0e-34
  Match length
                    134
  % identity
                    55
  NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    219343
  Seq. ID
                    LIB3149-021-Q1-K1-D8
 Method
                    BLASTX
 NCBI GI
                    g3334320
 BLAST score
                    717
 E value
                    4.0e-76
 Match length
                    138
  % identity
                    98
 NCBI Description
                   40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                    ribosome-associated protein p40 [Glycine max]
 Seq. No.
                    219344
 Seq. ID
                    LIB3149-021-Q1-K1-D9
 Method
                    BLASTX
 NCBI GI
                    g2677830
 BLAST score
                    550
 E value
                    1.0e-56
 Match length
                    117
 % identity
                    92
 NCBI Description
                   (U93168) ribosomal protein L12 [Prunus armeniaca]
 Seq. No.
                    219345
 Seq. ID
                    LIB3149-021-Q1-K1-E1
 Method
                    BLASTX
 NCBI GI
                    g2541876
 BLAST score
                    275
 E value
                    2.0e-24
 Match length
                    108
 % identity
                    46
 NCBI Description
                    (D26015) CND41, chloroplast nucleoid DNA binding protein
                    [Nicotiana tabacum]
```

Seq. No. 219346

Seq. ID LIB3149-021-Q1-K1-E10

Method BLASTX
NCBI GI 94220481
BLAST score 543
E value 9.0e-56
Match length 133

Match length

107



```
% identity
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  219347
Seq. ID
                  LIB3149-021-Q1-K1-E11
                  BLASTX
Method
NCBI GI
                  q1718097
BLAST score
                  214
                  3.0e-17
E value
                  85
Match length
% identity
                  46
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
                  219348
Seq. No.
Seq. ID
                  LIB3149-021-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q1747310
BLAST score
                  371
                  6.0e-36
E value
Match length
                  86
                  84
% identity
NCBI Description
                  (D58424) Myb-like DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  219349
Seq. ID
                  LIB3149-021-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q3036796
BLAST score
                  216
E value
                  2.0e-17
                  47
Match length
                  85
% identity
NCBI Description
                  (AL022373) putative protein [Arabidopsis thaliana]
                  >gi_3805858_emb_CAA21478_ (AL031986) putative protein
                  [Arabidopsis thaliana]
                  219350
Seq. No.
Seq. ID
                  LIB3149-021-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1143427
                  660
BLAST score
                  2.0e-69
E value
                  137
Match length
% identity
                  94
NCBI Description
                  (X73961) heat shock protein 70 [Cucumis sativus]
Seq. No.
                  219351
Seq. ID
                  LIB3149-021-Q1-K1-E7
Method
                  BLASTX
                  g1871577
NCBI GI
BLAST score
                  305
E value
                  7.0e-28
```

Method

NCBI GI

BLASTX

g1199772



% identity NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa] 219352 Seq. No. LIB3149-021-Q1-K1-F11 Seq. ID BLASTX Method g4559334 NCBI GI 516 BLAST score 1.0e-52E value 123 Match length % identity 70 (AC007087) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 219353 LIB3149-021-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI g4204281 BLAST score 239 4.0e-20 E value 72 Match length 65 % identity NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana] 219354 Seq. No. LIB3149-021-Q1-K1-F3 Seq. ID Method BLASTX NCBI GI g4455359 BLAST score 453 3.0e-45E value 118 Match length 78 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] 219355 Seq. No. Seq. ID LIB3149-021-Q1-K1-F4 Method BLASTX NCBI GI g3335341 BLAST score 144 5.0e-09 E value Match length 88 44 % identity NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana] 219356 Seq. No. LIB3149-021-Q1-K1-F5 Seq. ID Method BLASTX NCBI GI q3860247 BLAST score 610 E value 1.0e-63 Match length 129 % identity 89 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] 219357 Seq. No. Seq. ID LIB3149-021-Q1-K1-F8



```
BLAST score
                  197
                  3.0e-15
E value
Match length
                  43
                  88
% identity
NCBI Description
                  (D83226) extensin like protein [Populus nigra]
                  >gi 1199774 dbj BAA11855_ (D83227) extensin like protein
                  [Populus nigra]
                  219358
Seq. No.
                  LIB3149-021-Q1-K1-F9
Seq. ID
                  BLASTN
Method
                  g18483
NCBI GI
                  50
BLAST score
                  4.0e-19
E value
                  166
Match length
                  87
% identity
NCBI Description Cotton mRNA for cottonseed catalase subunit 1 (EC 1.11.1.6)
                  219359
Seq. No.
                  LIB3149-021-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g3319432
NCBI GI
                  261
BLAST score
                  1.0e-22
E value
                  103
Match length
% identity
                  54
                  (AF077534) similar to the proteasome regulatory subunit
NCBI Description
                   [Caenorhabditis elegans]
                  219360
Seq. No.
                  LIB3149-021-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2262173
BLAST score
                   608
E value
                   2.0e-63
Match length
                   135
% identity
                   88
                  (AC002329) NADPH thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   219361
Seq. No.
Seq. ID
                   LIB3149-021-Q1-K1-H10
Method
                   BLASTX
                   g1486472
NCBI GI
                   187
BLAST score
                   4.0e-14
E value
Match length
                   35
% identity
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   219362
```

Seq. ID LIB3149-022-Q1-K1-A10

Method BLASTX
NCBI GI g1172977
BLAST score 432
E value 6.0e-43

Match length 108 80 % identity 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic NCBI Description ribosomal protein L18 [Arabidopsis thaliana] 219363 Seq. No. LIB3149-022-Q1-K1-A2 Seq. ID BLASTX Method g1174621 NCBI GI 322 BLAST score 7.0e-30 E value Match length 131 47 % identity T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) NCBI Description (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus] 219364 Seq. No. LIB3149-022-Q1-K1-A3 Seq. ID BLASTX Method NCBI GI g166867 BLAST score 188 1.0e-21 E value 93 Match length 59 % identity (J05216) ribosomal protein S11 (probable start codon at bp NCBI Description 67) [Arabidopsis thaliana] 219365 Seq. No. LIB3149-022-Q1-K1-A5 Seq. ID BLASTX Method g1703108 NCBI GI 508 BLAST score 1.0e-51 E value

BLAST score 508
E value 1.0e-5
Match length 95
% identity 98
NCBI Description ACTIN

NCBI Description ACTIN 2/7 >gi 2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi 2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 219366

Seq. ID LIB3149-022-Q1-K1-A7

Method BLASTX
NCBI GI g4417280
BLAST score 150
E value 8.0e-10
Match length 45
% identity 71

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 219367

Seq. ID LIB3149-022-Q1-K1-B1

Method BLASTX



```
g4417280
NCBI GI
BLAST score
                   215
                   3.0e-17
E value
Match length
                   52
                   81
% identity
                   (AC007019) putative ATP synthase [Arabidopsis thaliana]
NCBI Description
                   219368
Seq. No.
                   LIB3149-022-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g1498053
NCBI GI
BLAST score
                   374
                   5.0e-36
E value
                   103
Match length
                   71
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                   219369
Seq. No.
Seq. ID
                   LIB3149-022-Q1-K1-B12
                   BLASTX
Method
                   q3687235
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
                   80
Match length
                   51
% identity
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   219370
Seq. No.
                   LIB3149-022-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   q625977
NCBI GI
BLAST score
                   143
                   2.0e-09
E value
Match length
                   51
                   61
% identity
                   p40 protein homolog - Arabidopsis thaliana >gi_402904
NCBI Description
                   (U01955) laminin receptor-like protein [Arabidopsis
                   thaliana]
                   219371
Seq. No.
                   LIB3149-022-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g2160322
NCBI GI
                   190
BLAST score
                   7.0e-16
E value
                   68
Match length
                   66
 % identity
                   (D16139) cytokinin binding protein CBP57 [Nicotiana
NCBI Description
                   sylvestris]
                   219372
 Seq. No.
                   LIB3149-022-Q1-K1-B7
 Seq. ID
                   BLASTX
Method
                   g3193316
 NCBI GI
                   360
 BLAST score
```

3.0e-34

E value



```
78
Match length
% identity
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  219373
Seq. No.
                  LIB3149-022-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  q3193316
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
                  78
Match length
                  76
% identity
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  219374
Seq. No.
Seq. ID
                  LIB3149-022-Q1-K1-C12
Method
                  BLASTX
                   q133088
NCBI GI
                   410
BLAST score
                   4.0e-40
E value
                   136
Match length
                   66
% identity
                   50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12)
NCBI Description
                   >gi_100377_pir__S21061 ribosomal protein L12.1 precursor,
                   chloroplast - common tobacco >gi_280406_pir__S21062
                   ribosomal protein L12.1a precursor, chloroplast - common
                   tobacco >gi_20018_emb_CAA44214_ (X62339) ribosomal protein
                   L12-1 [Nicotiana tabacum]
                   219375
Seq. No.
                   LIB3149-022-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g2829899
NCBI GI
                   193
BLAST score
                   9.0e-15
E value
                   84
Match length
                   45
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp_AJ001449_2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
                   219376
 Seq. No.
                   LIB3149-022-Q1-K1-C4
 Seq. ID
                   BLASTX
 Method
                   g3819164
 NCBI GI
                   180
 BLAST score
                   3.0e-13
 E value
                   63
 Match length
                   65
 % identity
                   (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
 NCBI Description
```

Seq. No. 219377

Seq. ID LIB3149-022-Q1-K1-C7

Method BLASTX



```
g3201613
NCBI GI
                  415
BLAST score
                  9.0e-41
E value
                  138
Match length
                  63
% identity
                  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
NCBI Description
                  219378
Seq. No.
                  LIB3149-022-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  g1197518
NCBI GI
                  36
BLAST score
                   3.0e-11
E value
                  52
Match length
                   92
% identity
NCBI Description N.pseudonarcissus mRNA for histone H3
                   219379
Seq. No.
                   LIB3149-022-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g2281101
NCBI GI
                   150
BLAST score
                   4.0e-10
E value
                   66
Match length
                   48
% identity
                   (AC002333) LecRK1 protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   219380
Seq. No.
                   LIB3149-022-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   g541818
NCBI GI
                   185
BLAST score
                   9.0e-20
E value
                   125
Match length
                   35
 % identity
                   protein kinase - common ice plant (fragment) .
NCBI Description
                   >gi_457693_emb_CAA82994_ (Z30333) protein kinase
                   [Mesembryanthemum crystallinum]
                   219381
 Seq. No.
 Seq. ID
                   LIB3149-022-Q1-K1-D3
                   BLASTX
 Method
                   q2529663
 NCBI GI
                   168
 BLAST score
 E value
                    9.0e-12
 Match length
                    110
 % identity
                   (AC002535) putative lysophospholipase [Arabidopsis
 NCBI Description
                    thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                    [Arabidopsis thaliana]
                    219382
 Seq. No.
                    LIB3149-022-Q1-K1-D5
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1173187
```

30864

663

BLAST score



```
7.0e-70
E value
                  133
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  219383
Seq. No.
                  LIB3149-022-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g3386615
NCBI GI
BLAST score
                  691
                  4.0e-73
E value
Match length
                  147
                  87
% identity
                  (AC004665) putative phosphomannomutase [Arabidopsis
NCBI Description
                   thaliana]
                   219384
Seq. No.
                  LIB3149-022-Q1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g267082
BLAST score
                   741
                   6.0e-79
E value
Match length
                   146
                   97
% identity
                  TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8
NCBI Description
                   chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8
                   tubulin [Arabidopsis thaliana]
                   219385
Seq. No.
                   LIB3149-022-Q1-K1-E10
Seq. ID
                   BLASTN
Method
                   g1654276
NCBI GI
                   156
BLAST score
                   2.0e-82
E value
Match length
                   156
                   100
% identity
NCBI Description Gossypium australe 5.8S ribosomal RNA gene and internal
                   transcribed spacer 1 and
                   219386
Seq. No.
                   LIB3149-022-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g1708314
NCBI GI
                   187
BLAST score
                   3.0e-18
E value
                   103
Match length
                   55
 % identity
                   HEAT SHOCK PROTEIN 83 >gi 169296 (M99431) heat shock
```

NCBI Description protein 83 [Pharbitis nil] >gi_445625_prf__1909372A heat

shock protein 83 [Ipomoea nil]

219387 Seq. No.

LIB3149-022-Q1-K1-E4 Seq. ID

BLASTX Method

E value



```
NCBI GI
                  q1495366
BLAST score
                  255
                  4.0e-22
E value
                  92
Match length
                  53
% identity
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
                  219388
Seq. No.
                  LIB3149-022-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  q4138265
NCBI GI
                  478
BLAST score
                  4.0e-48
E value
                  136
Match length
                  71
% identity
                  (AJ006228) Avr9 elicitor response protein [Nicotiana
NCBI Description
                  tabacum]
                   219389
Seq. No.
                   LIB3149-022-Q1-K1-F1
Seq. ID
                   BLASTX
Method
                   g4538993
NCBI GI
                   483
BLAST score
                   1.0e-48
E value
                   110
Match length
                   82
% identity
                  (AL049481) putative host response protein [Arabidopsis
NCBI Description
                   thaliana]
                   219390
Seq. No.
Seq. ID
                   LIB3149-022-Q1-K1-F12
                   BLASTX
Method
                   q4262232
NCBI GI
BLAST score
                   201
                   6.0e-16
E value
Match length
                   50
                   74
 % identity
NCBI Description (AC006200) putative ribosomal protein L7 [Arabidopsis
                   thaliana]
                   219391
 Seq. No.
                   LIB3149-022-Q1-K1-F3
 Seq. ID
                   BLASTX
 Method
                   q3184283
 NCBI GI
 BLAST score
                   514
                   3.0e-54
 E value
                   143
 Match length
                   77
 % identity
 NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis
                   thaliana]
                   219392
 Seq. No.
                   LIB3149-022-Q1-K1-F4
 Seq. ID
                   BLASTX
 Method
                   g3236242
 NCBI GI
                   213
 BLAST score
                   4.0e-17
```

Match length

% identity

85 82



```
51
Match length
                  86
% identity
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                  219393
Seq. No.
                  LIB3149-022-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  q2829900
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
                  128
Match length
                   30
% identity
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp_AJ001449_2465015 and major latex protein,
                   gp X91961_1107495 [Arabidopsis thaliana]
                   219394
Seq. No.
                   LIB3149-022-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   q3643602
NCBI GI
                   674
BLAST score
                   4.0e-71
E value
                   145
Match length
                   88
% identity
                  (AC005395) putative tonoplast intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   219395
Seq. No.
Seq. ID
                   LIB3149-022-Q1-K1-F9
Method
                   BLASTX
                   q2459418
NCBI GI
                   256
BLAST score
                   3.0e-22
E value
Match length
                   94
% identity
NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   219396
                   LIB3149-022-Q1-K1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703380
BLAST score
                   363
                   9.0e-35
E value
Match length
                   71
% identity
                   97
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607 (D17760)
                   ADP-ribosylation factor [Oryza sativa]
                   219397
Seq. No.
                   LIB3149-022-Q1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2760334
                   402
BLAST score
                   3.0e - 39
E value
```



```
(AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
                  219398
Seq. No.
Seq. ID
                  LIB3149-022-Q1-K1-G12
                  BLASTX
Method
                  g2493052
NCBI GI
                  322
BLAST score
                  7.0e-30
E value
                  68
Match length
                  82
% identity
                  ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
NCBI Description
                  >gi 1655486_dbj_BAA13602_ (D88377) epsilon subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana]
                  219399
Seq. No.
                  LIB3149-022-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g1172995
NCBI GI
BLAST score
                  244
                  1.0e-20
E value
                   96
Match length
                   55
% identity
                  60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
NCBI Description
                  protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
                   ribosomal protein L22 [Rattus norvegicus]
                   >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
                   norvegicus]
                   219400
Seq. No.
Seq. ID
                   LIB3149-022-Q1-K1-G4
                   BLASTX
Method
                   q974782
NCBI GI
                   221
BLAST score
                   5.0e-18
E value
Match length
                   66
                   57
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   219401
Seq. No.
                   LIB3149-022-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   q82512
NCBI GI
BLAST score
                   198
                   3.0e-15
E value
Match length
                   40
                   36
% identity
                   ubiquitin precursor - rice (fragment)
NCBI Description
                   >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
                   sativa]
                   219402
 Seq. No.
                   LIB3149-022-Q1-K1-G6
 Seq. ID
                   BLASTX
 Method
```

30868

q2764941

9.0e-40

407

NCBI GI

E value

BLAST score



```
Match length
                  106
% identity
                  69
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  219403
Seq. No.
                  LIB3149-022-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  q123650
NCBI GI
                  299
BLAST score
                  2.0e-27
E value
Match length
                  88
                  70
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat
NCBI Description
                  shock protein 70 (clone pMON9743) - garden petunia
                  >gi 20557 emb CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
Seq. No.
                  219404
Seq. ID
                  LIB3149-023-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g2129889
BLAST score
                   299
                   1.0e-31
E value
                  90
Match length
                   80
% identity
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
                   219405
Seq. No.
                  LIB3149-023-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g2160182
NCBI GI
                   162
BLAST score
                   4.0e-11
E value
                   59
Match length
                   54
% identity
                  (AC000132) ESTs gb ATTS1236,gb T43334,gb N97019,gb_AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   219406
Seq. No.
                   LIB3149-023-Q1-K1-A7
Seq. ID
Method
                   BLASTX
                   g136739
NCBI GI
                   253
BLAST score
E value
                   2.0e-22
Match length
                   67
                   70
% identity
                   UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                   PYROPHOSPHORYLASE) (UDPGP) >qi 67061 pir XNPOU
                   UTP--glucose-1-phosphate uridy Tyltransferase (EC 2.7.7.9) -
```

Seq. No. 219407

Seq. ID LIB3149-023-Q1-K1-B2

Method BLASTN

30869

potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Match length

% identity



```
NCBI GI
                    g2570118
BLAST score
                     49
                     1.0e-18
E value
                     81
Match length
                     90
% identity
                    S.latifolia mRNA, clone CCLS
NCBI Description
                     219408
Seq. No.
                     LIB3149-023-Q1-K1-B4
Seq. ID
                     BLASTX
Method
                     g2160182
NCBI GI
                     145
BLAST score
                     3.0e-09
E value
                     59
Match length
                     49
% identity
                     (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
NCBI Description
                     come from this gene. [Arabidopsis thaliana]
Seq. No.
                     219409
Seq. ID
                     LIB3149-023-Q1-K1-B7
                     BLASTX
Method
NCBI GI
                     g585973
                     324
BLAST score
                     3.0e-30
E value
                     82
Match length
                     82
% identity
                     FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823)
NCBI Description
                     fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A
                     fructokinase [Solanum tuberosum]
                     219410
 Seq. No.
                     LIB3149-023-Q1-K1-B8
 Seq. ID
                     BLASTX
Method
                     g3874563
 NCBI GI
                     201
 BLAST score
                     1.0e-15
 E value
 Match length
                     110
                     39
 % identity
                     (Z81042) similar to Yeast hypothetical protein YEY6 like;
 NCBI Description
                      cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5
                      comes from this gene; cDNA EST yk303h1.3 comes from this
                      gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...
                     >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast
hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes
                      from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5
                      comes from this gene; cDNA
                      219411
 Seq. No.
                      LIB3149-023-Q1-K1-C1
 Seq. ID
                      BLASTX
 Method
                      g4539543
 NCBI GI
                      364
 BLAST score
                      4.0e-35
 E value
                      91
```



```
(AJ133422) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                  [Nicotiana tabacum]
                  219412
Seq. No.
                  LIB3149-023-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  q1170567
NCBI GI
                  343
BLAST score
                  1.0e-32
E value
                  84
Match length
                  83
% identity
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                  >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
                  >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
                   219413
Seq. No.
                  LIB3149-023-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                   g1212921
NCBI GI
BLAST score
                   353
                   8.0e-34
E value
                   91
Match length
                   75
% identity
NCBI Description (X95953) aquaporin [Helianthus annuus]
Seq. No.
                   219414
                   LIB3149-023-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   g3894387
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   129
Match length
% identity
NCBI Description (AF053995) Hcr2-0B [Lycopersicon esculentum]
                   219415
Seq. No.
                   LIB3149-023-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   q445612
NCBI GI
BLAST score
                   263
                   6.0e-23
E value
                   54
Match length
                   94
 % identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                   219416
 Seq. No.
 Seq. ID
                   LIB3149-023-Q1-K1-D4
                   BLASTX
 Method
                   g4388728
 NCBI GI
                   251
 BLAST score
                   2.0e-21
 E value
                   82
 Match length
                   60
 % identity
 NCBI Description (AC006413) putative grrl-like protein [Arabidopsis
                   thaliana]
```

30871

219417

Seq. No.



LIB3149-023-Q1-K1-D6 Seq. ID BLASTX Method NCBI GI g2739046 353 BLAST score 2.0e-33 E value 99 Match length 64 % identity (AF024652) polyphosphoinositide binding protein Ssh2p NCBI Description [Glycine max] 219418 Seq. No. LIB3149-023-Q1-K1-E10 Seq. ID BLASTX Method g1181589 NCBI GI 344 BLAST score 1.0e-32 E value 83 Match length 75 % identity (D83070) high mobility group protein [Canavalia gladiata] NCBI Description >qi 1483173 dbj BAA13133 (D86594) high mobility group protein [Canavalia gladiata] 219419 Seq. No. Seq. ID LIB3149-023-Q1-K1-E3 BLASTX Method g3717946 NCBI GI 292 BLAST score 3.0e-26 E value 110 Match length 57 % identity (AJ005901) vag1 [Arabidopsis thaliana] NCBI Description 219420 Seq. No. Seq. ID LIB3149-023-Q1-K1-F4 BLASTX Method g2494261 NCBI GI 543 BLAST score 7.0e-56 E value 114 Match length 92 % identity ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) NCBI Description >gi 99903_pir__S21567 translation elongation factor Tu precursor - soybean chloroplast >gi_18776_emb_CAA46864_ (X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A elongation factor Tu [Glycine max] 219421 Seq. No. LIB3149-023-Q1-K1-F6 Seq. ID BLASTX Method NCBI GI g4105697 425 BLAST score 4.0e-42 E value 99 Match length 75 % identity

Seq. No. 219422

NCBI Description

30872

(AF049870) thaumatin-like protein [Arabidopsis thaliana]



```
LIB3149-023-Q1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3894190
                  302
BLAST score
                  2.0e-27
E value
Match length
                  82
                  68
% identity
                  (ACO05662) putative RNA polymerase [Arabidopsis thaliana]
NCBI Description
                  219423
Seq. No.
Seq. ID
                  LIB3149-023-Q1-K1-G10
                  BLASTX
Method
                  g4039152
NCBI GI
BLAST score
                  178
                   6.0e-13
E value
                  38
Match length
                  87
% identity
                  (AF104221) low temperature and salt responsive protein
NCBI Description
                  LTI6B [Arabidopsis thaliana] >gi 4325219 gb_AAD17303
                   (AF122006) hydrophobic protein [Arabidopsis thaliana]
                   219424
Seq. No.
                   LIB3149-023-Q1-K1-G5
Seq. ID
Method
                   BLASTX
                   g1362086
NCBI GI
BLAST score
                   366
                   2.0e-35
E value
Match length
                   87
% identity
                   80
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >qi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
Seq. No.
                   219425
                   LIB3149-023-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g2130109
NCBI GI
                   248
BLAST score
                   2.0e-21
E value
                   103
Match length
                   47
% identity
NCBI Description porin VDAC3 - wheat >gi_558652_emb_CAA57646_ (X82148)
                   Voltage dependent anion channel (VDAC) [Triticum aestivum]
                   219426
Seq. No.
                   LIB3149-023-Q1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2832685
BLAST score,
                   389
E value
                   8.0e-38
                   116
Match length
```

(AL021712) putative protein [Arabidopsis thaliana]

69

% identity

NCBI Description



```
219427
Seq. No.
                   LIB3149-023-Q1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3182981
                   567
BLAST score
                   1.0e-58
E value
                   121
Match length
                   83
% identity
                   CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj_BAA13096
NCBI Description
                   (D86494) diminuto [Pisum sativum]
                   219428
Seq. No.
                   LIB3149-023-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   q549063
NCBI GI
BLAST score
                   329
                   3.0e-31
E value
Match length
                   104
% identity
                   65
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835 dbj BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   219429
Seq. No.
                   LIB3149-023-Q1-K1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1168191
BLAST score
                   596
                   6.0e-62
E value
                   127
Match length
                   92
% identity
                   14-3-3-LIKE PROTEIN 4 (PBLT4) >gi 1362089_pir__S57272
NCBI Description
                   14-3-3 brain protein homolog (clone pBLT4) - tomato
                   >gi_466336 (L29150) 14-3-3 protein homologue [Solanum
                   lycopersicum] >gi 1090847_prf__2019487B 14-3-3 protein
                    [Lycopersicon esculentum]
Seq. No.
                   219430
Seq. ID
                   LIB3149-023-Q1-K1-H2
Method
                   BLASTX
                   q1729860
NCBI GI
                   357
BLAST score
                   3.0e-34
E value
                   83
Match length
                   84
% identity
                   26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                   PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1)
                   (LEMA-1) >gi_1362099_pir__S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426)
                   Mg-dependent ATPase 1 [Lycopersicon esculentum]
```

Seq. No. 219431

Seq. ID LIB3149-023-Q1-K1-H4

Method BLASTX NCBI GI g1917019

Method

NCBI GI

BLASTX

g481236



```
BLAST score
                  576
E value
                  1.0e-59
Match length
                  143
% identity
                  80
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                  219432
Seq. No.
                  LIB3149-023-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1946361
BLAST score
                  424
E value
                  8.0e-42
Match length
                  110
                  75
% identity
NCBI Description (U93215) C3HC4 zinc finger protein isolog [Arabidopsis
                  thaliana]
                  219433
Seq. No.
Seq. ID
                  LIB3149-023-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g1168191
BLAST score
                  389
E value
                  9.0e-38
Match length
                  116
% identity
NCBI Description 14-3-3-LIKE PROTEIN 4 (PBLT4) >gi 1362089 pir S57272
                  14-3-3 brain protein homolog (clone pBLT4) - tomato
                  >gi 466336 (L29150) 14-3-3 protein homologue [Solanum
                  lycopersicum] >gi_1090847_prf__2019487B 14-3-3 protein
                  [Lycopersicon esculentum]
                  219434
Seq. No.
                  LIB3149-024-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760830
BLAST score
                  182
E value
                  5.0e-14
Match length
                  44
% identity
NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana]
Seq. No.
                  219435
Seq. ID
                  LIB3149-024-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2754860
BLAST score
                  505
E value
                  2.0e-51
                  108
Match length
% identity
NCBI Description (AF039953) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
Seq. No.
                  219436
                  LIB3149-024-Q1-K1-A7
Seq. ID
```

Match length

% identity

56 57

```
BLAST score
                  167
                  9.0e-12
E value
                  56
Match length
                  64
% identity
                  hypothetical protein - Madagascar periwinkle
NCBI Description
                  >gi 407410 emb CAA81526_ (Z26880) 14 kDa polypeptide
                  [Catharanthus roseus]
                  219437
Seq. No.
                  LIB3149-024-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350777
                  392
BLAST score
                  4.0e-38
E value
                  90
Match length
                  86
% identity
                  60S RIBOSOMAL PROTEIN L9 >gi 971282 dbj BAA07209_ (D38012)
NCBI Description
                  ribosomal protein L9 [Oryza sativa]
                   219438
Seq. No.
                   LIB3149-024-Q1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3702620
                   413
BLAST score
                   9.0e-41
E value
                   97
Match length
                   76
% identity
NCBI Description (Y17329) calnexin [Pisum sativum]
                   219439
Seq. No.
                   LIB3149-024-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   q508304
NCBI GI
BLAST score
                   160
                   6.0e-11
 E value
                   63
Match length
                   51
 % identity
 NCBI Description (L22305) corC [Medicago sativa]
                   219440
 Seq. No.
                   LIB3149-024-Q1-K1-B2
 Seq. ID
                   BLASTX
 Method
                   g2829894
 NCBI GI
                   444
 BLAST score
                   3.0e-44
 E value
                   116
 Match length
                   75
 % identity
 NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
                   219441
 Seq. No.
                   LIB3149-024-Q1-K1-B5
 Seq. ID
                   BLASTX
 Method
                   g2583134
 NCBI GI
                   145
 BLAST score
                   4.0e-09
 E value
```

```
(AC002387) putative proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  219442
Seq. No.
                  LIB3149-024-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350777
BLAST score
                  148
                  6.0e-10
E value
Match length
                  61
                  57
% identity
                  60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
NCBI Description
                  ribosomal protein L9 [Oryza sativa]
                  219443
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q972931
BLAST score
                  326
                  1.0e-30
E value
                  94
Match length
                  69
% identity
NCBI Description (U18416) IAA14 [Arabidopsis thaliana]
                  219444
Seq. No.
                  LIB3149-024-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2829894
BLAST score
                   461
                   3.0e-46
E value
Match length
                  124
                  72
% identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
                   219445
Seq. No.
                   LIB3149-024-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   g3702620
NCBI GI
BLAST score
                   513
                   2.0e-52
E value
                   99
Match length
                   89
% identity
NCBI Description (Y17329) calnexin [Pisum sativum]
                   219446
Seq. No.
                   LIB3149-024-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1350742
NCBI GI
                   172
BLAST score
                   2.0e-12
E value
```

Match length 41 68 % identity

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA

yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA



yk64g1

220

91

5.0e-18

BLAST score

Match length

E value

```
219447
Seq. No.
                   LIB3149-024-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g4056462
NCBI GI
                   381
BLAST score
                   8.0e-37
E value
                   131
Match length
% identity
                   50
                   (AC005990) Strong similarity to gb_Y09876 aldehyde
NCBI Description
                   dehydrogenase (NAD+) from Nicotiana tabacum and a member of
                   the aldehyde dehydrogenase family PF_00171. ESTs
                   gb F15117, gb_R83958 and gb_586262 come from this gene.
                   [Arabidopsis thaliana]
                   219448
Seq. No.
                   LIB3149-024-Q1-K1-C7
Seq. ID
Method
                   BLASTN
                   q3236234
NCBI GI
                   72
BLAST score
                   3.0e-32
E value
                   158
Match length
                   89
% identity
                   Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   219449
Seq. No.
Seq. ID
                   LIB3149-024-Q1-K1-C9
Method
                   BLASTX
                   q3335375
NCBI GI
BLAST score
                    262
                    6.0e-23
E value
                   75
Match length
                    61
% identity
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
                    219450
Seq. No.
                    LIB3149-024-Q1-K1-D1
Seq. ID
Method
                    BLASTX
                    g549063
NCBI GI
                    326
BLAST score
                    2.0e-30
E value
Match length
                    101
                    63
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                    >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    219451
Seq. No.
                    LIB3149-024-Q1-K1-D5
Seq. ID
                    BLASTX
Method
NCBI GI
                    q4263770
```



```
% identity
                  (AC006218) unknown protein [Arabidopsis thaliana]
NCBI Description
                  219452
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-D7
                  BLASTX
Method
                  a2765140
NCBI GI
                  497
BLAST score
                  2.0e-50
E value
                  122
Match length
                  74
% identity
                  (Y11931) 1-phosphatidylinositol-4,5-bisphosphate
NCBI Description
                  phosphodiesterase [Nicotiana rustica]
                  219453
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                  g1272410
BLAST score
                  434
                  1.0e-45
E value
                  106
Match length
                  86
% identity
                  (U52045) immunophilin precursor [Vicia faba]
NCBI Description
                   219454
Seq. No.
                  LIB3149-024-Q1-K1-D9
Seq. ID
                   BLASTN
Method
                  g2687442
NCBI GI
BLAST score
                   87
                   8.0e-42
E value
                   106
Match length
                   95
% identity
NCBI Description Mitella pentandra large subunit 26S ribosomal RNA gene,
                   partial sequence
                   219455
Seq. No.
                   LIB3149-024-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g1313907
NCBI GI
BLAST score
                   338
                   2.0e-32
E value
Match length
                   65
                   97
% identity
NCBI Description (D84507) CDPK-related protein kinase [Zea mays]
Seq. No.
                   219456
                   LIB3149-024-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   q585338
NCBI GI
BLAST score
                   174
                   5.0e-13
E value
                   36
Match length
 % identity
                   86
                   ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >gi 391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
```

sativa]

Seq. ID



```
219457
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-E3
                  BLASTX
Method
                  g132944
NCBI GI
                  383
BLAST score
                  2.0e-37
E value
                  78
Match length
                  86
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
                  219458
Seq. No.
                  LIB3149-024-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g1707008
NCBI GI
                  495
BLAST score
                  4.0e-50
E value
                  130
Match length
                  75
% identity
                  (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
NCBI Description
                  thaliana]
                  219459
Seq. No.
                  LIB3149-024-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g629838
NCBI GI
                  642
BLAST score
                  2.0e-67
E value
                  124
Match length
                  98
% identity
NCBI Description tubulin beta-4 chain - maize >gi 416145 (L10635) beta-4
                  tubulin [Zea mays]
                   219460
Seq. No.
                  LIB3149-024-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  q1518540
NCBI GI
BLAST score
                  585
E value
                   9.0e-61
Match length
                  120
% identity
                   90
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                   219461
Seq. No.
                   LIB3149-024-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g4006858
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
Match length
                   124
% identity
                   32
NCBI Description (Z99707) cold acclimation protein homolog [Arabidopsis
                   thaliana]
                   219462
```

30880

LIB3149-024-Q1-K1-F4

NCBI Description



```
Method
                  BLASTX
                  q4006858
NCBI GI
BLAST score
                  318
                  2.0e-29
E value
Match length
                  102
                  55
% identity
                  (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                  thaliana]
                  219463
Seq. No.
                  LIB3149-024-Q1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4376815
BLAST score
                  278
                  9.0e-25
E value
Match length
                  125
% identity
                  46
                  (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia
NCBI Description
                  pneumoniae]
                   219464
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-G10
                  BLASTN
Method
NCBI GI
                  g2865522
BLAST score
                  38
                   6.0e-12
E value
                   54
Match length
                   93 -
% identity
                  Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
NCBI Description
                   complete cds
                   219465
Seq. No.
                   LIB3149-024-Q1-K1-G11
Seq. ID
Method
                   BLASTX
                   g114682
NCBI GI
                   253
BLAST score
                   6.0e-22
E value
                   60
Match length
% identity
                   80
                 ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                   >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, mitochondrial - sweet
                   potato >gi_168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
                   219466
Seq. No.
                   LIB3149-024-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g4406818
NCBI GI
BLAST score
                   232
                   7.0e-20
E value
                   62
Match length
                   68
% identity
```

30881

[Arabidopsis thaliana]

(AC006201) putative transcription factor-like protein

```
219467
Seq. No.
                  LIB3149-024-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g1709970
NCBI GI
BLAST score
                  349
                  4.0e-33
E value
                  113
Match length
                  61
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                  219468
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-H1
                  BLASTX
Method
                  g3415113
NCBI GI
                  250
BLAST score
                  2.0e-21
E value
Match length
                  119
                  37
% identity
NCBI Description (AF081201) villin 1 [Arabidopsis thaliana]
                  219469
Seq. No.
Seq. ID
                  LIB3149-024-Q1-K1-H2
                  BLASTX
Method
NCBI GI
                  q3643610
                   232
BLAST score
                   8.0e-20
E value
                   51
Match length
% identity
                  (AC005395) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   219470
Seq. No.
Seq. ID
                   LIB3149-024-Q1-K1-H6
Method
                   BLASTX
                   g1835154
NCBI GI
                   473
BLAST score
                   1.0e-47
E value
                   93
Match length
% identity
                   92
NCBI Description (Y10267) glutamine synthetase [Medicago truncatula]
                   219471
Seq. No.
                   LIB3149-024-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   g2865427
NCBI GI
                   140
BLAST score
                   7.0e-09
E value
                   79
Match length
```

% identity

NCBI Description (AF039372) polyprotein [Arabidopsis thaliana]

219472 Seq. No.

LIB3149-025-Q1-K1-A12 Seq. ID

41

BLASTX Method g1086252 NCBI GI 145 BLAST score 4.0e-09 E value

Method

NCBI GI

BLASTX

q4454451



```
Match length
                   37
                   68
% identity
                  sucrose cleavage protein - Potato >gi_707001_bbs_157931
NCBI Description
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                   tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                   [Solanum tuberosum]
                  219473
Seq. No.
                  LIB3149-025-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                   g2511574
NCBI GI
BLAST score
                   666
                   3.0e-70
E value
Match length
                   141
                   95
% identity
                   (Y13176) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                   thaliana] >gi 3421075 (AF043520) 20S proteasome subunit
                   PAB1 [Arabidopsis thaliana]
                   219474
Seq. No.
                   LIB3149-025-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3152562
                   188
BLAST score
                   1.0e-14
E value
                   81
Match length
                   53
% identity
                  (AC002986) Similar to proteosome component, micropain
NCBI Description
                   (multi-catalytic endopeptidase complex) subunit Y7,
                   gb X56731 from S. cerevisiae. EST gb_Z25719 comes from
                   this gene. [Arabidopsis thaliana]
                   219475
Seq. No.
                   LIB3149-025-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g3901014
NCBI GI
                   235
BLAST score
E value
                   1.0e-19
Match length
                   55
                   76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   219476
Seq. No.
                   LIB3149-025-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g1350983
NCBI GI
BLAST score
                   476
E value
                   6.0e-48
Match length
                   111
% identity
                   85
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
Seq. No.
                   219477
Seq. ID
                   LIB3149-025-Q1-K1-B12
```

Method

NCBI GI

BLASTX g3021510



```
186
BLAST score
                  2.0e-14
E value
                  64
Match length
                  52
% identity
                 (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  219478
Seq. No.
                  LIB3149-025-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g2804278
NCBI GI
                  492
BLAST score
                  8.0e-50
E value
                  113
Match length
                  79
% identity
                 (AB003516) squalene epoxidase [Panax ginseng]
NCBI Description
                  219479
Seq. No.
                  LIB3149-025-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q231504
                  681
BLAST score
                  6.0e-72
E value
                  138
Match length
                  96
% identity
                 ACTIN 100 >gi 100420_pir_ S20092 actin - potato (fragment)
NCBI Description
                  >gi 1345579 emb CAA39276 (X55746) actin [Solanum
                   tuberosum]
                   219480
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-B8
                  BLASTX
Method
                  g3123264
NCBI GI
                   474
BLAST score
                   1.0e-47
E value
Match length
                   123
                   76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   219481
Seq. No.
Seq. ID
                   LIB3149-025-Q1-K1-C11
                   BLASTX
Method
                   q585165
NCBI GI
                   675
BLAST score
                   3.0e-71
E value
Match length
                   133
                   94
 % identity
 NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
                   (G6PD) >gi 2129985_pir__S60287 glucose-6-phosphate
                   1-dehydrogenase (EC 1.1.1.49) - potato
                   >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
                   1-dehydrogenase [Solanum tuberosum]
 Seq. No.
                   219482
                   LIB3149-025-Q1-K1-C12
 Seq. ID
```



BLAST score E value 7.0e-10 73 Match length 57 % identity

(AJ001770) glucose-6-phosphate dehydrogenase [Nicotiana NCBI Description

tabacum]

219483 Seq. No. LIB3149-025-Q1-K1-C2 Seq. ID

BLASTX Method NCBI GI q122085 BLAST score 504 E value 3.0e-51 Match length 110 92 % identity

NCBI Description

HISTONE H3 >gi 81641 pir S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir S04099 histone H3 (variant H3R-21)

- rice >gi_1362194_pir__S57626 histone H3 - maize >gi 20251 emb CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >qi 168493 (M36658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays]

>gi 168497 (M13379) histone H3 [Zea mays] >gi 168506

(M35388) histone H3 [Zea mays] >gi 169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi 886738 emb CAA59111_ (X84377) histone 3 [Zea mays] >gi $1\overline{0}40764$ (M35 $\overline{3}87$) histone H3 [Arabidopsis thaliana] >gi 1314779 (U54827) histone H3

homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] $> \overline{gi}_1 \overline{1667592}$ (U $\overline{7}7296$) histone 3 [Oryza sativa] >gi 3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb H76511 gb H76255, gb AA712452, gb_N65260 and

 gb_{142306} come from this gene. [Arabidopsis thaliana] >gī 225459 prf 1303352A histone H3 [Helicoverpa zea] >gi_225839 prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 219484

LIB3149-025-Q1-K1-C3 Seq. ID

Method BLASTX NCBI GI q3915196 BLAST score 354 1.0e-33 E value 93 Match length

67 % identity

UBIQUITIN-CONJUGATING ENZYME E2-C (UBIQUITIN-PROTEIN NCBI Description

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 1493838 (U52949) cyclin-specific ubiquitin carrier protein E2-C [Spisula

solidissima]

219485 Seq. No.

LIB3149-025-Q1-K1-C4 Seq. ID

Method BLASTX NCBI GI g4417304

BLAST score

171



```
BLAST score
                  289
E value
                  4.0e-26
Match length
                  92
% identity
                  55
NCBI Description
                  (AC006446) putative beta-1,4-mannosyl-glycoprotein
                  beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                  thaliana]
                  219486
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4417304
BLAST score
                  242
E value
                  1.0e-20
Match length
                  100
% identity
                  46
NCBI Description
                  (AC006446) putative beta-1,4-mannosyl-glycoprotein
                  beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  219487
Seq. ID
                  LIB3149-025-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2894612
BLAST score
                  409
E value
                  5.0e-40
                  101
Match length
                  76
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                  219488
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  551
                  7.0e-57
E value
Match length
                  112
% identity
                  95
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
                  219489
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3702332
BLAST score
                  183
E value
                  2.0e-24
Match length
                  100
% identity
                  58
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  219490
Seq. ID
                  LIB3149-025-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g585963
```



```
3.0e-12
E value
Match length
                  51
                  73
% identity
                  PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
NCBI Description
                  219491
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-D2
                  BLASTX
Method
                  q1498053
NCBI GI
                  354
BLAST score
                  1.0e-33
E value
Match length
                  92
% identity
                  78
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  219492
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1762130
                   633
BLAST score
                   3.0e-66
E value
                  139
Match length
                   93
% identity
                  (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
NCBI Description
                   219493
Seq. No.
Seq. ID
                   LIB3149-025-Q1-K1-D5
                   BLASTX
Method
NCBI GI
                   g2462813
BLAST score
                   231
                   4.0e-19
E value
                   52
Match length
                   87
% identity
                  (U95230) NADH dehydrogenase [Rubus rosifolius]
NCBI Description
Seq. No.
                   219494
                   LIB3149-025-Q1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3413167
BLAST score
                   281
                   5.0e-25
E value
                   57
Match length
                   95
% identity
                  (AJ010225) elongation factor 1-alpha [Cicer arietinum]
NCBI Description
                   219495
Seq. No.
                   LIB3149-025-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g3193316
NCBI GI
                   349
BLAST score
                   6.0e-34
E value
                   102
Match length
                   76
% identity
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
```

30887

epimerases [Arabidopsis thaliana]



```
LIB3149-025-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  q3510259
NCBI GI
BLAST score
                  429
                  2.0e-42
E value
Match length
                  112
                  74
% identity
                  (AC005310) putative inorganic pyrophosphatase [Arabidopsis
NCBI Description
                  thaliana] >gi 3522960 (AC004411) putative inorganic
                  pyrophosphatase [Arabidopsis thaliana]
                  219497
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-E10
Method
                  BLASTX
                  g2501555
NCBI GI
BLAST score
                  115
                  6.0e-10
E value
Match length
                  83
                  45
% identity
                  POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >qi 549984 (U13148)
NCBI Description
                  possible apospory-associated protein [Pennisetum ciliare]
                  219498
Seq. No.
Seq. ID
                  LIB3149-025-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1077413
                  157
BLAST score
                  4.0e-11
E value
Match length
                  56
% identity
                  hypothetical protein YLR186w - yeast (Saccharomyces
NCBI Description
                  cerevisiae) > gi 577197 (U17246) Ylr186wp [Saccharomyces
                  cerevisiae]
Seq. No.
                  219499
Seq. ID
                  LIB3149-025-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2190550
BLAST score
                  549
E value
                  2.0e-56
Match length
                  127
% identity
                  82
                  (AC001229) ESTs gb T45673, gb N37512 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                  219500
Seq. No.
                  LIB3149-025-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  q1076809
NCBI GI
BLAST score
                  469
                   6.0e-48
E value
Match length
                  130
% identity
                  77
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                  >gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase
```

[Zea mays]



Seq. ID

219501

LIB3149-025-Q1-K1-E4

```
BLASTX
Method
                  g2462828
NCBI GI
                  137
BLAST score
                   6.0e-18
E value
                  72
Match length
                   60
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  219502
Seq. No.
                  LIB3149-025-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  g3885884
NCBI GI
BLAST score
                  514
                   2.0e-52
E value
                   114
Match length
                   86
% identity
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                   219503
Seq. No.
                   LIB3149-025-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g1170410
NCBI GI
                   145
BLAST score
                   4.0e-09
E value
                   54
Match length
                   59
% identity
                 HOMEOBOX PROTEIN HAT3.1 >gi_322519_pir__S31437 homeotic
NCBI Description
                   protein HAT 3.1 - Arabidopsis thaliana
                   >gi_16326_emb_CAA49263_ (X69512) HAT 3.1 [Arabidopsis
                   thaliana]
                   219504
Seq. No.
                   LIB3149-025-Q1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2738949
BLAST score
                   324
                   3.0e-30
E value
                   100
Match length
                   70
% identity
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                   ananassa]
                   219505
Seq. No.
                   LIB3149-025-Q1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4127456
BLAST score
                   194
                   3.0e-15
E value
                   68
Match length
% identity
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                   219506
                   LIB3149-025-Q1-K1-F5
Seq. ID
Method
                   BLASTX
```



```
g1173234
NCBI GI
                  286
BLAST score
                  9.0e-26
E value
                  64
Match length
                  88
% identity
                  40S RIBOSOMAL PROTEIN S25 >gi 481909 pir S40089 ribosomal
NCBI Description
                  protein S25 - tomato >gi 435679_emb_CAA54132_ (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                  >gi 1584836 prf__2123431A ribosomal protein S25
                  [Lycopersicon esculentum]
                  219507
Seq. No.
                  LIB3149-025-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  q3885884
NCBI GI
                  163
BLAST score
                  9.0e-12
E value
                  33
Match length
                  88
% identity
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                  219508
Seq. No.
                  LIB3149-025-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  g3885884
NCBI GI
BLAST score
                  312
E value
                  1.0e-28
                  102
Match length
                  63
% identity
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
Seq. No.
                  219509
                  LIB3149-025-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q1076738
NCBI GI
BLAST score
                  617
E value
                  2.0e-64
Match length
                  117
                  96
% identity
NCBI Description beta-tubulin R2242 - rice
Seq. No.
                  219510
                  LIB3149-025-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1351014
BLAST score
                  177
E value
                   5.0e-13
Match length
                  34
% identity
                   97
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
```

Seq. ID LIB3149-025-Q1-K1-G10

Method BLASTX NCBI GI g3759184 BLAST score 400



E value

5.0e-39

```
132
Match length
                  63
% identity
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  219512
Seq. No.
                  LIB3149-025-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  g3759184
NCBI GI
                  171
BLAST score
                  3.0e-12
E value
                  92
Match length
                  40
% identity
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  219513
Seq. No.
                  LIB3149-025-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                   g82307
NCBI GI
                   328
BLAST score
                   1.0e-30
E value
Match length
                   136
                   51
% identity
                  myb protein 306 - garden snapdragon >gi_256828_bbs_115017
NCBI Description
                   Myb oncoprotein homolog {clone 306} [Antirrhinum
                   majus=snapdragons, J1:522, flowers, Peptide, 316 aa]
                   219514
Seq. No.
                   LIB3149-025-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g531829
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
                   71
Match length
                   59
% identity
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector
                   pSport1]
                   219515
Seq. No.
Seq. ID
                   LIB3149-025-Q1-K1-G8
                   BLASTX
Method
                   q1762939
NCBI GI
                   386
BLAST score
                   2.0e-37
 E value
                   109
Match length
                   63
 % identity
                   (U66266) ORF; able to induce HR-like lesions [Nicotiana
 NCBI Description
                   tabacum]
                   219516
 Seq. No.
                   LIB3149-025-Q1-K1-H10
 Seq. ID
                   BLASTX
 Method
                   q1903359
 NCBI GI
 BLAST score
                   281
                   4.0e-25
 E value
                   115
 Match length
                    57
 % identity
```

NCBI GI



```
(AC000104) F19P19.21 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219517
Seq. ID
                  LIB3149-025-Q1-K1-H12
Method
                  BLASTX
                  q2104681
NCBI GI
BLAST score
                  217
                  1.0e-17
E value
                  128
Match length
% identity
                  43
                  (X97907) transcription factor [Vicia faba]
NCBI Description
Seq. No.
                  219518
                  LIB3149-025-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  529
                  4.0e-54
E value
Match length
                  123
% identity
                  77
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  219519
                  LIB3149-025-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2569938
BLAST score
                  488
E value
                  3.0e-49
Match length
                  112
% identity
                  79
                  (Y15193) GAI [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219520
                  LIB3149-025-Q1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3355477
                  236
BLAST score
                  9.0e-20
E value
                  127
Match length
                  44
% identity
                  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                  thaliana]
                  219521
Seq. No.
                  LIB3149-025-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485742
BLAST score
                  644
                  1.0e-67
E value
Match length
                  133
                  96
% identity
NCBI Description (L32791) pyrophosphatase [Beta vulgaris]
                  219522
Seq. No.
                  LIB3149-025-Q1-K1-H6
Seq. ID
Method
                  BLASTX
```

30892

g4567210



```
BLAST score
                  172
                   3.0e-12
E value
Match length
                  65
                   55
% identity
                  (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  219523
Seq. No.
                  LIB3149-025-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                   g1407705
NCBI GI
                   562
BLAST score
                   5.0e-58
E value
                   137
Match length
                   72
% identity
                  (U60202) lipoxygenase [Solanum tuberosum]
NCBI Description
                   219524
Seq. No.
                   LIB3149-026-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   q4510381
NCBI GI
                   186
BLAST score
                   7.0e-14
E value
                   56
Match length
                   70
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   219525
Seq. No.
                   LIB3149-026-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   g2736147
NCBI GI
                   373
BLAST score
                   7.0e-36
E value
                   92
Match length
                   75
% identity
                   (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
NCBI Description
                   thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,
                   FAH1 [Arabidopsis thaliana]
                   219526
Seq. No.
                   LIB3149-026-Q1-K1-A8
Seq. ID
                   BLASTX
Method
                   g1561575
NCBI GI
                   176
BLAST score
                   6.0e-13
E value
                   37
Match length
                   89
% identity
                  (Y08273) cyclophilin [Digitalis lanata]
NCBI Description
                   219527
Seq. No.
                   LIB3149-026-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   g2500376
NCBI GI
BLAST score
                   367
                   4.0e-35
E value
                   74
Match length
                   95
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_
```



(AC005508) 23552 [Arabidopsis thaliana]

```
Seq. No.
                  219528
                  LIB3149-026-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  q2565275
NCBI GI
BLAST score
                  540
                  2.0e-55
E value
                  116
Match length
                  84
% identity
                  (AF023611) Dimlp homolog [Homo sapiens]
NCBI Description
                  219529
Seq. No.
                  LIB3149-026-Q1-K1-B6
Seq. ID
Method
                  BLASTX
                  g3236242
NCBI GI
BLAST score
                  429
                  2.0e-42
E value
Match length
                  102
                  83
% identity
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                   219530
Seq. No.
                  LIB3149-026-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2160182
BLAST score
                   247
E value
                   4.0e-21
                  117
Match length
                   45
% identity
                  (AC000132) ESTs gb ATTS1236, gb T43334, gb N97019, gb_AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   219531
Seq. No.
                   LIB3149-026-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g1174592
NCBI GI
BLAST score
                   507
                   9.0e-52
E value
Match length
                   102
                   97
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   219532
Seq. No.
                   LIB3149-026-Q1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2583108
                   269
BLAST score
                   1.0e-23
E value
                   135
Match length
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
```

30894

219533

Seq. No.

```
Seq. ID
                  LIB3149-026-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2497486
BLAST score
                  428
E value
                  2.0e-42
                  108
Match length
                  81
% identity
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                  KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                  thaliana]
                  219534
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-C5
                  BLASTX
Method
                  q3776578
NCBI GI
                   385
BLAST score
                   3.0e-37
E value
                  139
Match length
% identity
                   49
NCBI Description
                  (AC005388) ESTs gb F13915 and gb F13916 come from this
                  gene. [Arabidopsis thaliana]
                   219535
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-C8
Method
                   BLASTX -
                   q2342682
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
Match length
                   63
% identity
                   67
                  (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                   protein kinase (gb X95577). [Arabidopsis thaliana]
                   219536
Seq. No.
Seq. ID
                   LIB3149-026-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   g2462761
BLAST score
                   226
E value
                   1.0e-18
Match length
                   83
% identity
                   55
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                   219537
Seq. No.
                   LIB3149-026-Q1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g464986
BLAST score
                   525
```

1.0e-53 E value 99 Match length 97 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating



enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. ID LIB3149-026-Q1-K1-D7 Method BLASTX NCBI GI g2293332 BLAST score 265 E value 4.0e-23 Match length 79 % identity 62

Seq. No.

NCBI Description (AF011338) unknown [Dictyostelium discoideum]

Seq. No. 219539

Seq. ID LIB3149-026-Q1-K1-E10

219538

Method BLASTX
NCBI GI g4193382
BLAST score 389
E value 1.0e-37
Match length 86

Match length 86 % identity 83

NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana]

>gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis

thaliana]

Seq. No. 219540

Seq. ID LIB3149-026-Q1-K1-E12

Method BLASTX
NCBI GI g2462741
BLAST score 323
E value 5.0e-30
Match length 76
% identity 82

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 219541

Seq. ID LIB3149-026-Q1-K1-E2

Method BLASTX
NCBI GI g4322940
BLAST score 292
E value 3.0e-26
Match length 104
% identity 36

NCBI Description (AF096299) DNA-binding protein 2 [Nicotiana tabacum]

Seq. No. 219542

Seq. ID LIB3149-026-Q1-K1-F12

Method BLASTX
NCBI GI g4415992
BLAST score 229
E value 5.0e-19
Match length 97



% identity

NCBI Description

```
219543
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-F3
                  BLASTX
Method
                  q4102861
NCBI GI
BLAST score
                  496
                  2.0e-50
E value
                  100
Match length
                   90
% identity
                   (AF016893) copper/zinc-superoxide dismutase [Populus
NCBI Description
                  tremuloides]
                   219544
Seq. No.
                  LIB3149-026-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4191785
BLAST score
                   264
E value
                   4.0e-23
                   119
Match length
                   54
% identity
                  (AC005917) putative hydrolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   219545
Seq. ID
                   LIB3149-026-Q1-K1-G10
                   BLASTX
Method
NCBI GI
                   g100535
BLAST score
                   130
E value
                   1.0e-17
                   70
Match length
% identity
                   hypothetical protein - swollen duckweed
NCBI Description
                   >gi 1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna
                   gibba]
Seq. No.
                   219546
                   LIB3149-026-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500376
BLAST score
                   364
                   9.0e-35
E value
Match length
                   74
                   93
% identity
                   60S RIBOSOMAL PROTEIN L34 >qi 4262177 qb AAD14494
NCBI Description
                   (AC005508) 23552 [Arabidopsis thaliana]
                   219547
Seq. No.
                   LIB3149-026-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   g3980393
NCBI GI
                   398
BLAST score
                   9.0e-39
E value
Match length
                   133
                   57
% identity
                  (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                                       30897
```

(AF059288) beta-tubulin 2 [Eleusine indica]



```
219548
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-G2
                  BLASTX
Method
                  g4191785
NCBI GI
                  336
BLAST score
                  3.0e - 34
E value
                  117
Match length
                  62
% identity
                  (AC005917) putative hydrolase [Arabidopsis thaliana]
NCBI Description
                  219549
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-G3
                  {\tt BLASTX}
Method
NCBI GI
                  g167367
                  379
BLAST score
                  1.0e-37
E value
                  100
Match length
                  77
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  219550
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-G5
                  BLASTX
Method
                  g167367
NCBI GI
BLAST score
                  160
                   3.0e-11
E value
                  79
Match length
                   46
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  219551
Seq. No.
Seq. ID
                  LIB3149-026-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                   q1173256
                   758
BLAST score
                   6.0e-81
E value
                   145
Match length
                   99
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
                   protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   219552
Seq. No.
Seq. ID
                   LIB3149-026-Q1-K1-G7
                   BLASTX
Method
NCBI GI
                   g464840
BLAST score
                   290
                   4.0e-26
E value
Match length
                   56
                   100
% identity
NCBI Description
                   TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
```

alpha-1 chain - fern (Anemia phyllitidis)

phyllitidis]

>gi 296494 emb CAA48927_ (X69183) alpha tubulin [Anemia

Seq. ID

219558

LIB3149-026-Q1-K1-H6



```
Seq. No.
                  219553
                  LIB3149-026-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510430
BLAST score
                  548
                  2.0e-56
E value
                  112
Match length
% identity
                  88
                   (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  219554
Seq. No.
                  LIB3149-026-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  q4249386
NCBI GI
BLAST score
                  372
E value
                   9.0e-36
                   125
Match length
% identity
                   63
                   (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1
NCBI Description
                   from Arabidopsis thaliana. EST gb H37393 comes from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                   219555
                  LIB3149-026-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g4097569
NCBI GI
BLAST score
                   382
E value
                   7.0e-37
Match length
                   107
% identity
                   67
                  (U64915) GMFP4 [Glycine max]
NCBI Description
Seq. No.
                   219556
                   LIB3149-026-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   g2864610
NCBI GI
BLAST score
                   175
                   1.0e-12
E value
Match length
                   61
                   52
% identity
                  (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4049336_emb_CAA22561_ (AL034567) putative protein
                   [Arabidopsis thaliana]
                   219557
Seq. No.
                   LIB3149-026-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g1732365
NCBI GI
BLAST score
                   152
                   3.0e-10
E value
                   67
Match length
                   51
% identity
                  (U80271) proline rich protein [Malus domestica]
NCBI Description
```



```
BLASTX
Method
NCBI GI
                  q2833373
                  285
BLAST score
                  2.0e-29
E value
                  87
Match length
                  75
% identity
                  DNA-3-METHYLADENINE GLYCOSIDASE (3-METHYLADENINE DNA
NCBI Description
                  GLYCOSYLASE) >qi 429157 emb CAA53763 (X76169)
                  3-methyladenine glycosylase [Arabidopsis thaliana]
                  219559
Seq. No.
                  LIB3149-026-Q1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4467130
BLAST score
                  265
                  3.0e-23
E value
                  68
Match length
                  72
% identity
                  (AL035538) glycosyltransferase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  219560
Seq. No.
                  LIB3149-027-Q1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4206196
                  290
BLAST score
                  3.0e-26
E value
                  90
Match length
                  67
% identity
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]
                  219561
Seq. No.
                  LIB3149-027-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1888557
BLAST score
                  508
                  9.0e-52
E value
Match length
                  118 😘
% identity
                  79
NCBI Description (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
                  [Lupinus angustifolius]
Seq. No.
                  219562
                  LIB3149-027-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                   423
                  1.0e-41
E value
                  85
Match length
                  74
% identity
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
```

219563 Seq. No. Seq. ID

LIB3149-027-Q1-K1-B1

(D13043) thiol protease [Arabidopsis thaliana]



```
BLASTX
Method
NCBI GI
                  q464707
                  457
BLAST score
                  1.0e-45
E value
                  104
Match length
                  84
% identity
                  40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343_emb CAA82273_ (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275_ (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >qi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                  qb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
                  219564
Seq. No.
Seq. ID
                  LIB3149-027-Q1-K1-B10
Method
                  BLASTX
                  g4512122
NCBI GI
BLAST score
                  488
                  2.0e-49
E value
                  132
Match length
                  73
% identity
                  (AF131219) chorismate mutase 3 [Arabidopsis thaliana]
NCBI Description
                   219565
Seq. No.
                  LIB3149-027-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g231660
BLAST score
                   359
                   3.0e - 34
E value
Match length
                   125
% identity
                   57
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
                   219566
Seq. No.
                   LIB3149-027-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g1899188
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
Match length
                   56
% identity
                   38
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.
                   219567
                   LIB3149-027-Q1-K1-B3
Seq. ID
```

30901

BLASTX

372

g3850823

Method

NCBI GI

BLAST score



E value 1.0e-35 Match length 133 54 % identity (Y18351) U2 snRNP auxiliary factor, large subunit NCBI Description [Nicotiana plumbaginifolia] 219568 Seq. No. LIB3149-027-Q1-K1-B4 Seq. ID BLASTX Method NCBI GI g3337361 BLAST score 316 1.0e-29 E value Match length 79 70 % identity (AC004481) ankyrin-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 219569 LIB3149-027-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI q2244734 622 BLAST score 5.0e-65 E value 122 Match length % identity 98 (D88414) actin [Gossypium hirsutum] NCBI Description 219570 Seq. No. LIB3149-027-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI g1545805 BLAST score 141 4.0e-09 E value 50 Match length % identity 64 (D64052) cytochrome P450 like_TBP [Nicotiana tabacum] NCBI Description 219571 Seq. No. LIB3149-027-Q1-K1-C5 Seq. ID Method BLASTX g132866 NCBI GI BLAST score 631 4.0e-66 E value 122 Match length 96 % identity CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71086_pir__R5NT2 NCBI Description ribosomal protein L2 - common tobacco chloroplast >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2
[Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi 225238_prf__1211235BW ribosomal protein L2 [Nicotiana tabacum] 219572 Seq. No. LIB3149-027-Q1-K1-C6 Seq. ID

Method BLASTX g2911044 NCBI GI 196 BLAST score



1.0e-20 E value Match length 121 50 % identity (AL021961) putative protein [Arabidopsis thaliana] NCBI Description 219573 Seq. No. LIB3149-027-Q1-K1-D1 Seq. ID Method BLASTX a2501578 NCBI GI 554 BLAST score 8.0e-57 E value Match length 125 91 % identity ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047 NCBI Description ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis] Seq. No. 219574 Seq. ID LIB3149-027-Q1-K1-D10 BLASTX Method NCBI GI g2384758 BLAST score 473 1.0e-47 E value Match length 95 94 % identity (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza NCBI Description sativa] Seq. No. 219575 LIB3149-027-Q1-K1-D11 Seq. ID Method BLASTX q2853081 NCBI GI BLAST score 155 E value 3.0e-10 Match length 55 55 % identity (AL021768) ATP binding protein - like [Arabidopsis NCBI Description thaliana] Seq. No. 219576 Seq. ID LIB3149-027-Q1-K1-D12 BLASTX Method NCBI GI q2853081 BLAST score 174 E value 2.0e-12 Match length 55 % identity 60

NCBI Description (AL021768) ATP binding protein - like [Arabidopsis

thaliana]

Seq. No. 219577

Seq. ID LIB3149-027-Q1-K1-D4

Method BLASTX
NCBI GI g4559388
BLAST score 321
E value 9.0e-30

Match length 90 % identity 58 (AC006526) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 219578 Seq. ID LIB3149-027-Q1-K1-D6 BLASTX Method NCBI GI q2911044 BLAST score 196 1.0e-20 E value 121 Match length % identity (AL021961) putative protein [Arabidopsis thaliana] NCBI Description 219579 Seq. No. LIB3149-027-Q1-K1-D7 Seq. ID Method BLASTX NCBI GI g3702332 BLAST score 486 4.0e-49 E value 130 Match length 69 % identity NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] Seq. No. 219580 Seq. ID LIB3149-027-Q1-K1-E10 Method BLASTX q1053047 NCBI GI BLAST score 416 E value 7.0e-41 83 Match length % identity (U38425) histone H3 [Glycine max] >gi 1053049 (U38426) NCBI Description histone H3 [Glycine max] >gi 1053051 (U38427) histone H3 [Glycine max] Seq. No. 219581 Seq. ID LIB3149-027-Q1-K1-E12

Method BLASTX
NCBI GI g2833311
BLAST score 193
E value 6.0e-15
Match length 54
% identity 63

NCBI Description HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III

>gi_630728_pir__S43605 R07E5.13 protein (clone R07E5) Caenorhabditis elegans >gi_3878946_emb_CAA83622_ (Z32683)

R07E5.13 [Caenorhabditis elegans]

Seq. No. 219582

Seq. ID LIB3149-027-Q1-K1-E4

Method BLASTX
NCBI GI g2829899
BLAST score 218
E value 1.0e-17
Match length 107
% identity 40



```
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   219583
Seq. ID
                   LIB3149-027-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   q1877397
BLAST score
                   184
                   1.0e-13
E value
                   44
Match length
                   80
% identity
                   (Y11591) shaggy-like kinase [Ricinus communis]
NCBI Description
                   219584
Seq. No.
                   LIB3149-027-Q1-K1-F1
Seq. ID
Method
                   BLASTX
                   q131276
NCBI GI
BLAST score
                   280
                   3.0e-48
E value
                   98
Match length
                   96
% identity
                   PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
NCBI Description
                   PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll
                   a-binding protein psbB - common tobacco chloroplast
                   >gi_11856_emb_CAA77373 (Z00044) PSII 47kD protein
[Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem
                   II P680 apoprotein [Nicotiana tabacum]
Seq. No.
                   219585
Seq. ID
                   LIB3149-027-Q1-K1-F11
                   BLASTX
Method
NCBI GI
                   g730645
BLAST score
                   520
                   4.0e-53
E value
                   114
Match length
                   90
% identity
                   40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal
NCBI Description
                   protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_
                   (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                   >gi 313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                   [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                   Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                   qb R29788, qb ATTS0365 come from this gene. [Arabidopsis
                   thaliana]
                   219586
Seq. No.
                   LIB3149-027-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   g4204095
NCBI GI
BLAST score
                   425
E value
                   5.0e-42
                   123
Match length
```

% identity

NCBI Description

63

(AF030260) CYP94A1 [Vicia sativa]



```
LIB3149-027-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g4454097
NCBI GI
BLAST score
                  288
                  6.0e-26
E value
Match length
                  67
                  79
% identity
NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]
                  219588
Seq. No.
                  LIB3149-027-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2055384
                  256
BLAST score
                  3.0e-22
E value
                  91
Match length
                  33
% identity
NCBI Description (U69633) cold-stress inducible protein [Solanum tuberosum]
                  219589
Seq. No.
Seq. ID
                  LIB3149-027-Q1-K1-G11
                  BLASTX
Method
NCBI GI
                  q2266949
BLAST score
                  641
                  3.0e-67
E value
                  134
Match length
                  93
% identity
                  (AF008940) phosphoenolpyruvate carboxylase 2 [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  219590
Seq. ID
                  LIB3149-027-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q2196878
BLAST score
                  545
                  5.0e-56
E value
Match length
                  108
% identity
                  92
NCBI Description
                  (Y08292) NADH glutamate dehydrogenase [Nicotiana
                  plumbaginifolia]
                  219591
Seq. No.
                  LIB3149-027-Q1-K1-G3
Seq. ID
Method
                  BLASTX
                  g4433048
NCBI GI
                   360
BLAST score
                  1.0e-42
E value
Match length
                  125
                  71
% identity
NCBI Description (D26578) DNA-binding protein [Daucus carota]
Seq. No.
                  219592
                  LIB3149-027-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g4530066
NCBI GI
```

235

1.0e-19

BLAST score

E value



```
Match length
                  107
% identity
NCBI Description
                  (AF060544) androgen receptor associated protein 54 [Homo
                  sapiens]
                  219593
Seq. No.
                  LIB3149-027-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q112863
NCBI GI
BLAST score
                  629
                  7.0e-66
E value
                  127
Match length
% identity
                  87
                  STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
NCBI Description
                  >gi 100227 pir S12209 hypothetical protein - tomato
                  >gi 19162 emb CAA38979 (X55193) 9612 [Lycopersicon
                  esculentum]
Seq. No.
                  219594
                  LIB3149-027-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g112863
NCBI GI
                  666
BLAST score
E value
                  3.0e-70
                  133
Match length
                  87
% identity
                  STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
NCBI Description
                  >gi_100227_pir__S12209 hypothetical protein - tomato
                  >gi 19162 emb CAA38979 (X55193) 9612 [Lycopersicon
                  esculentum]
Seq. No.
                  219595
Seq. ID
                  LIB3149-027-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4235430
BLAST score
                  461
E value
                  3.0e-46
Match length
                  136
% identity
                  69
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
                  219596
Seq. No.
                  LIB3149-027-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1477428
BLAST score
                  615
E value
                  3.0e-64
Match length
                  133
% identity
                  89
NCBI Description
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
                  219597
Seq. No.
Seq. ID
                  LIB3149-027-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3005065
BLAST score
                  517
```

30907

1.0e-52

E value



```
Match length
                  136
% identity
                   68
NCBI Description
                  (AF043325) N-myristoyltransferase 2 [Homo sapiens]
                  219598
Seq. No.
                  LIB3149-028-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1711572
BLAST score
                  487
                  3.0e-49
E value
Match length
                  119
% identity
                  77
NCBI Description
                  SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR
                   (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)
                  >gi 1076415 pir S30579 succinate--CoA ligase (GDP-forming)
                   (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment)
                  >gi 16510 emb CAA48891 (X69138) succinate--CoA ligase
                   (GDP-forming) [Arabidopsis thaliana]
                  219599
Seq. No.
                  LIB3149-028-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485514
BLAST score
                  335
                  2.0e-31
E value
Match length
                  72
                  88
% identity
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
Seq. No.
                  219600
                  LIB3149-028-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3687237
BLAST score
                  317
E value
                  2.0e-29
Match length
                  115
                  57
% identity
NCBI Description
                  (AC005169) putative Cys3His zinc-finger protein
                  [Arabidopsis thaliana]
Seq. No.
                  219601
                  LIB3149-028-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4098323
BLAST score
                  734
E value
                  4.0e-78
Match length
                  143
% identity
                  (U76746) beta-tubulin 3 [Triticum aestivum]
NCBI Description
```

Seq. ID LIB3149-028-Q1-K1-A6

Method BLASTX NCBI GI g1486472 BLAST score 651



```
E value
                  2.0e-68
Match length
                  134
                  90
% identity
NCBI Description
                  (X99853) oxoglutarate malate translocator [Solanum
                  tuberosum]
                  219603
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q485111
BLAST score
                  161
                  4.0e-11
E value
Match length
                  109
% identity
                  40
                  (U00050) similar to enoyl-CoA hydratases; highest
NCBI Description
                  similarity to YKRS_YEAST [Caenorhabditis elegans]
Seq. No.
                  219604
Seq. ID
                  LIB3149-028-Q1-K1-B1
Method
                  BLASTX
                  g1170409
NCBI GI
                  187
BLAST score
                  4.0e-14
E value
Match length
                  47
% identity
                  83
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
NCBI Description
                  >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana]
                  >gi 549888 (U09337) homeobox protein [Arabidopsis thaliana]
                  >gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein
                  HAT22 [Arabidopsis thaliana]
                  219605
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-B10
                  BLASTX
Method
NCBI GI
                  q3941543
BLAST score
                  293
                   2.0e-26
E value
Match length
                  70
                  84
% identity
NCBI Description
                  (AF069497) pelota [Arabidopsis thaliana]
                  >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                   [Arabidopsis thaliana]
Seq. No.
                  219606
Seq. ID
                  LIB3149-028-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                  g12292
BLAST score
                  230
                  1.0e-126
E value
Match length
                  362
% identity
                  91
```

Spinach chloroplast DNA homologous to ARS and ARC elements NCBI Description upstream of rDNA operon

Seq. No. 219607 LIB3149-028-Q1-K1-B3 Seq. ID

Method BLASTX

```
NCBI GI
                  g548774
BLAST score
                  387
E value
                  1.0e-37
Match length
                  100
                  74
% identity
                  60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  219608
                  LIB3149-028-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g70753
BLAST score
                  348
                  2.0e-33
E value
Match length
                  71
% identity
                  99
NCBI Description
                  histone H3 - garden pea >gi 82610 pir S00373 histone H3 -
Seq. No.
                  219609
Seq. ID
                  LIB3149-028-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3168840
BLAST score
                  148
                  2.0e-09
E value
Match length
                  65
% identity
NCBI Description
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
Seq. No.
                  219610
                  LIB3149-028-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462762
BLAST score
                  421
                  1.0e-41
E value
Match length
                  113
% identity
                  72
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  219611
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  q464849
                  397
BLAST score
                  6.0e-39
E value
                  92
Match length
                  87
% identity
                  TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                  chain - almond >gi 20413 emb CAA47635 (X67162)
                  alpha-tubulin [Prunus dulcis]
```

Seq. ID LIB3149-028-Q1-K1-C1

Method BLASTX NCBI GI g464849

E value Match length

136



```
BLAST score
                  592
E value
                  1.0e-61
Match length
                  118
% identity
                  100
NCBI Description
                  TUBULIN ALPHA CHAIN >qi 486847 pir S36232 tubulin alpha
                  chain - almond >gi 20413 emb CAA47635 (X67162)
                  alpha-tubulin [Prunus dulcis]
                  219613
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2661840
BLAST score
                  436
                  3.0e-43
E value
                  127
Match length
                  64
% identity
NCBI Description
                  (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  219614
Seq. ID
                  LIB3149-028-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g974782
BLAST score
                  382
E value
                  7.0e-37
Match length
                  76
                  99
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                  [Solenostemon scutellarioides]
Seq. No.
                  219615
                  LIB3149-028-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2688828
BLAST score
                  490
E value
                  1.0e-49
Match length
                  129
                  71
% identity
NCBI Description
                  (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
                  armeniaca]
Seq. No.
                  219616
Seq. ID
                  LIB3149-028-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2961300
BLAST score
                  586
E value
                  8.0e-61
Match length
                  121
% identity
                  93
                 (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
Seq. No.
                  219617
                  LIB3149-028-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g927575
BLAST score
                  566
                  2.0e-58
```



```
% identity
NCBI Description
                  (U12926) alpha galactosidase [Glycine max]
                  219618
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-C6
                  BLASTX
Method
NCBI GI
                  q4490705
BLAST score
                  272
                  2.0e-37
E value
                  111
Match length
                  75
% identity
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  219619
Seq. No.
                  LIB3149-028-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455338
BLAST score
                  298
E value
                  4.0e-27
Match length
                  81
% identity
                  70
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
                  219620
Seq. No.
                  LIB3149-028-Q1-K1-C9
Seq. ID
Method
                  BLASTX
                  q3298437
NCBI GI
BLAST score
                  193
E value
                  8.0e-15
                  57
Match length
% identity
                  65
                  (AB010877) chloroplast ribosomal protein L3 [Nicotiana
NCBI Description
                  tabacuml
Seq. No.
                  219621
Seq. ID
                  LIB3149-028-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  434
E value
                  4.0e-43
Match length
                  112
% identity
                  74
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  219622
                  LIB3149-028-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729618
BLAST score
                  246
                  2.0e-36
E value
Match length
                  113
% identity
                  70
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2)
NCBI Description
```

30912

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP 2) >gi_82172_pir__PQ0262 luminal binding protein BLP-2 - common tobacco (fragment) >gi 100338 pir S21878 heat shock



protein BiP homolog blp2 - common tobacco (fragment)
>gi_19807_emb_CAA42661_ (X60059) luminal binding protein
(BiP) [Nicotiana tabacum]

Seq. No. 219623

Seq. ID LIB3149-028-Q1-K1-E3

Method BLASTX
NCBI GI 92497752
BLAST score 291
E value 2.0e-26
Match length 100
% identity 58

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)

>gi 1321911 emb CAA65475 (X96714) lipid transfer protein

[Prunus dulcis]

Seq. No. 219624

Seq. ID LIB3149-028-Q1-K1-E6

Method BLASTX
NCBI GI g3980401
BLAST score 172
E value 2.0e-12
Match'length 55
% identity 56

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 219625

Seq. ID LIB3149-028-Q1-K1-F1

Method BLASTX
NCBI GI 94006858
BLAST score 419
E value 3.0e-41
Match length 130
% identity 62

NCBI Description (299707) cold acclimation protein homolog [Arabidopsis

thaliana]

Seq. No. 219626

Seq. ID LIB3149-028-Q1-K1-F12

Method BLASTX
NCBI GI 94432840
BLAST score 198
E value 3.0e-15
Match length 42
% identity 83

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 219627

Seq. ID LIB3149-028-Q1-K1-F2

Method BLASTX
NCBI GI g464734
BLAST score 612
E value 6.0e-64
Match length 124
% identity 92

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

Match length

% identity

123 40



HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]

Seq. No. 219628 Seq. ID LIB3149-028-Q1-K1-F4 Method BLASTX NCBI GI g2160166 BLAST score 270 9.0e-24 E value Match length 100 % identity 54 (AC000132) No definition line found [Arabidopsis thaliana] NCBI Description 219629 Seq. No. Seq. ID LIB3149-028-Q1-K1-F6 Method BLASTX NCBI GI g2058282 BLAST score 276 2.0e-24 E value Match length 80 64 % identity NCBI Description (X97377) atranbpla [Arabidopsis thaliana] Seq. No. 219630 Seq. ID LIB3149-028-Q1-K1-F7 Method BLASTX NCBI GI g2058282 236 BLAST score 8.0e-20 E value 112 Match length 46 % identity (X97377) atranbpla [Arabidopsis thaliana] NCBI Description 219631 Seq. No. LIB3149-028-Q1-K1-G10 Seq. ID Method BLASTX g2129915 NCBI GI BLAST score 180 3.0e-13E value 79 Match length 49 % identity ferredoxin precursor - sweet orange NCBI Description >gi 1360725 emb CAA87068 (Z46944) non-photosynthetic ferredoxin [Citrus sinensis] Seq. No. 219632 LIB3149-028-Q1-K1-G11 Seq. ID Method BLASTX NCBI GI g2598067 BLAST score 188 E value 3.0e-19

NCBI Description (AJ001486) Ser/Thr protein kinase [Zea mays]



```
219633
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3885515
BLAST score
                  426
                  3.0e-42
E value
                  103
Match length
% identity
                  78
                  (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                  sativa]
                  219634
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1084453
BLAST score
                  655
                  6.0e-69
E value
Match length
                  127
                  67
% identity
NCBI Description calmodulin - rice
                  219635
Seq. No.
                  LIB3149-028-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q3687243
NCBI GI
                  175
BLAST score
                  7.0e-13
E value
                  47
Match length
                  72
% identity
NCBI Description
                  (AC005169) putative ribosomal protein [Arabidopsis
                  thaliana]
Seq. No.
                   219636
Seq. ID
                  LIB3149-028-Q1-K1-G8
Method
                  BLASTN
                  g2160155
NCBI GI
BLAST score
                  38
E value
                   5.0e-12
Match length
                  74
% identity
                  88
NCBI Description
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   219637
Seq. ID
                  LIB3149-028-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2129840
BLAST score
                   268
                  1.0e-23
E value
Match length
                  68
                  74
% identity
NCBI Description nucleosome assembly protein 1 - soybean >gi 1161252
```

Seq. No. 219638

Seq. ID LIB3149-028-Q1-K1-H12

Method BLASTX

30915

(L38856) nucleosome assembly protein 1 [Glycine max]

```
g1498053
NCBI GI
BLAST score
                  264
E value
                  4.0e-23
                  53
Match length
                  92
% identity
                 (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  219639
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-H5
                  BLASTX
Method
NCBI GI
                  g4056420
BLAST score
                  139
                  1.0e-08
E value
                  40
Match length
                  70
% identity
                  (AC005322) ESTs gb T144077 and gb T43352 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
Seq. No.
                  219640
Seq. ID
                  LIB3149-028-Q1-K1-H6
                  BLASTN
Method
NCBI GI
                  g20412
BLAST score
                  39
                  3.0e-13
E value
                  67
Match length
                  90
% identity
NCBI Description P.amygdalus mRNA for alpha-tubulin
                  219641
Seq. No.
Seq. ID
                  LIB3149-028-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q231586
                  621
BLAST score
E value
                  5.0e-65
Match length
                  123
                  100
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 82027 pir S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
Seq. No.
                  219642
                  LIB3149-028-Q1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q231586
BLAST score
                  194
                  2.0e-24
E value
Match length
                  112
                  62
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
```

Seq. No. 219643

beta-subunit [Hevea brasiliensis]



```
LIB3149-029-Q1-K1-A1
Seq. ID
Method
                  BLASTX
                  q4027893
NCBI GI
BLAST score
                  475
E value
                  8.0e-48
                  108
Match length
                  78
% identity
                  (AF049351) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                  219644
Seq. No.
                  LIB3149-029-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4455351
                  222
BLAST score
                  3.0e-18
E value
                  59
Match length
                   66
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219645
Seq. ID
                  LIB3149-029-Q1-K1-A12
                  BLASTX
Method
                  q4324967
NCBI GI
BLAST score
                   628
                   1.0e-65
E value
                   119
Match length
                   99
% identity
                  (AF114796) ADP-ribosylation factor [Glycine max]
NCBI Description
Seq. No.
                   219646
                   LIB3149-029-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   q32532
NCBI GI
BLAST score
                   449
E value
                   8.0e-45
                   106
Match length
                   88
% identity
                  (X55715) ribosomal protein s3 [Homo sapiens]
NCBI Description
                   >gi 4506721 ref NP 000996.1 pRPS3 ribosomal protein S3
                   219647
Seq. No.
Seq. ID
                   LIB3149-029-Q1-K1-A8
                   BLASTX
Method
NCBI GI
                   g3660469
BLAST score
                   654
                   8.0e-69
E value
Match length
                   135
                   95
% identity
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi 4512693 gb AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.
                   219648
                   LIB3149-029-Q1-K1-A9
Seq. ID
                   BLASTX
Method
```

q417073

255

NCBI GI BLAST score



```
E value
                  8.0e-29
Match length
                  110
                  69
% identity
NCBI Description
                  GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
                  >gi 484529 pir JQ1977 glutamate synthase (NADH) (EC
                  1.4.1.14) - alfalfa >gi 166412 (L01660) NADH-glutamate
                  synthase [Medicago sativa]
                  219649
Seq. No.
                  LIB3149-029-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136063
BLAST score
                  620
                  8.0e-65
```

E value 144 Match length % identity 83

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description

> >gi_68426_pir__ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi 168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi 217974 dbj BAA00009 (D00012)

triosephosphate isomerase [Zea mays]

Seq. No. 219650

Seq. ID LIB3149-029-Q1-K1-B5

Method BLASTX q1771780 NCBI GI BLAST score 508 E value 1.0e-51 Match length 123 % identity

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

219651 Seq. No.

Seq. ID LIB3149-029-Q1-K1-B6

Method BLASTX NCBI GI g121907 BLAST score 147 E value 2.0e-09 Match length 33 % identity 91

NCBI Description HISTONE H1.2 >gi 70682 pir HSMU12 histone H1.2 -

Arabidopsis thaliana >gi 16320 emb CAA44316 (X62459) Histone H1-2 [Arabidopsis thaliana] >gi 1946357 (U93215)

histone H1-2C [Arabidopsis thaliana]

Seq. No. 219652

LIB3149-029-Q1-K1-B7 Seq. ID

Method BLASTX NCBI GI g322750 BLAST score 591 2.0e-61 E value Match length 117 % identity 97

ubiquitin / ribosomal protein CEP52 - wood tobacco NCBI Description

>gi_170217 (M74100) ubiquitin fusion protein [Nicotiana

sylvestris]

Method

NCBI GI

E value

BLAST score

BLASTN

41

q1732362

1.0e-13



```
Seq. No.
                  219653
Seq. ID
                  LIB3149-029-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                  q899307
BLAST score
                  33
E value
                  2.0e-09
Match length
                  57
% identity
                  89
NCBI Description H.vulgare chloroplast DNA for rps12 gene exons 2 and
Seq. No.
                  219654
Seq. ID
                  LIB3149-029-Q1-K1-C5
Method
                  BLASTN
                  g2275090
NCBI GI
BLAST score
                  79
E value
                  2.0e-36
Match length
                  95
% identity
                  96
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
                  219655
Seq. No.
Seq. ID
                  LIB3149-029-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3925703
BLAST score
                  307
E value
                  4.0e-28
Match length
                  70
                  90
% identity
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                  219656
Seq. ID
                  LIB3149-029-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1345592
BLAST score
                  204
E value
                  2.0e-16
Match length
                  58
                  76
% identity
NCBI Description 14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (U36446) GF14
                  epsilon isoform [Arabidopsis thaliana]
Seq. No.
                  219657
                  LIB3149-029-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4580455
BLAST score
                  356
E value
                  8.0e-34
Match length
                  97
                  73
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.
                  219658
Seq. ID
                  LIB3149-029-Q1-K1-D10
```



```
130
Match length
% identity
                  90
                  Malus domestica pAFD103 mRNA, partial cds
NCBI Description
                  219659
Seq. No.
                  LIB3149-029-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2642648
                  736
BLAST score
                  2.0e-78
E value
                  149
Match length
                  97
% identity
                  (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                  [Spinacia oleracea] >gi 2660768 (AF034616) cytosolic heat
                  shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                  cytosolic heat shock 70 protein [Spinacia oleracea]
                  219660
Seq. No.
Seq. ID
                  LIB3149-029-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q1737492
                  409
BLAST score
                  4.0e-40
E value
                  108
Match length
                  78
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
                  219661
Seq. No.
Seq. ID
                  LIB3149-029-Q1-K1-E1
Method
                  BLASTX
                  q3776577
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
Match length
                  69
% identity
                  46
NCBI Description (AC005388) T22H22.24 [Arabidopsis thaliana]
Seq. No.
                  219662
Seq. ID
                  LIB3149-029-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3122703
BLAST score
                  342
                  4.0e-32
E value
Match length
                  88
% identity
                  75
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                  protein L23a [Fritillaria agrestis]
Seq. No.
                  219663
                  LIB3149-029-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417103
                  432
BLAST score
                  5.0e-57
E value
Match length
                  121
```

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

98

% identity



H3.3-like protein - Arabidopsis thaliana >qi 16324 emb CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >qi 488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] $>g\overline{i}_38\overline{8}5890$ (AF $\overline{0}93633$) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 219664 LIB3149-029-Q1-K1-E4 Seq. ID BLASTX Method NCBI GI q1053047 387 BLAST score 1.0e-37 E value 92 Match length 87 % identity

NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

- -

Seq. No. 219665

Seq. ID LIB3149-029-Q1-K1-F10

Method BLASTX
NCBI GI g3024020
BLAST score 653
E value 1.0e-68
Match length 129
% identity 94

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 219666

Seq. ID LIB3149-029-Q1-K1-F11

Method BLASTX
NCBI GI g4455274
BLAST score 465
E value 1.0e-46
Match length 115
% identity 77

NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis

thaliana]

Seq. No. 219667

Seq. ID LIB3149-029-Q1-K1-F2

Method BLASTX

Seq. ID Method



```
NCBI GI
                  g1665777
BLAST score
                  342
E value
                  3.0e - 32
                  118
Match length
                  52
% identity
                  (D87444) Similar to S.cerevisiae EMP70 protein precursor
NCBI Description
                   (S25110) [Homo sapiens]
Seq. No.
                  219668
Seq. ID
                  LIB3149-029-Q1-K1-F3
                  BLASTX
Method
NCBI GI
                  q4128197
BLAST score
                  375
                  6.0e-37
E value
                  121
Match length
                  64
% identity
                  (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219669
Seq. ID
                  LIB3149-029-Q1-K1-F6
                  BLASTX
Method
                  g1171429
NCBI GI
                  407
BLAST score
                  3.0e-40
E value
Match length
                  81
                  63
% identity
                  (U44028) CKC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219670
Seq. ID
                  LIB3149-029-Q1-K1-F7
Method
                  BLASTX
                  g2160168
NCBI GI
BLAST score
                  610
                  1.0e-63
E value
Match length
                  137
                  87
% identity
NCBI Description
                  (AC000132) Strong similarity to R. communis
                  phosphoglycerate mutase (gb X70652). ESTs
                  gb T41853, gb T76648 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  219671
                  LIB3149-029-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  422
E value
                  1.0e-41
                  90
Match length
                  92
% identity
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                  sativa] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                   [Oryza sativa]
                  219672
Seq. No.
```

30922

LIB3149-029-Q1-K1-F9

BLASTX



```
NCBI GI
                   g2529675
BLAST score
                   231
                   3.0e-19
E value
Match length
                   77
% identity
                   61
                   (AC002535) putative AP2 domain containing protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   219673
Seq. ID
                   LIB3149-029-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g3482917
BLAST score
                   211
                   6.0e-17
E value
Match length
                   49
                   76
% identity
NCBI Description
                   (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
                   gi_2276344, gi_2829880, gi_2352919 and others. [Arabidopsis
                   thaliana]
Seq. No.
                   219674
Seq. ID
                   LIB3149-029-Q1-K1-G12
Method
                   BLASTN
NCBI GI
                   g2687434
BLAST score
                   334
E value
                   0.0e + 00
Match length
                   419
% identity
                   95
NCBI Description
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
                   partial sequence
                   219675
Seq. No.
                   LIB3149-029-Q1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4415996
BLAST score
                   531
E value
                   2.0e-54
Match length
                   115
% identity
                   87
NCBI Description
                  (AF059290) beta-tubulin 4 [Eleusine indica]
Seq. No.
                   219676
                   LIB3149-029-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3935167
BLAST score
                   203
                   2.0e-16
E value
                   43
Match length
% identity
                   88
NCBI Description
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
                   219677
Seq. No.
                   LIB3149-029-Q1-K1-G7
Seq. ID
```

Method BLASTX
NCBI GI g4580384
BLAST score 288
E value 6.0e-26

BLAST score

290

```
Match length
                  58
% identity
                  98
NCBI Description
                  (AC007184) putative histone H2B [Arabidopsis thaliana]
Seq. No.
                  219678
Seq. ID
                  LIB3149-029-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q464987
BLAST score
                  663
                  8.0e-70
E value
                  124
Match length
                  97
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi 421858 pir S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >gi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  219679
Seq. No.
                  LIB3149-029-Q1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2661840
BLAST score
                  382
                  6.0e-37
E value
                  116
Match length
% identity
                  59
NCBI Description
                 (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  219680
Seq. ID
                  LIB3149-029-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q2832664
BLAST score
                  187
                  4.0e-14
E value
Match length
                  78
% identity
                  45
NCBI Description
                  (AL021710) pollen-specific protein - like [Arabidopsis
                  thaliana]
                  219681
Seq. No.
                  LIB3149-029-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1370589
BLAST score
                  188
                  4.0e-14
E value
Match length
                  88
% identity
                  51
NCBI Description
                  (X98304) protein induced upon tuberization [Solanum
                  demissum]
                  219682
Seq. No.
                  LIB3149-030-Q1-K1-A10
Seq. ID
Method
                  BLASTX
                  g4206196
NCBI GI
```



E value 3.0e-26 Match length 90 % identity 67 NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] Seq. No. 219683 Seq. ID LIB3149-030-Q1-K1-A12 Method BLASTX NCBI GI q1888557 BLAST score 545 5.0e-56 E value Match length 124 % identity 78 NCBI Description (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius] Seq. No. 219684 Seq. ID LIB3149-030-Q1-K1-A2 Method BLASTX NCBI GI q1172873 BLAST score 423 8.0e-42 E value 85 Match length % identity 74 CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719 NCBI Description drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana] Seq. No. 219685 Seq. ID LIB3149-030-Q1-K1-A5 Method BLASTX NCBI GI q399900 BLAST score 189 E value 2.0e-14 Match length 96 47 % identity HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) NCBI Description (HD-ZIP PROTEIN ATHB-1) >gi 99659 pir S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana] 219686 Seq. No. Seq. ID LIB3149-030-Q1-K1-A8

Method BLASTX NCBI GI g2160322 BLAST score 422 1.0e-41 E value Match length 101 79 % identity

NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana

sylvestris]

219687 Seq. No.

LIB3149-030-Q1-K1-B1 Seq. ID

Method BLASTX

NCBI GI

E value

BLAST score

g3850823

329 9.0e-31



```
NCBI GI
                  q464707
BLAST score
                  457
E value
                  8.0e-46
                  104
Match length
                  84
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343 emb_CAA82273_ (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi_434906_emb CAA82275_ (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                  gb_R30430 come from this gene. [Arabidopsis thaliana]
                  >qi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
                  219688
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-B10
                  BLASTX
Method
NCBI GI
                  g4512122
BLAST score
                  543
E value
                  1.0e-55
                  145
Match length
                  74
% identity
NCBI Description
                 (AF131219) chorismate mutase 3 [Arabidopsis thaliana]
                  219689
Seq. No.
                  LIB3149-030-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g231660
BLAST score
                  360
E value
                  2.0e-34
Match length
                  122
% identity
                  57
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.
                  219690
Seq. ID
                  LIB3149-030-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1899188
BLAST score
                  260
E value
                  1.0e-22
Match length
                  103
% identity
                  38
NCBI Description
                 (U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.
                  219691
                  LIB3149-030-Q1-K1-B3
Seq. ID
Method
                  BLASTX
```



```
Match length 122
% identity 53
NCBI Description (Y1
[Ni
```

(Y18351) U2 snRNP auxiliary factor, large subunit

[Nicotiana plumbaginifolia]

Seq. No. 219692

Seq. ID LIB3149-030-Q1-K1-B4

Method BLASTX
NCBI GI g3337361
BLAST score 557
E value 2.0e-57
Match length 139
% identity 71

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 219693

Seq. ID LIB3149-030-Q1-K1-B7

Method BLASTX
NCBI GI g2244734
BLAST score 570
E value 4.0e-59
Match length 113
% identity 98

NCBI Description (D88414) actin [Gossypium hirsutum]

Seq. No. 219694

Seq. ID LIB3149-030-Q1-K1-B9

Method BLASTX
NCBI GI g1703108
BLAST score 482
E value 1.0e-48
Match length 122
% identity 80

NCBI Description ACTIN 2/7 >gi 2129525 pir S71210 actin 2 - Arabidopsis

thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 219695

Seq. ID LIB3149-030-Q1-K1-C5

Method BLASTX
NCBI GI g132866
BLAST score 609
E value 1.0e-63
Match length 116
% identity 97

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi 71086 pir R5NT2

ribosomal protein L2 - common tobacco chloroplast >gi_435269 emb_CAA77384_ (Z00044) ribosomal protein L2

[Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044)

ribosomal protein L2 [Nicotiana tabacum]

>gi_225238_prf__1211235BW ribosomal protein L2 [Nicotiana

tabacum]

Seq. No. 219696

Seq. ID LIB3149-030-Q1-K1-C6

Method

NCBI GI

BLASTX

g4559388



```
Method
                  BLASTX
NCBI GI
                  q2911044
BLAST score
                  119
                  9.0e-12
E value
Match length
                  107
% identity
                  43
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
                  219697
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2501578
BLAST score
                  577
                  8.0e-60
E value
Match length
                  127
% identity
                  91
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  219698
Seq. No.
                  LIB3149-030-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501850
BLAST score
                  502
                  6.0e-51
E value
Match length
                  101
% identity
                  92
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
Seq. No.
                  219699
Seq. ID
                  LIB3149-030-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2853081
BLAST score
                  174
E value
                  2.0e-12
Match length
                  55
% identity
                  60
                  (AL021768) ATP binding protein - like [Arabidopsis
NCBI Description
                  thaliana]
                  219700
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2853081
BLAST score
                  163
                  3.0e-11
E value
Match length
                  55
                  56
% identity
NCBI Description
                  (AL021768) ATP binding protein - like [Arabidopsis
                  thaliana]
Seq. No.
                  219701
                  LIB3149-030-Q1-K1-D4
Seq. ID
```

E value Match length

92



```
BLAST score
                 321
E value
                  1.0e-29
Match length
                  90
% identity
                  58
NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]
                  219702
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2911044
BLAST score
                  160
                  5.0e-15
E value
Match length
                  119
% identity
                  44
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219703
                  LIB3149-030-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3702332
BLAST score
                  465
                  1.0e-46
E value
                  127
Match length
% identity
                  68
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  219704
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-D8
Method
                  BLASTX
                  q2129709
NCBI GI
BLAST score
                  226
                  1.0e-18
E value
                  105
Match length
% identity
                  43
                  reverse transcriptase - Arabidopsis thaliana
NCBI Description
                  retrotransposon Tall-1 >gi_976278 (L47193) reverse
                  transcriptase [Arabidopsis thaliana]
Seq. No.
                  219705
                  LIB3149-030-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g2499498
NCBI GI
                  197
BLAST score
                  3.0e-15
E value
                  119
Match length
                  42
% identity
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC
NCBI Description
                  >gi 1161602 emb CAA88840 (Z48976) phosphoglycerate kinase
                   (PGK) [Nicotiana tabacum]
Seq. No.
                  219706
                  LIB3149-030-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1053047
BLAST score
                  460
                  5.0e-46
```

BLAST score

Match length

E value

591 2.0e-61

126



```
% identity
                   100
NCBI Description
                   (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
                   histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
                   219707
Seq. No.
Seq. ID
                   LIB3149-030-Q1-K1-E11
Method
                   BLASTX
NCBI GI
                   q1076583
BLAST score
                   147
                   2.0e-09
E value
Match length
                   38
% identity
                   82
NCBI Description histone H3 variant H3.3 - tomato (fragment)
                   219708
Seq. No.
Seq. ID
                   LIB3149-030-Q1-K1-E12
Method
                   BLASTX
NCBI GI
                   q2833311
BLAST score
                   261
E value
                   1.0e-22
Match length
                   75
                   64
% identity
NCBI Description
                   HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III
                   >gi 630728 pir S43605 R07E5.13 protein (clone R07E5) -
                   Caenorhabditis elegans >gi_3878946_emb_CAA83622_ (Z32683)
                   R07E5.13 [Caenorhabditis elegans]
Seq. No.
                   219709
Seq. ID
                   LIB3149-030-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g2829899
BLAST score
                   242
E value
                   2.0e-20
Match length
                   107
% identity
                   43
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   219710
                   LIB3149-030-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1877397
BLAST score
                   190
                   2.0e-14
E value
                   45
Match length
                   80
% identity
NCBI Description
                  (Y11591) shaggy-like kinase [Ricinus communis]
Seq. No.
                   219711
                   LIB3149-030-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131276
```



```
% identity
                   PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
NCBI Description
                   PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast
                   >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein
                   [Nicotiana tabacum] >gi 225224_prf__1211235BF photosystem
                   II P680 apoprotein [Nicotiana tabacum]
                   219712
Seq. No.
                   LIB3149-030-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g730645
NCBI GI
BLAST score
                   546
                   4.0e-56
E value
                   119
Match length
                   91
% identity
                   40S RIBOSOMAL PROTEIN S15 >gi 629556 pir _S43412 ribosomal
NCBI Description
                   protein S15 - Arabidopsis thaliana >gi 313152_emb_CAA80679_
                   (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                   >gi_313188_emb_CAA80681 (Z23162) ribosomal protein S15
                   [Arabidopsis thaliana] >gi 1903366 gb AAB70449 (AC000104)
                   Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                   gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                   thaliana]
                   219713
Seq. No.
                   LIB3149-030-Q1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4204095
BLAST score
                   425
                   5.0e-42
E value
Match length
                   123
                   63
% identity
NCBI Description (AF030260) CYP94A1 [Vicia sativa]
Seq. No.
                   219714
                   LIB3149-030-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454097
BLAST score
                   272
                   5.0e-24
E value
                   67
Match length
                   76
% identity
NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]
                   219715
Seq. No.
                   LIB3149-030-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   g2055384
NCBI GI
                   258
BLAST score
                   2.0e-22
E value
Match length
                   93
                   33
% identity
```

Seq. No. 219716

Seq. ID LIB3149-030-Q1-K1-G11

30931

NCBI Description (U69633) cold-stress inducible protein [Solanum tuberosum]



```
Method
                  BLASTX
NCBI GI
                  g2266949
BLAST score
                  627
                  1.0e-65
E value
Match length
                  131
                  92
% identity
                  (AF008940) phosphoenolpyruvate carboxylase 2 [Gossypium
NCBI Description
                  hirsutum]
                  219717
Seq. No.
                  LIB3149-030-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2196878
BLAST score
                  545
                  6.0e-56
E value
                  108
Match length
% identity
                  92
                  (Y08292) NADH glutamate dehydrogenase [Nicotiana
NCBI Description
                  plumbaginifolia]
                  219718
Seq. No.
                  LIB3149-030-Q1-K1-G3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q767700
BLAST score
                  .41
                  3.0e-14
E value
Match length
                  117
                  84
% identity
NCBI Description
                  Carrot mRNA for DNA-binding protein (transcriptional
                  regulator), partial cds, CHB6
Seq. No.
                  219719
                  LIB3149-030-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g4530066
NCBI GI
BLAST score
                  238
                  5.0e-20
E value
Match length
                  119
% identity
                  39
NCBI Description
                  (AF060544) androgen receptor associated protein 54 [Homo
                  sapiens]
                  219720
Seq. No.
```

LIB3149-030-Q1-K1-G7 Seq. ID

Method BLASTX NCBI GI g112863 BLAST score 670 1.0e-70 E value Match length 135 87 % identity

STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR NCBI Description

>gi_100227_pir__S12209 hypothetical protein - tomato >gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon

esculentum]

219721 Seq. No.

Seq. ID LIB3149-030-Q1-K1-G8



```
BLASTX
Method
NCBI GI
                  g112863
BLAST score
                  615
                  3.0e-64
E value
Match length
                  134
% identity
                  82
NCBI Description
                  STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
                  >gi 100227 pir S12209 hypothetical protein - tomato
                  >gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon
                  esculentum]
                  219722
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4235430
BLAST score
                  444
                  4.0e-44
E value
Match length
                  136
                  68
% identity
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
                  219723
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-H12
                  BLASTX
Method
NCBI GI
                  g1477428
BLAST score
                  652
                  2.0e-68
E value
Match length
                  141
                  89
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
                  219724
Seq. No.
Seq. ID
                  LIB3149-030-Q1-K1-H4
                  BLASTX
Method
NCBI GI
                  g3005065
BLAST score
                  471
                  2.0e-47
E value
Match length
                  125
                  68
% identity
NCBI Description (AF043325) N-myristoyltransferase 2 [Homo sapiens]
Seq. No.
                  219725
Seq. ID
                  LIB3149-030-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3212870
BLAST score
                  165
E value
                  5.0e-12
Match length
                  54
% identity
                  67
NCBI Description
                  (AC004005) putative N-myristoyltransferase [Arabidopsis
                  thaliana]
```

Seq. No. 219726

Seq. ID LIB3149-030-Q1-K1-H8

Method BLASTX NCBI GI g1173194 BLAST score 531



2.0e-54 E value Match length 117 85 % identity 30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) NCBI Description >gi 2119093 pir S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi 16767 emb CAA79013 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021 (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi 1515107 emb CAA60413 (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana] 219727 Seq. No.

Seq. ID LIB3149-030-Q1-K1-H9 Method BLASTX NCBI GI g1173194 BLAST score 348 E value 4.0e-33 98 Match length 71 % identity

NCBI Description

30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi 2119093 pir S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]

>gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi 1515107 emb CAA60413 (X86734) plastid ribosomal protein S13 [Arabidopsis

thaliana]

219728 Seq. No.

Seq. ID LIB3149-031-Q1-K1-A1

Method BLASTX q2497543 NCBI GI BLAST score 277 1.0e-24 E value Match length 112 % identity 50

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir \$41379

pyruvate kinase - common tobacco >qi 444023 emb CAA82628

(Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 219729

Seq. ID LIB3149-031-Q1-K1-A10

Method BLASTX NCBI GI g303742 BLAST score 472 E value 2.0e-47 Match length 95 % identity 97

NCBI Description (D12544) GTP-binding protein [Pisum sativum]

>gi 738936 prf 2001457D GTP-binding protein [Pisum

sativum]

Method

NCBI GI

E value

BLAST score

BLASTX

162

q3914136

4.0e-11



```
Seq. No.
                  219730
Seq. ID
                  LIB3149-031-Q1-K1-A11
                  BLASTX
Method
NCBI GI
                  g2829275
BLAST score
                  275
                  2.0e-24
E value
                  108
Match length
% identity
                  55
                  (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                  thaliana] >qi 3513740 (AF080118) contains similarity to
                  nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                  301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1
                  (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                  [Arabidopsis thaliana]
                  219731
Seq. No.
Seq. ID
                  LIB3149-031-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  q2764941
                  303
BLAST score
                  9.0e-28
E value
Match length
                  82
% identity
                  66
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  219732
Seq. No.
Seq. ID
                  LIB3149-031-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2500376
BLAST score
                  486
E value
                  4.0e-49
Match length
                  102
% identity
                  92
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
                  (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.
                  219733
Seq. ID
                  LIB3149-031-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q267073
BLAST score
                  419
E value
                  3.0e-58
Match length
                  118
                  99
% identity
                 TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  219734
                  LIB3149-031-Q1-K1-B2
Seq. ID
```

```
Match length
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein
                  [Cicer arietinum]
                  219735
Seq. No.
Seq. ID
                  LIB3149-031-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q1711572
BLAST score
                  472
                  1.0e-47
E value
                  94
Match length
                  91
% identity
                  SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR
NCBI Description
                  (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)
                  >gi 1076415 pir S30579 succinate--CoA ligase (GDP-forming)
                  (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment)
                  >gi 16510 emb CAA48891 (X69138) succinate--CoA ligase
                  (GDP-forming) [Arabidopsis thaliana]
                  219736
Seq. No.
Seq. ID
                  LIB3149-031-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  g2642435
BLAST score
                  305
                  4.0e-28
E value
Match length
                  70
                  76
% identity
NCBI Description (AC002391) MYB-related protein [Arabidopsis thaliana]
Seq. No.
                  219737
                  LIB3149-031-Q1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3334197
BLAST score
                  629
E value
                  7.0e-66
Match length
                  127
                  94
% identity
NCBI Description
                  AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T
                  PROTEIN) >gi 2894400 emb CAA94902 (Z71184) T-protein
                  [Flaveria anomala]
Seq. No.
                  219738
Seq. ID
                  LIB3149-031-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g547886
BLAST score
                  384
                  2.0e-43
E value
Match length
                  111
% identity
                  83
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                  (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >qi 542102 pir S42939 malate dehydrogenase
```

30936

(oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor - Flaveria pringlei >gi_1084444_pir__S52016 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)



(EC 1.1.1.40) - Flaveria pringlei >gi_459441_emb_CAA54986_ (X78069) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Flaveria pringlei]

Seq. No. 219739

Seq. ID LIB3149-031-Q1-K1-C4

Method BLASTX
NCBI GI g1222552
BLAST score 494
E value 3.0e-50
Match length 107
% identity 82

NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]

Seq. No. 219740

Seq. ID LIB3149-031-Q1-K1-C7

Method BLASTX
NCBI GI g4490705
BLAST score 497
E value 2.0e-50
Match length 113
% identity 88

NCBI Description (AL035680) ribosomal protein L14-like protein [Arabidopsis

thaliana]

Seq. No. 219741

Seq. ID LIB3149-031-Q1-K1-C9

Method BLASTX
NCBI GI g3297815
BLAST score 248
E value 3.0e-21
Match length 60
% identity 78

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 219742

Seq. ID LIB3149-031-Q1-K1-D3

Method BLASTX
NCBI GI g2829899
BLAST score 283
E value 3.0e-25
Match length 121
% identity 46

NCBI Description (AC002311) similar to ripening-induced protein,

gp_AJ001449_2465015 and major#latex protein,

gp X91961 1107495 [Arabidopsis thaliana]

Seq. No. 219743

Seq. ID LIB3149-031-Q1-K1-D4

Method BLASTX
NCBI GI g2970641
BLAST score 695
E value 1.0e-73
Match length 131
% identity 92

NCBI Description (AF052194) xyloglucan endotransglycosylase precursor

[Actinidia deliciosa]

```
Seq. No.
                  219744
Seq. ID
                  LIB3149-031-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3395432
BLAST score
                  314
                  6.0e-29
E value
Match length
                  69
                  81
% identity
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
                  219745
Seq. No.
Seq. ID
                  LIB3149-031-Q1-K1-D6
                  BLASTX
Method
NCBI GI
                  q1439609
BLAST score
                  114
E value
                  1.0e-13
Match length
                  67
% identity
                  69
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  219746
Seq. ID
                  LIB3149-031-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3096949
BLAST score
                  338
                  8.0e-32
E value
Match length
                  82
% identity
                  82
NCBI Description
                  (Y16328) putative cyclic nucleotide-regulated ion channel
                   [Arabidopsis thaliana] >qi 3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.
                  219747
                  LIB3149-031-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  341
E value
                  4.0e-32
Match length
                  92
                  76
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
Seq. No.
                  219748
Seq. ID
                  LIB3149-031-Q1-K1-E1
Method
                  BLASTX
                  g112697
NCBI GI
BLAST score
                  301
                  2.0e-27
E value
Match length
                  107
                  62
% identity
NCBI Description
                  14 KD PROLINE-RICH PROTEIN DC2.15 PRECURSOR
```

>gi 486809 pir S35714 proline-rich protein, 14K, embryonic



- carrot >gi 18316 emb CAA33476 (X15436) 14 kD protein (AA

1-137) [Daucus carota] 219749 Seq. No. Seq. ID LIB3149-031-Q1-K1-E2 BLASTX Method NCBI GI g1653767 BLAST score 152 2.0e-10 E value 61 Match length 49 % identity (D90916) oligopeptidase A [Synechocystis sp.] NCBI Description 219750 Seq. No. LIB3149-031-Q1-K1-E4 Seq. ID ${\tt BLASTX}$ Method NCBI GI g3395441 BLAST score 378 1.0e-36 E value Match length 98 % identity 80 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana] 219751 Seq. No. Seq. ID LIB3149-031-Q1-K1-E6 Method BLASTX NCBI GI g120669 463 BLAST score 2.0e-46 E value 92 Match length 92 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66014 pir DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905_ (X60347) glyceraldehyde

3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 219752

LIB3149-031-Q1-K1-E7 Seq. ID

Method BLASTX q120669 NCBI GI BLAST score 285 6.0e-27 E value 82 Match length 79 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66014 pir DEJMG glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 219753

Seq. ID LIB3149-031-Q1-K1-E8

Method BLASTX NCBI GI g1420936 BLAST score 531 E value 2.0e-54

Match length

% identity

73

74



```
Match length
                  126
% identity
                  77
                  (U61396) Vigna unquiculata aspartic proteinase mRNA,
NCBI Description
                  complete cds. [Vigna unguiculata]
                  219754
Seq. No.
Seq. ID
                  LIB3149-031-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q2500354
BLAST score
                  293
                  2.0e-26
E value
                  63
Match length
% identity
                  87
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                  (AB001891) QM family protein [Solanum melongena]
Seq. No.
                  219755
                  LIB3149-031-Q1-K1-F3
Seq. ID
Method
                  BLASTN
                  q557681
NCBI GI
BLAST score
                  43
                  6.0e-15
E value
                  119
Match length
% identity
                  84
NCBI Description Z.mays mRNA for ribosomal protein S28
Seq. No.
                  219756
                  LIB3149-031-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                  438
                  2.0e-43
E value
Match length
                  104
                  80
% identity
                 40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  219757
Seq. ID
                  LIB3149-031-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  583
E value
                  2.0e-60
Match length
                  128
% identity
                  86
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  219758
                  LIB3149-031-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980781
BLAST score
                  273
E value
                  4.0e-24
```

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  219759
Seq. ID
                  LIB3149-031-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1856971
BLAST score
                  388
                  1.0e-37
E value
Match length
                  83
% identity
                  89
                  (D26058) This gene is specifically expressed at the S phase
NCBI Description
                  during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
Seq. No.
                  219760
Seq. ID
                  LIB3149-031-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3860250
BLAST score
                   377
                  2.0e-36
E value
Match length
                   129
% identity
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  219761
Seq. ID
                  LIB3149-031-Q1-K1-H7
                  BLASTN
Method
NCBI GI
                  g2244733
BLAST score
                   33
E value
                   4.0e-09
Match length
                   33
% identity
                  100
NCBI Description Cotton mRNA for actin, clone CF456, partial cds
Seq. No.
                  219762
                  LIB3149-031-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1666173
BLAST score
                   278
E value
                   4.0e-25
Match length
                  70
% identity
                  80
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
NCBI Description
Seq. No.
                  219763
                  LIB3149-031-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g498906
BLAST score
                   235
E value
                   3.0e-20
                  53
Match length
% identity
                   83
NCBI Description (U10046) ribosomal protein L27 homolog [Pisum sativum]
```

219764 Seq. No.

LIB3149-032-Q1-K1-A10 Seq. ID

Method BLASTX NCBI GI g3319342



```
279
BLAST score
                   8.0e-25
E value
                  95
Match length
                   30
% identity
                  (AF077407) similar to mitochondrial carrier proteins (Pfam:
NCBI Description
                  mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                  thaliana]
                   219765
Seq. No.
                  LIB3149-032-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  g3688177
NCBI GI
                   531
BLAST score
                  2.0e-54
E value
                  142
Match length
                   70
% identity
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   219766
Seq. No.
                  LIB3149-032-Q1-K1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1399380
BLAST score
                   649
                   3.0e-68
E value
                   133
Match length
                   87
% identity
NCBI Description
                  (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
                  methyltransferase [Glycine max]
                   219767
Seq. No.
                  LIB3149-032-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                   g2739376
NCBI GI
                   383
BLAST score
                   5.0e - 37
E value
                   112
Match length
% identity
                   69
                  (AC002505) putative permease [Arabidopsis thaliana]
NCBI Description
                   219768
Seq. No.
                   LIB3149-032-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3688177
BLAST score
                   183
E value
                   4.0e-14
Match length
                   66
% identity
                   58
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
                   219769
Seq. No.
                   LIB3149-032-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1171978
BLAST score
                   257
E value
                   3.0e-22
```

76

67

Match length % identity

Method

NCBI GI

BLASTX

g1710424



```
NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                  (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                  [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                  219770
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2136139
                  297
BLAST score
                  5.0e-27
E value
Match length
                  124
% identity
                  14
                  sds22 protein homolog - human >gi 1085028 emb CAA90626
NCBI Description
                  (Z50749) yeast sds22 homolog [Homo sapiens]
                  >qi 1585165 prf 2124310A sds22 gene [Homo sapiens]
                  >gi 4506013 ref NP 002703.1 pPPP1R7 protein phosphatase 1,
                  regulatory subunit
Seq. No.
                  219771
Seq. ID
                  LIB3149-032-Q1-K1-B10
                  BLASTX
Method
NCBI GI
                  g1928981
BLAST score
                  558
                  1.0e-57
E value
Match length
                  117
                  62
% identity
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  219772
                  LIB3149-032-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710424
                  305
BLAST score
                  1.0e-28
E value
                  79
Match length
                  86
% identity
                  50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
NCBI Description
                  >gi 2129718_pir__S71282 ribosomal protein L21 - Arabidopsis
                  thaliana >gi 1149573_emb_CAA89887_ (Z49787) chloroplast
                  ribosomal large subunit protein L21 [Arabidopsis thaliana]
Seq. No.
                  219773
                  LIB3149-032-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g3738315
NCBI GI
BLAST score
                  153
E value
                  3.0e-27
Match length
                  95
                  73
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                  219774
Seq. No.
                  LIB3149-032-Q1-K1-B6
Seq. ID
```



```
197
BLAST score
E value
                  2.0e-15
                  90
Match length
                  61
% identity
                  50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
NCBI Description
                  >gi 2129718 pir S71282 ribosomal protein L21 - Arabidopsis
                  thaliana >gi 1149573_emb_CAA89887_ (Z49787) chloroplast
                  ribosomal large subunit protein L21 [Arabidopsis thaliana]
                  219775
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-B7
                  BLASTX
```

Method BLASTX
NCBI GI g3695383
BLAST score 572
E value 3.0e-59
Match length 118
% identity 88

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis

thaliana]

Seq. No. 219776

Seq. ID LIB3149-032-Q1-K1-B9

Method BLASTN
NCBI GI g3128141
BLAST score 33
E value 6.0e-09
Match length 45

Match length 45
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQD22, complete sequence [Arabidopsis thaliana]

Seq. No. 219777

Seq. ID LIB3149-032-Q1-K1-C10

Method BLASTX
NCBI GI g495725
BLAST score 453
E value 3.0e-45
Match length 133
% identity 69

NCBI Description (L25042) acetyl-CoA carboxylase [Medicago sativa]

Seq. No. 219778

Seq. ID LIB3149-032-Q1-K1-C11

Method BLASTX
NCBI GI g445612
BLAST score 353
E value 2.0e-33
Match length 70
% identity 96

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 219779

Seq. ID LIB3149-032-Q1-K1-C12

Method BLASTX NCBI GI g3600047 BLAST score 456



67

% identity

```
E value
                  1.0e-45
Match length
                  124
                  71
% identity
                  (AF080120) similar to elongation factor EF-Ts [Arabidopsis
NCBI Description
                  thaliana]
                  219780
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3319882
BLAST score
                  661
                  1.0e-69
E value
                  129
Match length
                  98
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                  arietinum]
                  219781
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-C3
Method
                  BLASTX
                  g2894592
NCBI GI
BLAST score
                  407
                  8.0e-40
E value
                  92
Match length
                  78
% identity
NCBI Description (AL021889) predicted protein [Arabidopsis thaliana]
                  219782
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-C4
Method
                  BLASTX
                  q495725
NCBI GI
                  313
BLAST score
                  6.0e-29
E value
                  117
Match length
% identity
                  56
                  (L25042) acetyl-CoA carboxylase [Medicago sativa]
NCBI Description
                  219783
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4158221
BLAST score
                  679
                  1.0e-71
E value
Match length
                  140
                  88
% identity
NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
Seq. No.
                  219784
                  LIB3149-032-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351365
BLAST score
                  183
E value
                  1.0e-13
                  51
Match length
```

30945

(CR6) >gi 2130002 pir S68969 ubiquinol--cytochrome-c

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN



reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768_
(X82325) cytochrome c reductase subunit [Solanum tuberosum]

Seq. No. 219785

Seq. ID LIB3149-032-Q1-K1-C9

Method BLASTX
NCBI GI 94204761
BLAST score 353
E value 1.0e-33
Match length 92
% identity 73

NCBI Description (U51192) peroxidase precursor [Glycine max]

Seq. No. 219786

Seq. ID LIB3149-032-Q1-K1-D12

Method BLASTX
NCBI GI g1707955
BLAST score 614
E value 4.0e-64
Match length 119
% identity 97

NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1

(GLUTAMATE--AMMONIA LIGASE) >gi 1134896 emb CAA63981

(X94320) glutamine synthetase [Vitis vinifera]

Seq. No. 219787

Seq. ID LIB3149-032-Q1-K1-D3

Method BLASTX
NCBI GI g1350930
BLAST score 281
E value 4.0e-25
Match length 55
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S13

Seq. No. 219788

Seq. ID LIB3149-032-Q1-K1-D4

Method BLASTX
NCBI GI g119530
BLAST score 266
E value 3.0e-23
Match length 140
% identity 18

NCBI Description PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR

(ERP72) >gi_87320_pir__A23723 protein disulfide-isomerase (EC 5.3.4.1) ERp72 precursor - human >gi_181508 (J05016) protein disulfide isomerase-related protein [Homo sapiens]

Seq. No. 219789

Seq. ID LIB3149-032-Q1-K1-D5

Method BLASTX
NCBI GI g119530
BLAST score 230
E value 4.0e-19
Match length 100
% identity 17

NCBI Description PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR

90

% identity

(ERP72) >gi_87320_pir__A23723 protein disulfide-isomerase (EC 5.3.4.1) ERp72 precursor - human >gi_181508 (J05016) protein disulfide isomerase-related protein [Homo sapiens]

219790 Seq. No. LIB3149-032-Q1-K1-D7 Seq. ID BLASTX Method NCBI GI q3297815 506 BLAST score 1.0e-51 E value 119 Match length 79 % identity (AL031032) putative protein [Arabidopsis thaliana] NCBI Description 219791 Seq. No. LIB3149-032-Q1-K1-D8 Seq. ID BLASTX Method NCBI GI g3288823 BLAST score 292 2.0e-26 E value 81 Match length 68 % identity (AF063852) FUS5 [Arabidopsis thaliana] NCBI Description 219792 Seq. No. Seq. ID LIB3149-032-Q1-K1-E1 BLASTX Method q3281858 NCBI GI BLAST score 547 E value 3.0e-56129 Match length 81 % identity (AL031004) ribosomal protein S6 - like [Arabidopsis NCBI Description thaliana] 219793 Seq. No. LIB3149-032-Q1-K1-E11 Seq. ID BLASTX Method g1173218 NCBI GI BLAST score 452 2.0e-45 E value Match length 99 98 % identity 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal NCBI Description protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] 219794 Seq. No. LIB3149-032-Q1-K1-F1 Seq. ID Method BLASTX g120669 NCBI GI 619 BLAST score 1.0e-64 E value Match length 136

30947

>gi 66014 pir DEJMG glyceraldehyde-3-phosphate

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

Seq. ID



dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >qi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

```
219795
Seq. No.
                  LIB3149-032-Q1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2245069
                  263
BLAST score
                  3.0e-24
E value
                  78
Match length
                  71
% identity
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  219796
Seq. No.
Seq. ID
                  LIB3149-032-Q1-K1-F2
Method
                  BLASTX
                   g3820648
NCBI GI
BLAST score
                   308
                   3.0e-28
E value
                   78
Match length
                   71
% identity
                  (Y12636) allene oxide synthase [Arabidopsis thaliana]
NCBI Description
                   219797
Seq. No.
                   LIB3149-032-Q1-K1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1931652
BLAST score
                   347
E value
                   9.0e-33
Match length
                   93
                   70
% identity
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   219798
Seq. No.
                   LIB3149-032-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   g1332579
NCBI GI
BLAST score
                   663
                   7.0e-70
E value
Match length
                   135
                   10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                   219799
                   LIB3149-032-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4539350
NCBI GI
BLAST score
                   159
                   1.0e-10
E value
Match length
                   48
% identity
                   60
                  (AL035539) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   219800
Seq. No.
                   LIB3149-032-Q1-K1-G4
```

% identity



```
Method
                  BLASTX
NCBI GI
                  g3023651
BLAST score
                  150
                  1.0e-09
E value
Match length
                  49
                  59
% identity
                  D-LACTATE DEHYDROGENASE [CYTOCHROME] PRECURSOR (D-LACTATE
NCBI Description
                  FERRICYTOCHROME C OXIDOREDUCTASE) (D-LCR)
                  >gi 1076962 pir S51528 D-lactate dehydrogenase
                  (cytochrome) (EC 1.1.2.4) - yeast (Kluyveromyces marxianus
                  var. lactis) >gi 602029 emb CAA50635 (X71628) D-lactate
                  dehydrogenase (cytochrome) [Kluyveromyces lactis]
Seq. No.
                  219801
Seq. ID
                  LIB3149-032-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  q1495251
BLAST score
                  559
E value
                  1.0e-57
                  123
Match length
% identity
                  86
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219802
                  LIB3149-032-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  q4406780
NCBI GI
BLAST score
                  420
E value
                  2.0e-41
Match length
                  93
% identity
                  84
                  (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  219803
                  LIB3149-032-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346524
BLAST score
                  468
E value
                   5.0e-47
Match length
                   94
% identity
                   96
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 497900
                   (M73430) S-adenosyl methionine synthetase [Populus
                  deltoides]
                   219804
Seq. No.
                  LIB3149-032-Q1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score
                   41
E value
                  5.0e-14
                  53
Match length
                   94
```

30949

MSJ1, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:



```
Seq. No.
                  219805
                  LIB3149-032-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2493045
                   470
BLAST score
                   3.0e-47
E value
Match length
                   110
% identity
                   81
                  ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi 1655484 dbj BAA13601 (D88376) delta-prime subunit of
                   mitochondrial F1-ATPase [Arabidopsis thaliana]
Seq. No.
                   219806
                   LIB3149-033-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3880858
BLAST score
                   161
E value
                   5.0e-11
Match length
                   115
                   32
% identity
                  (AL031633) predicted using Genefinder; cDNA EST yk304f12.5
NCBI Description
                   comes from this gene [Caenorhabditis elegans]
Seq. No.
                   219807
Seq. ID
                   LIB3149-033-Q1-K1-A12
                   BLASTX
Method
NCBI GI
                   g266945
BLAST score
                   531
E value
                   2.0e-54
Match length
                   122
                   87
% identity
                   60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                   >qi 100065 pir S19978 ribosomal protein L9 - garden pea
                   >qi 20727 emb CAA46273 (X65155) GA [Pisum sativum]
                   >gi_12796\overline{4}5 emb CAA659\overline{8}7 (X97322) ribosomal protein L9
                   [Pisum sativum]
Seq. No.
                   219808
Seq. ID
                   LIB3149-033-Q1-K1-A6
                   BLASTX
Method
NCBI GI
                   q464981
BLAST score
                   636
                   1.0e-66
E value
Match length
                   119
% identity
                   98
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
                   219809
Seq. No.
                   LIB3149-033-Q1-K1-A7
Seq. ID
Method
                   BLASTX
                   q135452
NCBI GI
BLAST score
                   605
```

30950

5.0e-63

136

E value

Match length



```
% identity
                  TUBULIN BETA-1 CHAIN >gi_170060 (M21296) S-beta-1 tubulin
NCBI Description
                  [Glycine max]
                  219810
Seq. No.
                  LIB3149-033-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  q3080428
NCBI GI
                  421
BLAST score
                  2.0e-41
E value
                  124
Match length
                  63
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  219811
Seq. No.
                  LIB3149-033-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g1173223
NCBI GI
                  490
BLAST score
E value
                  2.0e-49
                  100
Match length
                  93
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal
                  protein S11 [Glycine max]
                  219812
Seq. No.
                  LIB3149-033-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g2760330
NCBI GI
BLAST score
                  496
                  3.0e-50
E value
                  123
Match length
                  75
% identity
NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]
                   219813
Seq. No.
Seq. ID
                   LIB3149-033-Q1-K1-B12
                   BLASTX
Method
                   g3757522
NCBI GI
BLAST score
                   368
                   3.0e - 35
E value
Match length
                   98
                   68
% identity
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                   219814
                   LIB3149-033-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g1222552
NCBI GI
BLAST score
                   626
E value
                   2.0e-65
Match length
                   132
                   86
% identity
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
```

 Seq. No.
 219815

 Seq. ID
 LIB3149-033-Q1-K1-B4

```
BLASTX
 Method
 NCBI GI
                    q3212869
                    341
 BLAST score
                    2.0e-32
 E value
 Match length
                    98
 % identity
                    (AC004005) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    219816
 Seq. No.
                    LIB3149-033-Q1-K1-B6
 Seq. ID
                    BLASTX
 Method
                    q133939
 NCBI GI
 BLAST score
                    185
                    2.0e-14
 E value
                    36
 Match length
                    92
  % identity
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70865 pir R3NT3
 NCBI Description
                    ribosomal protein S3 - common tobacco chloroplast
                    >gi_11865_emb_CAA77381_ (Z00044) ribosomal protein S3
                    [Nicotiana tabacum] >qi 225235 prf 1211235BT ribosomal
                    protein S3 [Nicotiana tabacum]
                    219817
  Seq. No.
  Seq. ID
                    LIB3149-033-Q1-K1-B7
Method
                    BLASTX
                    q544134
  NCBI GI
                    340
  BLAST score
                    6.0e-32
  E value
  Match length
                    124
  % identity
                    59
                    DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
  NCBI Description
                    >gi_99720_pir__S22863 hypothetical protein - Arabidopsis
                    thaliana >gi_421844_pir__A46260 RecA functional analog
                    DRT100 - Arabidopsis thaliana (fragment)
                    219818
  Seq. No.
                    LIB3149-033-Q1-K1-C1
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q3860277
  BLAST score
                    584
                    1.0e-60
  E value
                    143
  Match length
                    81
  % identity
                    (ACO05824) putative ribosomal protein L10 [Arabidopsis
  NCBI Description
                    thaliana] >gi 4314394 gb AAD15604_ (AC006232) putative
                    ribosomal protein L10A [Arabidopsis thaliana]
```

Seq. ID LIB3149-033-Q1-K1-C11

Method BLASTX
NCBI GI g285741
BLAST score 434
E value 6.0e-43
Match length 140
% identity 62

NCBI Description (D14550) EDGP precursor [Daucus carota]



```
219820
Seq. No.
                  LIB3149-033-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  q3860277
NCBI GI
BLAST score
                  344
                  2.0e-32
E value
                  123
Match length
                  61
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi 4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  219821
Seq. No.
                  LIB3149-033-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g1895084
NCBI GI
BLAST score
                   306
                   2.0e-46
E value
Match length
                   116
                   84
% identity
                  (U89897) golgi associated protein se-wap41 [Zea mays]
NCBI Description
                   219822
Seq. No.
                   LIB3149-033-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g1890152
NCBI GI
                   204
BLAST score
                   4.0e-16
E value
Match length
                   80
% identity
                   50
                  (X92510) allene oxide synthase [Arabidopsis thaliana]
NCBI Description
                   219823
Seq. No.
                   LIB3149-033-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g4467095
NCBI GI
                   211
BLAST score
                   8.0e-17
E value
Match length
                   140
                   37
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   219824
Seq. No.
                   LIB3149-033-Q1-K1-C7
Seq. ID
Method
                   BLASTN
                   g167312
NCBI GI
                   58
BLAST score
                   6.0e-24
E value
                   58
Match length
                   100
% identity
                  Gossypium hirsutum vacuolar H+-ATPase catalytic subunit
NCBI Description
                   mRNA, complete cds
```

Seq. ID LIB3149-033-Q1-K1-C8

Method BLASTX NCBI GI g3193292



```
389
BLAST score
                   9.0e-38
E value
                   108
Match length
% identity
                   74
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   219826
Seq. No.
                   LIB3149-033-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1353157
                   221
BLAST score
E value
                   5.0e-18
Match length
                   114
                   39
% identity
                   HYPOTHETICAL 108.5 KD PROTEIN RO6F6.2 IN CHROMOSOME II
NCBI Description
                   >gi_3878900_emb_CAA86774_ (Z46794) similar to vacuolar biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from
                   this gene; cDNA EST EMBL:D34974 comes from this gene
                   [Caenorhabditis elegans]
                   219827 -
Seq. No.
                   LIB3149-033-Q1-K1-D3
Seq. ID
                 BLASTX
Method
NCBI GI
                   g3860247
BLAST score
                   678
E value
                   1.0e-71
                   134
Match length
                   95
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                   219828
Seq. No.
                   LIB3149-033-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2275215
BLAST score
                   372
E value
                   1.0e-35
Match length
                   131
                   57
% identity
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   219829
                   LIB3149-033-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2275215
BLAST score
                   386
E value
                   2.0e-37
Match length
                   125
% identity
                   62
```

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 219830

Seq. ID LIB3149-033-Q1-K1-D6

Method BLASTX NCBI GI g1125691 BLAST score 322

% identity

49



```
E value
                  8.0e-30
Match length
                  96
% identity
                  64
                  (X94301) DnaJ protein [Solanum tuberosum]
NCBI Description
Seq. No.
                  219831
Seq. ID
                  LIB3149-033-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2702268
BLAST score
                  555
                  4.0e-57
E value
Match length
                  140
% identity
                  71
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219832
                  LIB3149-033-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q567893
BLAST score
                  165
E value
                   9.0e-12
Match length
                  75
                  48
% identity
NCBI Description
                  (L37382) beta-galactosidase-complementation protein
                   [Cloning vector]
Seq. No.
                  219833
Seq. ID
                  LIB3149-033-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2369766
BLAST score
                  537
                  5.0e-55
E value
Match length
                  138
% identity
                  75
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                  219834
Seq. No.
                  LIB3149-033-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4377374
                  239
BLAST score
                   4.0e-20
E value
Match length
                  139
% identity
                   37
                  (AE001684) Adenosylmethionine-8-Amino-7-Oxononanoate
NCBI Description
                  Aminotransferase [Chlamydia pneumoniae]
                  219835
Seq. No.
                  LIB3149-033-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g3878134
NCBI GI
BLAST score
                   219
E value
                   9.0e-18
                  75
Match length
```

NCBI Description (Z68218) K01H12.1 [Caenorhabditis elegans]

Match length

% identity

110

75



```
Seq. No.
                   219836
Seq. ID
                   LIB3149-033-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   q3024127
BLAST score
                   752
                   3.0e-80
E value
                   141
Match length
% identity
                   98
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
                   219837
Seq. No.
Seq. ID
                  LIB3149-033-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   q544134
BLAST score
                   343
E value
                   3.0e-32
                   131
Match length
% identity
                   61
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
NCBI Description
                   >gi 99720 pir S22863 hypothetical protein - Arabidopsis
                   thaliana >gi 421844 pir A46260 RecA functional analog
                   DRT100 - Arabidopsis thaliana (fragment)
                   219838
Seq. No.
                   LIB3149-033-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   451
E value
                   6.0e-45
Match length
                   128
                   65
% identity
NCBI Description
                  (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   219839
                   LIB3149-033-Q1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4102858
BLAST score
                   40
                   2.0e-13
E value
                   44
Match length
                   98
% identity
NCBI Description
                  Populus tremuloides cytoplasmic superoxide dismutase 1
                   (SODcyt1) mRNA, complete cds
Seq. No.
                   219840
Seq. ID
                   LIB3149-033-Q1-K1-F8
Method
                  BLASTX
                   g122007
NCBI GI
BLAST score
                   408
                   5.0e-40
E value
```

>gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1

NCBI Description HISTONE H2A >gi 100161 pir S11498 histone H2A - parsley



42

% identity

- 149) [Petroselinum crispum]

```
219841
Seq. No.
                  LIB3149-033-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334441
                  301
BLAST score
                  2.0e-27
E value
                  142
Match length
                  29
% identity
                  HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II
NCBI Description
                  >gi 2642161 (AC003000) hypothetical protein [Arabidopsis
                  thaliana]
                  219842
Seq. No.
Seq. ID
                  LIB3149-033-Q1-K1-G11
                  BLASTX
Method
NCBI GI
                  q4337189
BLAST score
                  343
E value
                  2.0e-32
Match length
                  88
                  72
% identity
                  (AC006403) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  219843
Seq. No.
                  LIB3149-033-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  q3421413
NCBI GI
BLAST score
                  193
                  1.0e-14
E value
                  43
Match length
% identity
                   84
                  (AF081922) protein phosphatase 2A 55 kDa B regulatory
NCBI Description
                   subunit [Oryza sativa] >gi 3421415 (AF081923) protein
                  phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
                   219844
Seq. No.
                  LIB3149-033-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512667
BLAST score
                   609
                   2.0e-63
E value
Match length
                   144
                   77
% identity
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                   219845
                   LIB3149-033-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160166
BLAST score
                   281
E value
                   5.0e-25
Match length
                   136
```

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]



Seq. No. Seq. ID

219846

LIB3149-033-Q1-K1-G8

```
BLASTX
 Method
 NCBI GI
                   q116343
 BLAST score
                   236
                   8.0e-20
 E value
                   114
 Match length
 % identity
                   42
 NCBI Description BASIC ENDOCHITINASE PRECURSOR
                   219847
 Seq. No.
 Seq. ID
                   LIB3149-033-Q1-K1-G9
 Method
                   BLASTX
                   g4337189
 NCBI GI
                   386
 BLAST score
                   2.0e-37
 E value
                   130
 Match length
                   61
 % identity
 NCBI Description
                   (AC006403) putative calmodulin-binding protein [Arabidopsis
                   thaliana]
                   219848
 Seq. No.
                   LIB3149-033-Q1-K1-H1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2498882
 BLAST score
                   201
                   1.0e-15
 E value
                   101
 Match length
                   45
 % identity
                   SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120)
 NCBI Description
                   >qi 2146975 pir S60735 splicing factor SF3a 120K chain -
                   human >qi 899298 emb CAA59494 (X85237) human splicing
                   factor [Homo sapiens] >qi 3212998 (AC004997) spliceosome
                   associated protein 114 (SF3a) [Homo sapiens]
                   219849
 Seq. No.
 Seq. ID
                   LIB3149-033-Q1-K1-H5
                   BLASTX
 Method
NCBI GI
                   q542059
 BLAST score
                   476
                   7.0e-48
 E value
 Match length
                   94
 % identity
                   99
                   inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
 NCBI Description
                   >qi 457744 emb CAA54869 (X77915) inorganic pyrophosphatase
                    [Nicotiana tabacum]
                   219850
 Seq. No.
                   LIB3149-033-Q1-K1-H6
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g1854386
 BLAST score
                   484
 E value
                   8.0e-49
                   108
 Match length
                   83
 % identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
 NCBI Description
                   vinifera]
```

20 Sec. 15

```
219851
Seq. No.
Seq. ID
                  LIB3149-033-Q1-K1-H7
                  BLASTX
Method
                  g2582665
NCBI GI
BLAST score
                  653
                  1.0e-68
E value
                  142
Match length
                  89
% identity
                  (Z82983) thi [Citrus sinensis]
NCBI Description
                  219852
Seq. No.
Seq. ID
                  LIB3149-033-Q1-K1-H8
                  BLASTX
Method
                  g3805847
NCBI GI
                  377
BLAST score
                  3.0e-36
E value
                  140
Match length
                  54
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                  219853
Seq. No.
                  LIB3149-033-Q1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4090943
BLAST score
                  337
                  1.0e-31
E value
                  92
Match length
                  84
% identity
                  (AF029984) COP1 homolog [Lycopersicon esculentum]
NCBI Description
                  219854
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-A11
                  BLASTX
Method
NCBI GI
                  q464707
                  187
BLAST score
                  6.0e-26
E value
                  75
Match length
                  81
% identity
                  40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_434345_emb CAA82274 (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                   gb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
```

Seq. ID LIB3149-034-Q1-K1-A3

```
BLASTX
Method
NCBI GI
                  q3954807
                  562
BLAST score
                  5.0e-58
E value
Match length
                  133
% identity
                  (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus
NCBI Description
                  roseus]
                  219856
Seq. No.
                  LIB3149-034-Q1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244851
BLAST score
                  242
                  1.0e-20
E value
Match length
                  111
                  45
% identity
                  (Z97337) amine oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219857
Seq. ID
                  LIB3149-034-Q1-K1-B10
                  BLASTX
Method
                  g2282584
NCBI GI
BLAST score
                  496
E value
                  3.0e-50
Match length
                  101
                  94
% identity
                  (U76259) elongation factor 1-alpha [Zea mays]
NCBI Description
Seq. No.
                  219858
                  LIB3149-034-Q1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q731821
BLAST score
                   147
E value
                   3.0e-09
Match length
                   69
                   43
% identity
                  HYPOTHETICAL 36.1 KD PROTEIN IN RNR3-ARC15 INTERGENIC
NCBI Description
                   REGION >gi 626331 pir S48416 hypothetical protein YIL063c
                   - yeast (Saccharomyces cerevisiae) >gi_557806 emb_CAA86160_
                   (Z38060) orf, len: 327, CAI: 0.17, some similarity to
                   NUP2 YEAST P32499 NUCLEOPORIN NUP2 [Saccharomyces
                   cerevisiae]
Seq. No.
                   219859
Seq. ID
                  LIB3149-034-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g465820
BLAST score
                   185
E value
                   7.0e-14
Match length
                   48
% identity
                   65
                  HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
NCBI Description
```

C40H1.6 [Caenorhabditis elegans]

>gi_280536_pir__S28301 hypothetical protein C40H1.6 Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)



219860

```
Seq. ID
                  LIB3149-034-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  125
                  1.0e-10
E value
                  43
Match length
                  88
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  219861
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2392895
BLAST score
                  511
                  4.0e-52
E value
Match length
                  126
% identity
                  79
                  (AF017056) brassinosteroid insensitive 1 [Arabidopsis
NCBI Description
                  thaliana]
                  219862
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3914535
BLAST score
                  164
                  1.0e-11
E value
Match length
                  37
% identity
                  89
                  60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283
NCBI Description
                  (AJ223363) ribosomal protein L13a [Lupinus luteus]
                  219863
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-C10
                  BLASTX
Method
NCBI GI
                  g2129915
BLAST score
                  424
                  8.0e-42
E value
Match length
                  104
                  74
% identity
NCBI Description
                  ferredoxin precursor - sweet orange
                  >gi 1360725 emb CAA87068 (Z46944) non-photosynthetic
                  ferredoxin [Citrus sinensis]
Seq. No.
                  219864
Seq. ID
                  LIB3149-034-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2661840
BLAST score
                  496
                  3.0e-50
E value
Match length
                  134
% identity
                  69
                  (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
Seq. No.
                  219865
                  LIB3149-034-Q1-K1-C12
Seq. ID
```

95

% identity

```
Method
                  BLASTX
NCBI GI
                  q729882
BLAST score
                  149
                  1.0e-20
E value
                  99
Match length
                  57
% identity
                  CASEIN KINASE II BETA' CHAIN (CK II)
NCBI Description
                  >gi 1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta
                  chain CKB2 - Arabidopsis thaliana >gi 467975 (U03984)
                  casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                  >gi 2245122_emb_CAB10544_ (Z97343) unnamed protein product
                  [Arabidopsis thaliana]
                  219866
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-C2
                  BLASTN
Method
                  g2865522
NCBI GI
                  33
BLAST score
E value
                  6.0e-09
Match length
                  101
                  90
% identity
NCBI Description Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
                  complete cds
Seq. No.
                  219867
                  LIB3149-034-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2497752
BLAST score
                  209
E value
                  1.0e-16
Match length
                  64
% identity
                  61
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                  [Prunus dulcis]
Seq. No.
                  219868
Seq. ID
                  LIB3149-034-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3687251
BLAST score
                  151
                  7.0e-10
E value
Match length
                  37
% identity
                  78
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
                  219869
Seq. No.
                  LIB3149-034-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352664
BLAST score
                  449
E value
                  1.0e-44
                  85
Match length
```

30962

(EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana

SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC

>gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

219870 Seq. No. LIB3149-034-Q1-K1-D10 Seq. ID Method BLASTX NCBI GI q4454464 246 BLAST score 6.0e-21 E value 73 Match length 67 % identity

(AC006234) unknown protein [Arabidopsis thaliana] NCBI Description

219871 Seq. No.

LIB3149-034-Q1-K1-D11 Seq. ID

Method BLASTX NCBI GI g547712 BLAST score 603 7.0e-63 E value Match length 121 % identity 98

EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) NCBI Description

>gi_542153_pir__ S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

219872 Seq. No.

LIB3149-034-Q1-K1-D2 Seq. ID

BLASTX Method NCBI GI g2454184 685 BLAST score 2.0e-72 E value 135 Match length 95 % identity

(U80186) pyruvate dehydrogenase El beta subunit NCBI Description

[Arabidopsis thaliana]

219873 Seq. No.

Seq. ID LIB3149-034-Q1-K1-D3

BLASTX Method g3281870 NCBI GI BLAST score 146 3.0e-09 E value 32 Match length 88 % identity

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

219874 Seq. No.

LIB3149-034-Q1-K1-D5 Seq. ID

BLASTX Method q477226 NCBI GI BLAST score 253 3.0e-26E value 99 Match length 66 % identity



```
NCBI Description heat shock protein HSP82 - maize >gi 300083 bbs 130886
                  (S59780) HSP82=82 kda heat shock protein [Zea mays,
                  seedling, leaves, Peptide, 715 aa] [Zea mays]
                  219875
Seq. No.
                  LIB3149-034-Q1-K1-D7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2267582
                  269
BLAST score
                  1.0e-150
E value
                  280
Match length
                  99
% identity
                  Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA,
NCBI Description
                  complete cds
                  219876
Seq. No.
                  LIB3149-034-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  g2464852
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
                  141
Match length
                   44
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   219877
Seq. No.
                  LIB3149-034-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  q1350720
NCBI GI
BLAST score
                   451
E value
                   6.0e-45
                  111
Match length
                   77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
                   219878
Seq. No.
Seq. ID
                   LIB3149-034-Q1-K1-E3
                  BLASTX
Method
                   q2431771
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
Match length
                   113
% identity
                   48
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
                   219879
Seq. No.
                   LIB3149-034-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g3192929
NCBI GI
BLAST score
                   166
E value
                   6.0e-12
Match length
                   73
                   53
```

NCBI Description (AF068688) malate dehydrogenase [Glycine max] Seq. No. 219880

% identity

LIB3149-034-Q1-K1-F1 Seq. ID



```
BLASTX
Method
NCBI GI
                  g2129915
                  182
BLAST score
                  2.0e-13
E value
                  71
Match length
                  51
% identity
                  ferredoxin precursor - sweet orange
NCBI Description
                  >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
                  ferredoxin [Citrus sinensis]
                  219881
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  g2369766
BLAST score
                  302
                  1.0e-27
E value
                  114
Match length
                  56
% identity
                 (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                  219882
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-F2
                  BLASTX
Method
                  g2369766
NCBI GI
BLAST score
                  427
                  3.0e-42
E value
                  128
Match length
                  67
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
                  219883
Seq. No.
                  LIB3149-034-Q1-K1-F3
Seq. ID
Method
                  BLASTN
                  q2244747
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
Match length
                  76
                  87
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  219884
Seq. ID
                  LIB3149-034-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q76358
BLAST score
                  159
E value
                  3.0e-11
Match length
                  37
% identity
                  84
NCBI Description hypothetical protein C-123 - maize chloroplast
                  219885
Seq. No.
Seq. ID
                  LIB3149-034-Q1-K1-F7
                  BLASTX
Method
```

BLAST score 211 E value 8.0e-17

g3169287

NCBI GI



```
42
Match length
                   100
% identity
                   (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
NCBI Description
                   hirsutum]
                   219886
Seq. No.
Seq. ID
                   LIB3149-034-Q1-K1-F9
                   BLASTX
Method
                   g1168196
NCBI GI
BLAST score
                   318
                   2.0e-29
E value
                   70
Match length
                   89
% identity
                  14-3-3-LIKE PROTEIN >gi 555974 (U15036) 14-3-3-like protein
NCBI Description
                   [Pisum sativum]
                   219887
Seq. No.
                   LIB3149-034-Q1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3264769
BLAST score
                   212
                   4.0e-17
·E value
                   44
Match length
                   86
% identity
                  (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                   armeniaca]
                   219888
Seq. No.
Seq. ID
                   LIB3149-034-Q1-K1-G4
                   {\tt BLASTX}
Method
NCBI GI
                   g4099090
BLAST score
                   191
                   1.0e-14
E value
                   95
Match length
                   46
% identity
NCBI Description (U83178) unknown [Arabidopsis thaliana]
                   219889
Seq. No.
                   LIB3149-034-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263713
BLAST score
                   188
                   4.0e-14
E value
                   113
Match length
% identity
                   45
NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]
                   219890
Seq. No.
                   LIB3149-034-Q1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1871184
BLAST score
                   212
                   4.0e-17
E value
Match length
                   113
% identity
                   42
```

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  219891
Seq. ID
                  LIB3149-034-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4204300
BLAST score
                  233
E value
                  1.0e-19
Match length
                  74
% identity
                  66
NCBI Description
                  (AC003027) Unknown protein [Arabidopsis thaliana]
                  219892
Seq. No.
                  LIB3149-034-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1171978
                  545
BLAST score
                  5.0e-56
E value
Match length
                  131
% identity
NCBI Description
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                  (PABP 2) >qi 304109 (L19418) poly(A)-binding protein
                  [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                  219893
Seq. ID
                  LIB3149-034-Q1-K1-H4
                  BLASTX
Method
NCBI GI
                  q2281649
BLAST score
                  264
E value
                  3.0e-23
Match length
                  100
                  57
% identity
NCBI Description
                  (AF003105) AP2 domain containing protein RAP2.12
                  [Arabidopsis thaliana]
Seq. No.
                  219894
                  LIB3149-034-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464986
BLAST score
                  316
E value
                  4.0e-39
Match length
                  104
% identity
                  75
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
```

Seq. ID LIB3149-034-Q1-K1-H9

Method BLASTX

ligase UBC9 [Arabidopsis thaliana]

```
g1550814
NCBI GI
                  281
BLAST score
                  1.0e-26
E value
                  76
Match length
% identity
                  84
                  (Y07959) 60S acidic ribosomal protein P0 [Zea mays]
NCBI Description
                  219896
Seq. No.
                  LIB3149-035-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3881450
BLAST score
                  141
                  1.0e-08
E value
                  91
Match length
                  33
% identity
                  (Z47073) similar to phosphatidylserine synthase I; cDNA EST
NCBI Description
                  yk345c1.5 comes from this gene [Caenorhabditis elegans]
                  219897
Seq. No.
                  LIB3149-035-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464985
                   269
BLAST score
                   3.0e-24
E value
                   58
Match length
% identity
                   86
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                   >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana]
Seq. No.
                   219898
                   LIB3149-035-Q1-K1-A3 . .
Seq. ID
Method
                   BLASTX
                   g4580468
NCBI GI
BLAST score
                   475
                   8.0e-48
E value
                   128
Match length
                   66
% identity
                  (AC006081) putative protein kinase; similar to human PKX1
NCBI Description
                   and Drosophila DC2 [Arabidopsis thaliana]
                   219899
Seq. No.
Seq. ID
                   LIB3149-035-Q1-K1-A6
                   BLASTX
Method
NCBI GI
                   q100379
BLAST score
                   17.2
                   2.0e-12
E value
                   39
Match length
                   95
% identity
```

NCBI Description ribosomal protein S6 - common tobacco

>gi_20022_emb_CAA48187_ (X68050) ribosomal protein S6

[Nicotiana tabacum]

Seq. No. 219900

Seq. ID LIB3149-035-Q1-K1-B10

Method BLASTX

```
q3860259
NCBI GI
BLAST score
                  141
                  1.0e-08
E value
                  91
Match length
                  35
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                  219901
Seq. No.
                  LIB3149-035-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g1173043
NCBI GI
                  312
BLAST score
                  1.0e-28
E value
                  69
Match length
                  88
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi 479441 pir S33899 ribosomal
NCBI Description
                  protein L38 - tomato (cv. Moneymaker)
                  >gi 313027 emb CAA49599 (X69979) ribosomal protein L38
                  [Lycopersicon esculentum]
                  219902
Seq. No.
                  LIB3149-035-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g322750
NCBI GI
BLAST score
                  658
                  3.0e-69
E value
                  128
Match length
                  99
% identity
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                  >qi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
                  219903
Seq. No.
Seq. ID
                  LIB3149-035-Q1-K1-B5
Method
                  BLASTX
                  g1707642
NCBI GI
                  330
BLAST score
E value
                  9.0e-31
                  137
Match length
                  52
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
                  219904
Seq. No.
                  LIB3149-035-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3334405
BLAST score
                  453
                  2.0e-71
E value
Match length
                  141
                  98
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                  219905
Seq. No.
                  LIB3149-035-Q1-K1-B9
Seq. ID
```

30969

BLASTX

Method



NCBI GI g4105180 BLAST score 162 E value 2.0e-11 Match length 39 % identity 77

NCBI Description (AF043905) plastoglobule associated protein PG1 precursor

[Pisum sativum]

Seq. No. 219906

Seq. ID LIB3149-035-Q1-K1-C12

Method BLASTX
NCBI GI g4204285
BLAST score 140
E value 1.0e-08
Match length 50

% identity 52

NCBI Description (AC003027) lcl prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 219907

Seq. ID LIB3149-035-Q1-K1-C2

Method BLASTX
NCBI GI g122085
BLAST score 539
E value 3.0e-55
Match length 126
% identity 87

NCBI Description

HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21)

- rice >gi 1362194 pir S57626 histone H3 - maize >gi 20251 emb CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi 168493 (M36658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays] >gi 168497 (M13379) histone H3 [Zea mays] >gi 168506 (M35388) histone H3 [Zea mays] >gi 169655 (M77493) histone H3 [Zea mays] >gi 169657 (M77494) histone H3

H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and

gb_T42306 come from this gene. [Arabidopsis thaliana]
>gi_225459_prf__1303352A histone H3 [Helicoverpa zea]
>gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 219908

Seq. ID LIB3149-035-Q1-K1-C8

Method BLASTX NCBI GI g2462733 BLAST score 619

```
Active (A)
```

```
E value
                  1.0e-64
Match length
                  143
                  90
% identity
NCBI Description
                  (AC002292) Putative enoyl-CoA hydratase/isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  219909
Seq. ID
                  LIB3149-035-Q1-K1-D12
                  BLASTN
Method
                  g2961299
NCBI GI
BLAST score
                  59
                  2.0e-24
E value
Match length
                  123
% identity
                  87
NCBI Description Cicer arietinum mRNA for ribosomal protein L24
Seq. No.
                  219910
Seq. ID
                  LIB3149-035-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2500347
                  344
BLAST score
                  2.0e-32
E value
Match length
                  103
                  69
% identity
                  NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG
NCBI Description
                  >gi 3878691 emb CAA90127 (Z49911) similar to ribosomal
                  protein (L7AE family); cDNA EST EMBL:D73957 comes from this
                  gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST
                  EMBL: D74077 comes from this gene; cDNA EST EMBL: D71393
                  comes from this gene; cD
Seq. No.
                  219911
Seq. ID
                  LIB3149-035-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  409
E value
                  4.0e-40
Match length
                  118
% identity
                  63
NCBI Description 40S RIBOSOMAL PROTEIN S19
                  219912
Seq. No.
                  LIB3149-035-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q445613
BLAST score
                  324
E value
                  4.0e-30
Match length
                  109
                  61
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
```

Seq. ID LIB3149-035-Q1-K1-E2

Method BLASTX
NCBI GI g3953471
BLAST score 322
E value 4.0e-30



Match length 84 % identity 65 NCBI Description (A)

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No.

219914

Seq. ID

LIB3149-035-Q1-K1-E3

Method NCBI GI BLASTX g1256259

BLAST score E value Match length 224 4.0e-22 87

% identity

69

NCBI Description

(U50900) voltage-dependent anion channel protein [Spinacia

oleracea]

Seq. No.

219915

Seq. ID

LIB3149-035-Q1-K1-E5

Method NCBI GI BLAST score E value BLASTX g464849 385 2.0e-37

Match length % identity

99 81

NCBI Description

TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha

chain - almond $>gi_2041\overline{3}_emb_C\overline{A}A47\overline{63}5_$ (X67162)

alpha-tubulin [Prunus dulcis]

Seq. No.

219916

Seq. ID

LIB3149-035-Q1-K1-F1

Method BLASTX
NCBI GI g3776559
BLAST score 465
E value 1.0e-46
Match length 144
% identity 63

NCBI Description

(AC005388) Strong similarity to gene F14J9.26 gi_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No.

219917

Seq. ID

LIB3149-035-Q1-K1-F11

Method BLASTN
NCBI GI g2252639
BLAST score 35
E value 3.0e-10
Match length 55

% identity
NCBI Description

NCBI Description Genomic sequence of Arabidopsis BAC F8A5, complete sequence

[Arabidopsis thaliana]

Seq. No.

219918

91

Seq. ID

LIB3149-035-Q1-K1-F12

Method BLASTX
NCBI GI g2961390
BLAST score 632
E value 3.0e-66

BLAST score

E value

36 1.0e-10



```
Match length
                  136
% identity
                  79
NCBI Description
                  (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  219919
Seq. No.
Seq. ID
                  LIB3149-035-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q464840
BLAST score
                   674
                   4.0e-71
E value
                  131
Match length
% identity
                   98
                  TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
NCBI Description
                  alpha-1 chain - fern (Anemia phyllitidis)
                  >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia
                  phyllitidis]
Seq. No.
                  219920
                  LIB3149-035-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115525
BLAST score
                   640
E value
                   3.0e-67
                  125
Match length
% identity
                   66
                  CALMODULIN >gi_71685_pir__MCSP calmodulin - spinach
NCBI Description
Seq. No.
                  219921
Seq. ID
                  LIB3149-035-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  g3128196
BLAST score
                  159
E value
                   1.0e-10
Match length
                   55
                   53
% identity
                   (AC004521) putative cellulase [Arabidopsis thaliana]
NCBI Description
                   >gi 3341674 (AC003672) putative glycosyl hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   219922
                   LIB3149-035-Q1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4580468
BLAST score
                   555
                   4.0e-57
E value
                   138
Match length
                   71
% identity
                  (AC006081) putative protein kinase; similar to human PKX1
NCBI Description
                   and Drosophila DC2 [Arabidopsis thaliana]
                   219923
Seq. No.
                   LIB3149-035-Q1-K1-G10
Seq. ID
                   BLASTN
Method
                   g170293
NCBI GI
```



```
Match length
                  136
% identity
                  82
NCBI Description
                  Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3)
                  mRNA, complete cds
                  219924
Seq. No.
Seq. ID
                  LIB3149-035-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2501850
BLAST score
                  737
                  2.0e-78
E value
Match length
                  143
% identity
                  95
                  (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
NCBI Description
                  219925
Seq. No.
                  LIB3149-035-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2960216
BLAST score
                  689
E value
                  7.0e-73
Match length
                  147
                  90
% identity
NCBI Description
                  (AJ223384) 26S proteasome regulatory ATPase subunit 10b
                  (S10b) [Manduca sexta]
                  219926
Seq. No.
Seq. ID
                  LIB3149-035-Q1-K1-G5
Method
                  BLASTX
                  g2970051
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
Match length
                  121
% identity
                  88
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
                  219927
Seq. No.
Seq. ID
                  LIB3149-035-Q1-K1-G6
Method
                  BLASTX
                  g134892
NCBI GI
                  145
BLAST score
                  3.0e-12
E value
Match length
                  97
                  43
% identity
                  SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
NCBI Description
                  (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                  >gi 88607 pir A29440 signal recognition particle receptor
                  - human >gi 30866 emb CAA29608 (X06272) docking protein
                  [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal
                  recognition particle receptor ('docking protein')
```

Seq. ID LIB3149-035-Q1-K1-G8

Method BLASTN
NCBI GI g1199773
BLAST score 33
E value 6.0e-09

Seq. ID



```
45
  Match length
                    93
  % identity
  NCBI Description Populus nigra gene for extensin like protein, complete cds
                    219929
  Seq. No.
  Seq. ID
                    LIB3149-035-Q1-K1-H10
                    BLASTX
  Method
                    q3413167
  NCBI GI
  BLAST score
                    383
                    5.0e-37
  E value
                    77
  Match length
                    95
  % identity
  NCBI Description (AJ010225) elongation factor 1-alpha [Cicer arietinum]
                    219930
  Seq. No.
  Seq. ID
                    LIB3149-035-Q1-K1-H2
                    BLASTX
  Method
  NCBI GI
                    g4567310
  BLAST score
                    319
  E value
                    2.0e-29
                    104
  Match length
                    67
  % identity
  NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                    219931
  Seq. No.
                    LIB3149-035-Q1-K1-H5
  Seq. ID
                    BLASTX
Method
                    g4006890
  NCBI GI
  BLAST score
                    540
  E value
                    2.0e-55
                    105
  Match length
                    90
  % identity
                   (Z99708) ubiquitin--protein ligase-like protein
  NCBI Description
                    [Arabidopsis thaliana]
                    219932
  Seq. No.
  Seq. ID
                    LIB3149-035-Q1-K1-H6
                    BLASTN
  Method
                    g18058
  NCBI GI
  BLAST score
                    65
                    3.0e-28
  E value
  Match length
                    69
                    99
  % identity
  NCBI Description Citrus limon cistron for 26S ribosomal RNA
                    219933
  Seq. No.
                    LIB3149-035-Q1-K1-H9
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    g1397319
  BLAST score
                    214
  E value
                     3.0e-17
  Match length
                    103
                     46
  % identity
  NCBI Description (U61953) No definition line found [Caenorhabditis elegans]
  Seq. No.
                     219934
```

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LIB3149-036-Q1-K1-A11



```
Method
                  BLASTX
NCBI GI
                  q2495724
BLAST score
                  155
                  2.0e-10
E value
Match length
                  83
                  42
% identity
                 HYPOTHETICAL PROTEIN KIAA0249 >qi 1665767 dbj BAA13380
NCBI Description
                  (D87436) Similar to Human KIAA0188 protein [Homo sapiens]
                  219935
Seq. No.
Seq. ID
                  LIB3149-036-Q1-K1-A2
                  BLASTX
Method
NCBI GI
                  g3122703
BLAST score
                  280
                  5.0e-25
E value
Match length
                  95
% identity
                  60
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                  protein L23a [Fritillaria agrestis]
Seq. No.
                  219936
Seq. ID
                  LIB3149-036-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q3123745
BLAST score
                  607
                  3.0e-63
E value
Match length
                  130
% identity
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  219937
                  LIB3149-036-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461498
BLAST score
                  466
                  8.0e-47
E value
                  124
Match length
% identity
                  72
NCBI Description
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >gi 320619 pir S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                  alanine aminotransferase [Panicum miliaceum]
                  219938
Seq. No.
                  LIB3149-036-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244734
BLAST score
                  694
                  2.0e-73
E value
Match length
                  135
                  100
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
```

30976

219939

BLASTX

LIB3149-036-Q1-K1-B3

Seq. No.

Seq. ID Method



```
NCBI GI
                   g3108209
BLAST score
                   544
                   1.0e-56
E value
Match length
                  123
                   85
% identity
NCBI Description
                  (AF028809) eukaryotic cap-binding protein [Arabidopsis
                  thaliana]
                   219940
Seq. No.
                  LIB3149-036-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g170920
                   557
BLAST score
                   2.0e-57
E value
Match length
                  105
% identity
                   98
                  (M62396) ribosomal protein L41 [Candida maltosa]
NCBI Description
Seq. No.
                   219941
                  LIB3149-036-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1053063
BLAST score
                   143
                   1.0e-09
E value
Match length
                   43
% identity
                   84
NCBI Description
                  (U38464) small GTP-binding protein [Solanum lycopersicum]
Seq. No.
                   219942
                   LIB3149-036-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q466160
BLAST score
                   362
                   1.0e-34
E value
                   84
Match length
                   82
% identity
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi 289769 (L14429) putative [Caenorhabditis
                   elegans]
                   219943
Seq. No.
                   LIB3149-036-Q1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3702336
BLAST score
                   268
E value
                   1.0e-23
Match length
                   81
% identity
                   60
NCBI Description
                  (AC005397) putative 3-methyl-2-oxobutanoate
                   hydroxy-methyl-transferase [Arabidopsis thaliana]
```

Seq. ID LIB3149-036-Q1-K1-D3

Method BLASTX NCBI GI g2244759 BLAST score 566



```
E value
                  2.0e-58
Match length
                  126
% identity
                  82
NCBI Description
                 (Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.
                  219945
Seq. ID
                  LIB3149-036-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3914386
BLAST score
                  143
                  6.0e-09
E value
Match length
                  56
% identity
                  50
NCBI Description
                  ALLERGEN MF1 >gi 3445490 dbj BAA32435 (AB011804) MF1
                  [Malassezia furfur]
Seq. No.
                  219946
Seq. ID
                  LIB3149-036-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  562
                  5.0e-58
E value
                  127
Match length
% identity
                  87
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  219947
Seq. No.
Seq. ID
                  LIB3149-036-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q120629
BLAST score
                  268
                  2.0e-23
E value
Match length
                  120
% identity
                  42
NCBI Description
                  PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, HEAVY CHAIN
                  (PKCSH) (80K-H PROTEIN) >gi 105167 pir A32469 80K protein
                  H precursor - human >gi 1438753 bbs 177421 p90,
                  80K-H=tyrosine-phosphorylated protein/FGF signaling protein
                  [human, MRC-5 bFGF-stimulated fibroblast cells, Peptide,
                  527 aa] >gi 182855 (J03075) 80K-H protein [Homo sapiens]
                  >gi 1293640 (U50327) protein kinase C substrate 80K-H [Homo
                  sapiens] >gi 4506077 ref NP 002734.1 pPRKCSH protein
                  kinase C substrate 80K-H
                  219948
Seq. No.
                  LIB3149-036-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220527
BLAST score
                  482
```

BLAST score 482 E value 9.0e-49 Match length 114 % identity 71

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 219949

Seq. ID LIB3149-036-Q1-K1-E2



```
Method
                  BLASTX
NCBI GI
                  q1354849
BLAST score
                   440
E value
                  1.0e-43
Match length
                  119
                  70
% identity
NCBI Description
                 (U57350) epoxide hydrolase [Nicotiana tabacum]
                  219950
Seq. No.
                  LIB3149-036-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
```

BLAST score 544 E value 6.0e - 56Match length 103 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 219951 Seq. ID LIB3149-036-Q1-K1-E4 Method BLASTX NCBI GI g1729971 BLAST score 271 7.0e-24 E value Match length 71

% identity 69

TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) NCBI Description

(AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza

satival

Seq. No. 219952

Seq. ID LIB3149-036-Q1-K1-E6

Method BLASTX NCBI GI g2493694 BLAST score 257 E value 3.0e-22 Match length 102 % identity 53

NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi 1076268 pir S53025 photosystem II

protein - spinach > gi 728716 emb CAA59409 (X85038) protein

of photosystem II [Spinacia oleracea]

219953 Seq. No.

Seq. ID LIB3149-036-Q1-K1-E9

Method BLASTX NCBI GI g2760334 BLAST score 416 6.0e-41E value Match length 91 % identity 80

(AC002130) F1N21.5 [Arabidopsis thaliana] NCBI Description

```
Seq. No.
                   219954
Seq. ID
                   LIB3149-036-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q2541876
BLAST score
                   173
                   1.0e-12
E value
Match length
                   100
                   38
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   219955
Seq. ID
                   LIB3149-036-Q1-K1-F5
                   BLASTX
Method
                   q3747044
NCBI GI
BLAST score
                   204
                   5.0e-16
E value
Match length
                   107
% identity
                   36
                  (AF093537) blue copper protein [Zea mays]
NCBI Description
                   219956
Seq. No.
Seq. ID
                   LIB3149-036-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4510345
BLAST score
                   259
                   2.0e-22
E value
Match length
                   65
% identity
                   69
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   219957
Seq. No.
Seq. ID
                   LIB3149-036-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g124200
BLAST score
                   261
                   1.0e-22
E value
Match length
                   113
% identity
                   41
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT
NCBI Description
                   (EIF-2-ALPHA) >gi 181995 (J02645) translational initiation
                   factor eIF-2, alpha subunit [Homo sapiens]
                   >gi 4503501 ref NP 001404.1 pEIF2A eukaryotic translation
                   initiation factor 2A
                   219958
Seq. No.
                   LIB3149-036-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g70753
BLAST score
                   414
                   1.0e-40
E value
Match length
                   105
% identity
                   80
```

30980

NCBI Description histone ${\tt H3}$ - garden pea >gi_82610_pir__S00373 histone ${\tt H3}$ -

wheat

```
219959
Seq. No.
Seq. ID
                  LIB3149-036-Q1-K1-G11
Method
                  BLASTX
                  g136140
NCBI GI
                  235
BLAST score
                  1.0e-19
E value
                  99
Match length
                  47
% identity
                 PUTATIVE AC9 TRANSPOSASE >gi 72973 pir__TQZMCA probable
NCBI Description
                  transposase - maize transposon Ac9
                  219960
Seq. No.
Seq. ID
                  LIB3149-036-Q1-K1-G2
                  BLASTX
Method
NCBI GI
                  g629483
                  295
BLAST score
                  1.0e-26
E value
                  115
Match length
                  54
% identity
NCBI Description gene 1-Sc3 protein - European white birch
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi_1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
                  219961
Seq. No.
                  LIB3149-036-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g2970051
NCBI GI
                  225
BLAST score
                  2.0e-18
E value
Match length
                  64
% identity
                  64
NCBI Description (AB012110) ARG10 [Vigna radiata]
                  219962
Seq. No.
                  LIB3149-036-Q1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g974782
                  497
BLAST score
                  2.0e-50
E value
Match length
                  122
                  79
% identity
NCBI Description (Z49150) cobalamine-independent methionine synthase
                  [Solenostemon scutellarioides]
                  219963
Seq. No.
                  LIB3149-036-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q3759184
NCBI GI
BLAST score
                  331
E value
                  6.0e-31
                  94
Match length
                  69
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
```

30981

219964

LIB3149-036-Q1-K1-H1

Seq. No. Seq. ID

Seq. ID

```
BLASTX
Method
NCBI GI
                  g266945
BLAST score
                  343
                  2.0e-32
E value
Match length
                  95
% identity
                  72
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi 100065 pir S19978 ribosomal protein L9 - garden pea
                  >gi 20727 emb CAA46273 (X65155) GA [Pisum sativum]
                  >gi 1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
                  219965
Seq. No.
Seq. ID
                  LIB3149-036-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4008159
BLAST score
                  532
E value
                  2.0e-54
Match length
                  118
% identity
                  85
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
                  219966
Seq. No.
Seq. ID
                  LIB3149-036-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3892057
BLAST score
                  562
                  5.0e-58
E value
Match length
                  125
% identity
                  49
NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]
                  219967
Seq. No.
                  LIB3149-036-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462744
BLAST score
                  294
E value
                  1.0e-26
Match length
                  128
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  219968
Seq. ID
                  LIB3149-036-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4056432
BLAST score
                  566
                  2.0e-58
E value
Match length
                  131
% identity
                  77
NCBI Description
                  (AC005990) Similar to gi 2245014 glucosyltransferase
                  homolog from Arabidopsis thaliana chromosome 4 contig
                  gb Z97341. ESTs gb T20778 and gb AA586281 come from this
```

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gene. [Arabidopsis thaliana]

LIB3149-036-Q1-K1-H9

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                  576
                  1.0e-59
E value
Match length
                  116
                  92
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  219970
                  LIB3149-037-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245098
BLAST score
                  485
E value
                  6.0e-49
Match length
                  141
                  68
% identity
NCBI Description (Z97343) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  219971
                 LIB3149-037-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2384758
BLAST score
                  310
E value
                  1.0e-28
Match length
                  81
                  75
% identity
                 (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                  sativa]
Seq. No.
                  219972
                  LIB3149-037-Q1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4262149
BLAST score
                  174
E value
                  2.0e-25
Match length
                  125
                  53
% identity
NCBI Description (AC005275) putative xyloglucan endotransglycosylase
                  [Arabidopsis thaliana]
Seq. No.
                  219973
                  LIB3149-037-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352316
BLAST score
                  472
E value
                  2.0e-47
Match length
                  97
                  93
% identity
NCBI Description DR1 PROTEIN HOMOLOG >gi 633026 dbj BAA07288 ~(D38110) Dr1
                  [Arabidopsis thaliana]
```

LIB3149-037-Q1-K1-B10

Method

NCBI GI

BLAST score

BLASTX

374

g1771780

```
Method
                   BLASTX
NCBI GI
                   g2500443
BLAST score
                   232
E value
                   3.0e-19
Match length
                  49
                  96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 1762931 (U66262) ribosomal
                  protein S14 [Nicotiana tabacum]
Seq. No.
                  219975
Seq. ID
                  LIB3149-037-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4490751
BLAST score
                  348
                  7.0e-33
E value
Match length
                  111
% identity
                  61
NCBI Description
                  (AL035708) proliferating-cell nucleolar antigen-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  219976
Seq. ID
                  LIB3149-037-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1350956
BLAST score
                  171
E value
                  3.0e-12
Match length
                  38
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
Seq. No.
                  219977
Seq. ID
                  LIB3149-037-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4432844
BLAST score
                  187
                  5.0e-14
E value
                  40
Match length
                  93
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  219978
Seq. ID
                  LIB3149-037-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1346181
BLAST score
                  231
E value
                  3.0e-19
Match length
                  53
                  85
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN GRP2A >qi 496237 (L31377)
                  homology with RNA-binding proteins in meristematic tissue
                  [Sinapis alba]
                  219979
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-B9
```

30984



```
E value
                  6.0e-36
Match length
                  124
                  45
% identity
NCBI Description
                  (Y10024) ubiquitin extension protein [Solanum tuberosum]
                  219980
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3024020
BLAST score
                  628
                  1.0e-65
E value
                  126
Match length
% identity
                  94
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                  219981
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-C3
Method
                  BLASTX
                  q4220476
NCBI GI
BLAST score
                  549
                  2.0e-56
E value
Match length
                  130
                  79
% identity
                  (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
NCBI Description
                  219982
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4220476
BLAST score
                  265
E value
                  3.0e-23
Match length
                  97
                  54
% identity
                  (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  219983
Seq. ID
                  LIB3149-037-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2098705
BLAST score
                   304
                  8.0e-28
E value
                  122
Match length
                  55
% identity
NCBI Description
                  (U82973) pectinesterase [Citrus sinensis]
                  219984
Seq. No.
                  LIB3149-037-Q1-K1-D11
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g2829205
BLAST score 174
E value 4.0e-93
Match length 405
% identity 17

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

```
Seq. No.
                  219985
                  LIB3149-037-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1362093
                  254
BLAST score
                  5.0e-22
E value
Match length
                  71
                  69
% identity
                  hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                  >qi 924632 (U20595) unknown [Solanum lycopersicum]
                  219986
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-D5
                  BLASTX
Method
NCBI GI
                  g2388575
BLAST score
                  198
E value
                  2.0e-15
Match length
                  110
% identity
                  38
                 (AC000098) YUP8H12.18 [Arabidopsis thaliana]
NCBI Description
                  219987
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4539321
                  309
BLAST score
                  3.0e-28
E value
Match length
                  88
% identity
                  66
                 (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                  219988
Seq. No.
                  LIB3149-037-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706551
BLAST score
                  298
E value
                  5.0e-27
Match length
                  84
% identity
NCBI Description
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
                  ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                  1,3-glucanase [Triticum aestivum]
                  219989
Seq. No.
                  LIB3149-037-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82537
BLAST score
                  100
                  4.0e-10
E value
                  51
Match length
% identity
                  65
                  hypothetical 8K protein (rps12-trnN intergenic region) -
NCBI Description
                  rice chloroplast >gi 12039 emb CAA33943 (X15901) ORF72
```

30986

[Oryza sativa] >gi_1\overline{2063_emb_CAA33917_ (X15901) ORF72 [Oryza sativa] >gi_226659 prf 1603356CK ORF 71 [Oryza



sativa]

```
Seq. No.
                  219990
Seq. ID
                  LIB3149-037-Q1-K1-E4
                  BLASTX
Method
NCBI GI
                  g220838
                  363
BLAST score
                  1.0e-34
E value
                  127
Match length
                  57
% identity
                 (D10655) dihydrolipoamide acetyltransferase [Rattus rattus]
NCBI Description
                  219991
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2218152
BLAST score
                  640
                  3.0e-67
E value
                  130
Match length
                  86
% identity
                  (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                  unguiculata]
                  219992
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-E7
Method
                  BLASTX
                  g1170507
NCBI GI
BLAST score
                  467
                  7.0e-47
E value
Match length
                  114
% identity
                  81
                  EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
NCBI Description
                  >gi 100276 pir S22579 translation initiation factor eIF-4A
                   - curled-leaved tobacco >qi 19699 emb CAA43514 (X61206)
                  nicotiana eukaryotic translation initiation factor 4A
                   [Nicotiana plumbaginifolia]
Seq. No.
                  219993
                  LIB3149-037-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  q417103
NCBI GI
BLAST score
                  601
                  1.0e-62
E value
                  122
Match length
                  98
% identity
NCBI Description
                  HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
                  H3.3-like protein - Arabidopsis thaliana
```

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2

[Medicago sativa] $>gi_488577$ (U09465) histone H3.2

[Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]



>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

219994 Seq. No. LIB3149-037-Q1-K1-E9 Seq. ID BLASTX Method q4454097 NCBI GI BLAST score 253 9.0e-22 E value 80 Match length % identity (X85206) hybrid proline-rich protein [Catharanthus roseus] NCBI Description Seq. No. 219995 Seq. ID LIB3149-037-Q1-K1-F9 BLASTX Method q4056432 NCBI GI 470 BLAST score 3.0e-47E value 124 Match length % identity (AC005990) Similar to gi_2245014 glucosyltransferase NCBI Description homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No. 219996 Seq. ID LIB3149-037-Q1-K1-G1

Method BLASTX
NCBI GI g2104712
BLAST score 184
E value 6.0e-14
Match length 91
% identity 46

NCBI Description (U95180) endosperm specific protein [Zea mays]

Seq. No. 219997

Seg. ID LIB3149-037-Q1-K1-G10

Method BLASTX
NCBI GI g3757514
BLAST score 389
E value 6.0e-38
Match length 87
% identity 84

NCBI Description (AC005167) putative plasma membrane intrinsic protein

[Arabidopsis thaliana]

Seq. No. 219998

Seq. ID LIB3149-037-Q1-K1-G12

Method BLASTX NCBI GI g1352088 BLAST score 479



```
E value
                  3.0e-48
Match length
                  121
% identity
                  78
                  CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi 624676
NCBI Description
                  (U19481) citrate synthase precursor [Citrus maxima]
Seq. No.
                  219999
                  LIB3149-037-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454097
BLAST score
                  292
E value
                  2.0e-26
Match length
                  75
% identity
                  76
NCBI Description
                  (X85206) hybrid proline-rich protein [Catharanthus roseus]
                  220000
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q730583
BLAST score
                  213
                  1.0e-17
E value
Match length
                  57
% identity
                  74
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
Seq. No.
                   220001
                  LIB3149-037-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                   q1943720
NCBI GI
                   343
BLAST score
                   2.0e-32
E value
                  81
Match length
                   72
% identity
                  (U76831) thioredoxin-m [Brassica napus]
NCBI Description
Seq. No.
                   220002
                  LIB3149-037-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2632061
BLAST score
                   383
                   2.0e-42
E value
                   124
Match length
                   75
% identity
                  (AJ002597) membrane-associated salt-inducible protein like
NCBI Description
                   [Arabidopsis thaliana]
                   220003
Seq. No.
                   LIB3149-037-Q1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2564237
```

Method BLASTX
NCBI GI g2564237
BLAST score 528
E value 5.0e-54
Match length 108
% identity 87



```
NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]
                  220004
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-H10
Method
                  BLASTX
                  g2827143
NCBI GI
                  516
BLAST score
E value
                  1.0e-52
                  116
Match length
% identity
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                  [Arabidopsis thaliana]
                  220005
Seq. No.
Seq. ID
                  LIB3149-037-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  197
E value
                  4.0e-20
Match length
                  61
                  92
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  220006
Seq. No.
                  LIB3149-037-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362162
BLAST score
                  328
E value
                  1.0e-30
Match length
                  76
                  75
% identity
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                  220007
                  LIB3149-037-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173027
BLAST score
                  264
E value
                  5.0e-25
Match length
                  92
% identity
                  62
                  60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                  220008
                  LIB3149-038-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498464
BLAST score
                  211
E value
                  6.0e-17
Match length
                  70
                  61
% identity
                  28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF
NCBI Description
```

30990

ASSOCIATED PROTEIN) >gi_1136584 (U41745) PDGF associated

platelet-derived growth factor-associated protein [Homo

protein [Homo sapiens] >gi_1589642_prf__2211382B



sapiens]

```
Seq. No.
                  220009
                  LIB3149-038-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023182
BLAST score
                  520
E value
                   4.0e-53
Match length
                  112
                  91
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN 5 >gi 1771172 emb CAA65148.1 (X95903)
                  14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                  220010
Seq. ID
                  LIB3149-038-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q2529680
BLAST score
                  412
E value
                  1.0e-40
Match length
                  101
                  56
% identity
NCBI Description
                  (AC002535) putative protein disulfide-isomerase precursor
                  [Arabidopsis thaliana]
Seq. No.
                  220011
Seq. ID
                  LIB3149-038-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4235644
BLAST score
                  529
                  4.0e-54
E value
Match length
                  137
% identity
                  72
                 (AF119040) polyprotein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  220012
Seq. ID
                  LIB3149-038-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g729442
BLAST score
                  169
                  4.0e-13
E value
Match length
                  83
                  52
% identity
                  PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR
NCBI Description
                  >gi_166380 (M80235) glucose-regulated endoplasmic reticular
                  protein precursor [Medicago sativa]
                  220013
Seq. No.
Seq. ID
                  LIB3149-038-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g3024126
BLAST score
                  493
E value
                  6.0e-50
Match length
                  96
% identity
                  98
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
```

30991

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 1655576 emb CAA95856 (Z71271) S-adenosyl-L-methionine

NCBI Description



synthetase 1 [Catharanthus roseus]

```
220014
Seq. No.
Seq. ID
                  LIB3149-038-Q1-K1-B3
Method
                  BLASTX
                  q3377797
NCBI GI
                  554
BLAST score
E value
                  5.0e-57
                  136
Match length
                  79
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  220015
                  LIB3149-038-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  q1703375
NCBI GI
                  604
BLAST score
                   6.0e-63
E value
                  120
Match length
% identity
                  97
                  ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
Seq. No.
                   220016
Seq. ID
                  LIB3149-038-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q3885884
BLAST score
                  168
                  7.0e-12
E value
Match length
                  33
                   91
% identity
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                  220017
Seq. No.
Seq. ID
                  LIB3149-038-Q1-K1-C3
Method
                  BLASTX
                  g3193316
NCBI GI
                   397
BLAST score
                   5.0e-45
E value
Match length
                  136
                   69
% identity
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
Seq. No.
                   220018
Seq. ID
                  LIB3149-038-Q1-K1-C4
                  BLASTX
Method
                  g1864017
NCBI GI
BLAST score
                   723
                  7.0e-77
E value
Match length
                  139
% identity
```

30992

(D63396) elongation factor-1 alpha [Nicotiana tabacum]



```
Seq. No.
                  220019
Seq. ID
                  LIB3149-038-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g224293
BLAST score
                  410
                  3.0e-40
E value
Match length
                  82
                  100
% identity
NCBI Description histone H4 [Triticum aestivum]
                  220020
Seq. No.
Seq. ID
                  LIB3149-038-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q585963
BLAST score
                  262
E value
                  7.0e-23
                  69
Match length
% identity
                  78
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
                  220021
Seq. No.
Seq. ID
                  LIB3149-038-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1931654
BLAST score
                  169
                  5.0e-12
E value
Match length
                  78
% identity
                  41
NCBI Description
                 (U95973) BRCA1-associated RING domain protein isolog
                  [Arabidopsis thaliana]
Seq. No.
                  220022
Seq. ID
                  LIB3149-038-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2689631
BLAST score
                  426
E value
                  2.0e-42
Match length
                  87
% identity
                  95
NCBI Description (AF022389) ADP-ribosylation factor [Vigna unguiculata]
Seq. No.
                  220023
                  LIB3149-038-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056469
BLAST score
                  300
                  2.0e-27
E value
Match length
                  110
% identity
                  58
NCBI Description
                  (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
                  factor from Arabidopsis thaliana. ESTs gb Z25826,
                  gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967,
```

Seq. No. 220024

gb Z25043 come from t

gb AA712956, gb T46403, gb T46050, gb AI100391 and

% identity

NCBI Description

59



```
LIB3149-038-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3122258
BLAST score
                  441
E value
                  5.0e-44
                  106
Match length
                  80
% identity
NCBI Description
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) (B4
                  INTEGRIN INTERACTOR) (CAB) >gi 2809383 (AF022229)
                  translation initiation factor 6 [Homo sapiens]
                  >gi 2910997 emb CAA72243 (Y11435) b4 integrin interactor
                  [Homo sapiens] >gi 3335506 (AF047433) b(2)gcn homolog [Homo
                  sapiens] >gi_4504771_ref_NP_002203.1_pITGB4BP_ integrin
                  beta 4 binding protein
                  220025
Seq. No.
Seq. ID
                  LIB3149-038-Q1-K1-E2
                  BLASTN
Method
NCBI GI
                  q1418705
BLAST score
                  130
                  7.0e-67
E value
                  326
Match length
% identity
                  94
NCBI Description G.hirsutum metallothionein-like gene
                  220026
Seq. No.
                  LIB3149-038-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q728880
BLAST score
                  349
E value
                  5.0e-33
Match length
                  107
                  65
% identity
NCBI Description
                 N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
                  >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase
                  homologue [Homo sapiens] >gi 1302661 (U52112) ARD1 N-acetyl
                  transferase related protein [Homo sapiens]
Seq. No.
                  220027
Seq. ID
                  LIB3149-038-Q1-K1-F1
Method
                  BLASTN
NCBI GI
                  q633680
BLAST score
                  41
                  6.0e-14
E value
Match length
                  132
                  83
% identity
NCBI Description S.tuberosum (Desiree) cr14 mRNA
Seq. No.
                  220028
                  LIB3149-038-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522011
BLAST score
                  163
E value
                  5.0e-14
Match length
                  76
```

30994

(AC007069) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                    220029
 Seq. ID
                    LIB3149-038-Q1-K1-G1
 Method
                    BLASTX
 NCBI GI
                    g133940
 BLAST score
                    178
 E value
                    4.0e-13
 Match length
                    46
                    76
 % identity
 NCBI Description
                    40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851 pir R3XL3A
                    ribosomal protein S3a - African clawed frog
                    >gi 65091 emb CAA40592 (X57322) ribosomal protein S1a
                    [Xenopus laevis]
 Seq. No.
                    220030
 Seq. ID
                    LIB3149-038-Q1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    q3341688
 BLAST score
                    153
 E value
                    5.0e-10
 Match length
                    99
                    40
 % identity
                    (AC003672) putative casein kinase II beta subunit
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    220031
 Seq. ID
                    LIB3149-038-Q1-K1-G3
 Method
                    BLASTX
 NCBI GI
                    q3237190
 BLAST score
                    179
 E value
                    3.0e-13
 Match length
                    72
 % identity
                    51
 NCBI Description
                    (AB014760) cystein proteinase inhibitor [Cucumis sativus]
 Seq. No.
                    220032
                    LIB3149-038-Q1-K1-G4
⊸ Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2780194
 BLAST score
                    140
                    9.0e-09
 E value
                    45
 Match length
                    67
 % identity
 NCBI Description
                    (AJ003197) adenine nucleotide translocator [Lupinus albus]
                    220033
 Seq. No.
                    LIB3149-038-Q1-K1-G5
 Seq. ID
 Method
                    BLASTX
```

Method BLASTX
NCBI GI g544134
BLAST score 228
E value 6.0e-19
Match length 98
% identity 54

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__\$22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__\$46260 RecA functional analog

DRT100 - Arabidopsis thaliana (fragment)

30995

```
Seq. No.
                  220034
Seq. ID
                  LIB3149-038-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1172571
BLAST score
                  626
                  2.0e-65
E value
Match length
                  136
                  84
% identity
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
NCBI Description
                  >gi 1076277 pir S52637 phosphoenolpyruvate carboxykinase
                   (ATP) (EC 4.1.1.49) - cucumber >gi 567102 (L31899)
                  phosphoenolpyruvate carboxykinase [Cucumis sativus]
Seq. No.
                  220035
Seq. ID
                  LIB3149-038-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q133793
BLAST score
                  144
                  2.0e-09
E value
Match length
                  28
                  100
% identity
                  40S RIBOSOMAL PROTEIN S15A (PPCB8) >gi 99825 pir S20945
NCBI Description
                  ribosomal protein S15a - rape >gi 1786\overline{3} emb \overline{CAA42599}
                   (X59983) r-protein BnS15a [Brassica napus]
Seq. No.
                  220036
Seq. ID
                  LIB3149-039-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2765366
BLAST score
                  198
E value
                  3.0e-15
Match length
                  109
% identity
                  39
NCBI Description
                 (Y14038) putative Ole e 1 protein [Betula pendula]
                  220037
Seq. No.
                  LIB3149-039-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1922251
BLAST score
                  726
                  3.0e-77
E value
Match length
                  136
                  100
% identity
NCBI Description
                  (Y12072) farnesyl pyrophosphate synthase [Gossypium
                  arboreum]
                  220038
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g121953
BLAST score
                  194
E value
                  6.0e-15
Match length
                  48
                  83
% identity
NCBI Description HISTONE H1 > gi 81905 pir S00033 histone H1.b - garden pea
                  >gi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263)
```

30996



[Pisum sativum] Seq. No. 220039 LIB3149-039-Q1-K1-A5 Seq. ID Method BLASTX NCBI GI g2351380 BLAST score 247 4.0e-21 E value Match length 122 % identity 44 (U54559) translation initiation factor eIF3 p40 subunit NCBI Description [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN 220040 Seq. No. Seq. ID LIB3149-039-Q1-K1-A7 BLASTX Method NCBI GI q3063453 BLAST score 159 E value 9.0e-11 40 Match length 72 % identity (AC003981) F22013.15 [Arabidopsis thaliana] NCBI Description Seq. No. 220041 LIB3149-039-Q1-K1-B1 Seq. ID BLASTX Method NCBI GI q3820648 BLAST score 286 E value 1.0e-25 Match length 72 71 % identity NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana] Seq. No. 220042 LIB3149-039-Q1-K1-B11 Seq. ID Method BLASTX g3492803 NCBI GI BLAST score 261 E value 1.0e-22 Match length 84 57 % identity NCBI Description (AJ002479) ENBP1 [Medicago truncatula] Seq. No. 220043 LIB3149-039-Q1-K1-B12 Seq. ID BLASTX Method g4098129 NCBI GI BLAST score 288 E value 2.0e-26 59 Match length

Seq. No. 220044

% identity

Seq. ID LIB3149-039-Q1-K1-B6

95

Method BLASTX NCBI GI g3747050

30997

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]



```
BLAST score
                   450
                  7.0e-45
E value
Match length
                  114
% identity
                   78
                  (AF093540) ribosomal protein L26 [Zea mays]
NCBI Description
                  220045
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-B7
                  BLASTX
Method
NCBI GI
                  g4100433
BLAST score
                   405
                   1.0e-39
E value
Match length
                   97
                   84
% identity
NCBI Description
                  (AF000378) beta-glucosidase [Glycine max]
Seq. No.
                   220046
Seq. ID
                   LIB3149-039-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q120672
BLAST score
                   538
                   3.0e-55
E value
Match length
                   126
% identity
                   85
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66016_pir__DEPZG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - parsley
                   >gi_20549_emb_CAA42902_ (X60344) glyceraldehyde 3-phosphate
                   dehydrogenase [Petroselinum crispum]
                   220047
Seq. No.
                   LIB3149-039-Q1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1362086
                   532
BLAST score
                   1.0e-54
E value
                   134
Match length
                   82
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_2129919_pir__$65957
                   5\hbox{-}methyltet \overline{r}ahy \overline{dr}opter oyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471 emb CAA58474 (X83499) methionine synthase
                   [Catharanthus roseus]
                   220048
Seq. No.
                   LIB3149-039-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539292
                   442
BLAST score
                   6.0e-44
E value
Match length
                   93
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
```

thaliana]

% identity

56



```
220049
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  265
                  4.0e-23
E value
                  100
Match length
                  54
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                  220050
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-C7
                  BLASTX
Method
NCBI GI
                  g547886
BLAST score
                  503
                  4.0e-51
E value
                  137
Match length
                  73
% identity
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                  (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi 542102_pir__S42939 malate dehydrogenase
                  (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40)
                  precursor - Flaveria pringlei >gi_1084444_pir__S52016
                  malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)
                  (EC 1.1.1.40) - Flaveria pringlei >gi 459441_emb_CAA54986_
                  (X78069) malate dehydrogenase (oxaloacetate
                  decarboxylating) (NADP+) [Flaveria pringlei]
                  220051
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  a1498053
                  411
BLAST score
                  2.0e-40
E value
Match length
                  133
% identity
                  66
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
                  220052
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3367591
BLAST score
                  256
                  3.0e-22
E value
Match length
                  121
% identity
                  45
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                  220053
Seq. No.
                  LIB3149-039-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063465
BLAST score
                  319
E value
                  2.0e-29
Match length
                  129
```

30999

NCBI Description (AC003981) F22013.27 [Arabidopsis thaliana]

```
220054
Seq. No.
Seq. ID
                  LIB3149-039-Q1-K1-D5
                  BLASTX
Method
                  g4193382
NCBI GI
BLAST score
                  338
                  1.0e-31
E value
                  66
Match length
                  91
% identity
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
                  220055
Seq. No.
                  LIB3149-039-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g3522938
NCBI GI
BLAST score
                  346
                  1.0e-32
E value
Match length
                  132
                  58
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220056
Seq. No.
                  LIB3149-039-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3023816
                  159
BLAST score
                  6.0e-11
E value
Match length
                  33
% identity
                  91
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  220057
Seq. No.
                  LIB3149-039-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                  q1174592
NCBI GI
BLAST score
                   605
                   5.0e-63
E value
Match length
                  119
                   96
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                   220058
                  LIB3149-039-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g120941
BLAST score
                   285
E value
                  1.0e-25
                  86
Match length
                   60
% identity
NCBI Description GAR1 PROTEIN >gi 83030 pir__S19634 nucleolar protein GAR1 -
                   yeast (Saccharomyces cerevisiae) >gi_3728_emb_CAA45162_
```

31000



(X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Gar1p: Small nucleolar RNA protein required for pre-rRNA splicing [Saccharomyces cerevisiae]

220059 Seq. No. LIB3149-039-Q1-K1-F12 Seq. ID Method BLASTX g4432837 NCBI GI BLAST score 219 8.0e-18 E value Match length 132 % identity 42

NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No. 220060

Seq. ID LIB3149-039-Q1-K1-F3 Method BLASTX

Method BLASTX
NCBI GI g4490332
BLAST score 344
E value 2.0e-32
Match length 119
% identity 59

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 220061

Seq. ID LIB3149-039-Q1-K1-F4

Method BLASTX
NCBI GI g4098129
BLAST score 700
E value 4.0e-74
Match length 138
% identity 96

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 220062

Seq. ID LIB3149-039-Q1-K1-F5

Method BLASTN
NCBI GI g1777727
BLAST score 51
E value 5.0e-20
Match length 160
% identity 82

NCBI Description Gossypium hirsutum 18S ribosomal RNA gene, partial sequence

Seq. No. 220063

Seq. ID LIB3149-039-Q1-K1-F6

Method BLASTX
NCBI GI g2190992
BLAST score 346
E value 1.0e-32
Match length 104
% identity 64

NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops

tauschii]

Seq. No. 220064

Seq. ID LIB3149-039-Q1-K1-F7



```
BLASTX
Method
                  g1771780
NCBI GI
                  533
BLAST score
                  1.0e-54
E value
                  132
Match length
                  83
% identity
                  (Y10024) ubiquitin extension protein [Solanum tuberosum]
NCBI Description
                  220065
Seq. No.
                  LIB3149-039-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g1346524
NCBI GI
                  390
BLAST score
                  7.0e-38
E value
                  125
Match length
                  67
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 497900
                   (M73430) S-adenosyl methionine synthetase [Populus
                  deltoides]
                   220066
Seq. No.
                  LIB3149-039-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g3122703
NCBI GI
                   289
BLAST score
                   5.0e-26
E value
                  76
Match length
                  74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                  protein L23a [Fritillaria agrestis]
                   220067
Seq. No.
                   LIB3149-039-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   q1173043
NCBI GI
                   213
BLAST score
                   4.0e-17
E value
Match length
                   48
                   88
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi_479441 pir__S33899 ribosomal
NCBI Description
                   protein L38 - tomato (cv. Moneymaker)
                   >gi 313027 emb CAA49599 (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
Seq. No.
                   220068
                   LIB3149-039-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   q1709061
NCBI GI
BLAST score
                   286
E value
                   3.0e - 34
Match length
                   131
```

53 % identity

NCBI Description PROBABLE METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE

PRECURSOR (ACYLATING) (MMSDH) >gi 3875820 emb CAA88946_

(Z49127) similar to methylmalonate-semialdehyde

dehydrogenase; cDNA EST EMBL: Z14764 comes from this gene;



cDNA EST EMBL: Z14949 comes from this gene; cDNA EST EMBL: D26762 comes from this gene; cDNA EST EMBL: D26766 comes from thi

220069 Seq. No. LIB3149-039-Q1-K1-H2 Seq. ID Method BLASTX q567893 NCBI GI BLAST score 155 2.0e-10 E value Match length 77 48 % identity (L37382) beta-galactosidase-complementation protein NCBI Description [Cloning vector] Seq. No. 220070 LIB3149-039-Q1-K1-H4 Seq. ID Method BLASTX NCBI GI g2829899 BLAST score 317 3.0e-29 E value Match length 140 45 % identity (AC002311) similar to ripening-induced protein, NCBI Description gp AJ001449 2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana] Seq. No. 220071 LIB3149-039-Q1-K1-H7 Seq. ID Method BLASTX q1113861 NCBI GI 208 BLAST score 1.0e-16 E value Match length 84 55 % identity (U39930) nitrate reductase [Chlorella vulgaris] >gi_1113863 NCBI Description (U39931) nitrate reductase [Chlorella vulgaris] 220072 Seq. No. LIB3149-039-Q1-K1-H8 Seq. ID Method BLASTX NCBI GI g3549669 173 BLAST score 1.0e-12 E value 49 Match length 71 % identity NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 220073

Seq. ID LIB3149-040-Q1-K1-A12

Method BLASTX
NCBI GI g2911042
BLAST score 465
E value 1.0e-46
Match length 135
% identity 69

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein



[Arabidopsis thaliana]

```
Seq. No.
                  220074
Seq. ID
                  LIB3149-040-Q1-K1-A2
Method
                  BLASTX
                  q3169028
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
                  65
Match length
                  48
% identity
                  (AL023702) putative cationic amino acid transporter
NCBI Description
                  [Streptomyces coelicolor]
                  220075
Seq. No.
                  LIB3149-040-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q4544432
NCBI GI
                   472
BLAST score
E value
                  2.0e-47
                  135
Match length
                   70
% identity
                  (AC006955) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   220076
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-A7
                   BLASTX
Method
                   q2842480
NCBI GI
BLAST score
                   492
E value
                   8.0e-50
Match length
                   116
                   53
% identity
                  (AL021749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   220077
Seq. No.
                   LIB3149-040-Q1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760325
BLAST score
                   293
E value
                   2.0e-26
                   127
Match length
% identity
                   48
NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]
                   220078
Seq. No.
                   LIB3149-040-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g1172977
NCBI GI
                   553
BLAST score
                   6.0e-57
E value
Match length
                   124
                   86
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                   ribosomal protein L18 [Arabidopsis thaliana]
```

Seq. No. 220079



```
LIB3149-040-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076314
BLAST score
                  511
E value
                  5.0e-52
                  110
Match length
                  85
% identity
NCBI Description
                  cystathionine gamma-lyase (EC 4.4.1.1) 1 - Arabidopsis
                  thaliana (fragment) >gi_499166_emb_CAA56143_ (X79707) CYS1
                  [Arabidopsis thaliana]
                  220080
Seq. No.
                  LIB3149-040-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3219353
BLAST score
                  195
                  3.0e-15
E value
Match length
                  39
% identity
                  90
                  (AF061514) manganese superoxide dismutase [Gossypium
NCBI Description
                  hirsutum]
                  220081
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3915847
                  649
BLAST score
                  3.0e-68
E value
Match length
                  134
% identity
                  91
                  40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  220082
Seq. ID
                  LIB3149-040-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g994736
BLAST score
                  142
E value
                  5.0e-09
Match length
                  53
% identity
                  55
NCBI Description
                  (M18327) LacOPZ-alpha peptide from pUC9; putative [cloning
                  vectors] >gi 994738 (M18328) LacOPZ-alpha peptide from
                  pUC9; putative [cloning vectors] >qi 994740 (M18329)
                  LacOPZ-alpha peptide from pUC9; putative [cloning vectors]
                  220083
Seq. No.
                  LIB3149-040-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4163997
BLAST score
                  264
```

E value 4.0e-23 Match length 108 50 % identity

(AF087483) alpha-xylosidase precursor [Arabidopsis NCBI Description

thaliana]

E value

Match length

NCBI Description

% identity

95

68



```
220084
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-C1
                  BLASTX
Method
                  q3738329
NCBI GI
BLAST score
                  181
                  2.0e-13
E value
                  46
Match length
                  83
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220085
Seq. No.
                  LIB3149-040-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                  q2911042
NCBI GI
BLAST score
                  175
                  1.0e-12
E value
Match length
                  58
                  59
% identity
NCBI Description
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
                  [Arabidopsis thaliana]
                  220086
Seq. No.
                  LIB3149-040-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  q129248
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
                  100
Match length
% identity
                  21
NCBI Description
                  ORGAN SPECIFIC PROTEIN S2 >gi 72318 pir KNPMS2 protein S2
                  - garden pea >gi_295831_emb_CAA35944_ (X51595) S2 protein
                   [Pisum sativum]
                  220087
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g133829
BLAST score
                  195
E value
                   6.0e-15
Match length
                  72
% identity
                  57
                  30S RIBOSOMAL PROTEIN S17, CHLOROPLAST PRECURSOR (CS17)
NCBI Description
                  >gi 81948 pir B35542 ribosomal protein S17 - garden pea
                   (fragment) >gi 169068 (M31025) ribosomal protein S17 [Pisum
                   sativum]
                  220088
Seq. No.
                  LIB3149-040-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3176687
BLAST score
                  354
                  1.0e-33
```

31006

(AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and



gb R64855 come from this gene. [Arabidopsis thaliana]

220089 Seq. No. Seq. ID LIB3149-040-Q1-K1-D3 Method BLASTX q3550661 NCBI GI BLAST score 210 E value 9.0e-17 54 Match length % identity NCBI Description

(AJ001310) 39 kDa EF-Hand containing protein [Solanum

tuberosum]

220090 Seq. No.

LIB3149-040-Q1-K1-D4 Seq. ID

Method BLASTX NCBI GI g4103154 BLAST score 357 5.0e - 34E value 130 Match length % identity 55

NCBI Description (AF020717) histidyl-tRNA synthetase [Triticum aestivum]

220091 Seq. No.

LIB3149-040-Q1-K1-D6 Seq. ID

Method BLASTX q124226 NCBI GI BLAST score 383 E value 5.0e-37 Match length 79 94 % identity

INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) NCBI Description

> >qi 100278 pir S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi 19702 emb CAA45104 (X63542) eukaryotic initiation factor 5A ($\overline{2}$) [Nicotiana

plumbaginifolia]

220092 Seq. No.

Seq. ID LIB3149-040-Q1-K1-D7

Method BLASTX g124226 NCBI GI 337 BLAST score 1.0e-31 E value 79 Match length % identity 84

NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)

>gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana

plumbaginifolia]

220093 Seq. No.

LIB3149-040-Q1-K1-D8 Seq. ID

Method BLASTX g464734 NCBI GI BLAST score 229 3.0e-19 E value



```
53
Match length
                  85
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi 481237 pir S38379
                  adenosylhomocysteinase (EC\overline{3.3.1.1}) - Madagascar periwinkle
                  >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine
                  hydrolase [Catharanthus roseus]
                  220094
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-D9
                  BLASTX
Method
                  q549056
NCBI GI
                  398
BLAST score
                  8.0e-39
E value
                  129
Match length
                   64
% identity
                  T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA)
NCBI Description
                   >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1)
                  beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT
                   (chaperonin containing TCP-1) beta subunit [Mus musculus]
                   220095
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-E12
                  BLASTX
Method
                   g3860277
NCBI GI
                   299
BLAST score
                   4.0e-27
E value
                   62
Match length
                   92
% identity
                   (ACO05824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   220096
Seq. No.
Seq. ID
                   LIB3149-040-Q1-K1-E2
Method
                   BLASTX
                   q1136298
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
Match length
                   102
                   87
% identity
NCBI Description (D61377) WIPK [Nicotiana tabacum]
                   220097
Seq. No.
Seq. ID
                   LIB3149-040-Q1-K1-E6
Method
                   BLASTN
NCBI GI
                   g2924257
```

Method BLASTN
NCBI GI g2924257
BLAST score 36
E value 3.0e-11
Match length 80
% identity 86

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 220098

Seq. ID LIB3149-040-Q1-K1-E7

Method BLASTX NCBI GI 92760325

31008

```
BLAST score
                  320
                  1.0e-29
E value
                  131
Match length
                  51
% identity
                  (AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                  220099
Seq. No.
                  LIB3149-040-Q1-K1-E9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2264305
BLAST score
                  44
                  2.0e-15
E value
                  81
Match length
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK23, complete sequence [Arabidopsis thaliana]
                  220100
Seq. No.
                  LIB3149-040-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  g4490332
NCBI GI
BLAST score
                  174
                  2.0e-12
E value
                  80
Match length
                  51
% identity
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  220101
                  LIB3149-040-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  g4455194
NCBI GI
BLAST score
                   260
                  1.0e-22
E value
                  65
Match length
                   75
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   220102
                  LIB3149-040-Q1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2980795
BLAST score
                   567
E value
                   1.0e-58
                   119
Match length
                   91
% identity
                 (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   220103
Seq. No.
                   LIB3149-040-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q729618
```

Method BLASTX
NCBI GI g729618
BLAST score 519
E value 5.0e-53
Match length 134
% identity 78

NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2)

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP

2) >gi 82172 pir PQ0262 luminal binding protein BLP-2 common tobacco (fragment) >gi_100338_pir__S21878 heat shock protein BiP homolog blp2 - common tobacco (fragment) >gi 19807 emb CAA42661 (X60059) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No. 220104 LIB3149-040-Q1-K1-F6 Seq. ID BLASTX Method g3986119 NCBI GI 305 BLAST score E value 4.0e-32 Match length 131 % identity 60

NCBI Description (AB013101) 1-aminocyclopropane-1-carboxylate oxidase

[Lycopersicon esculentum]

Seq. No. 220105 LIB3149-040-Q1-K1-F7 Seq. ID Method BLASTX NCBI GI q1439609 BLAST score 552 E value 7.0e-57 110

Match length % identity 53

(U62778) delta-tonoplast intrinsic protein [Gossypium NCBI Description

hirsutum]

Seq. No. 220106

LIB3149-040-Q1-K1-F9 Seq. ID

Method BLASTX q3582436 NCBI GI BLAST score 474 1.0e-47 E value 131 Match length

70 % identity

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 220107

LIB3149-040-Q1-K1-G1 Seq. ID

Method BLASTX NCBI GI g3413170 BLAST score 628 9.0e-66 E value 128 Match length 95 % identity

(AJ010227) 40S ribosomal protein S6 [Cicer arietinum] NCBI Description

220108 Seq. No.

LIB3149-040-Q1-K1-G10 Seq. ID

Method BLASTX NCBI GI q508304 BLAST score 149 E value 7.0e-10 Match length 63 49 % identity

(L22305) corC [Medicago sativa] NCBI Description

NCBI GI

```
220109
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2275213
BLAST score
                  407
                  8.0e-40
E value
Match length
                  125
                  61
% identity
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  220110
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-G5
                  BLASTX
Method
NCBI GI
                  q3318611
BLAST score
                  261
E value
                  2.0e-23
Match length
                  57
% identity
                  97
NCBI Description
                  (AB016063) mitochondrial phosphate transporter [Glycine
                  max]
Seq. No.
                  220111
Seq. ID
                  LIB3149-040-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g4539422
BLAST score
                  629
E value
                  7.0e-66
Match length
                  135
% identity
                  81
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  220112
Seq. ID
                  LIB3149-040-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2935529
BLAST score
                  412
                  2.0e-40
E value
Match length
                  105
% identity
                   69
NCBI Description
                  (AF049069) No definition line found [Pinus radiata]
                  220113
Seq. No.
                  LIB3149-040-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123264
                   417
BLAST score
                   4.0e-41
E value
                  85
Match length
% identity
                  91
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                  220114
Seq. No.
                  LIB3149-040-Q1-K1-H11
Seq. ID
Method
                  BLASTX
```

31011

g4539543

NCBI GI

E value Match length

BLAST score

% identity

```
484
BLAST score
E value
                  6.0e-49
                  116
Match length
                  83
% identity
                  (AJ133422) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                  [Nicotiana tabacum]
                  220115
Seq. No.
                  LIB3149-040-Q1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1469930
                  211
BLAST score
E value
                  4.0e-17
Match length
                  69
                  70
% identity
                  (U48777) fiber-specific acyl carrier protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  220116
                  LIB3149-040-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q3452497
NCBI GI
BLAST score
                  597
                  4.0e-62
E value
                  133
Match length
                  87
% identity
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]
                  220117
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-H8
Method
                  BLASTX
                  q4090533
NCBI GI
BLAST score
                  558
                  2.0e-57
E value
Match length
                  136
                  79
% identity
NCBI Description (U68215) ACC oxidase [Carica papaya]
                  220118
Seq. No.
Seq. ID
                  LIB3149-040-Q1-K1-H9
                  BLASTX
Method
NCBI GI
                  q2829862
BLAST score
                  146
                  2.0e-09
E value
                  99
Match length
% identity
NCBI Description (AC002396) Similar to glucosyltransferases [Arabidopsis
                  thaliana]
Seq. No.
                  220119
                  LIB3149-042-Q1-K1-A1
Seq. ID
Method
                  BLASTX
```

31012

.

g1495768

401 3.0e-39

110 69

E value

Match length

% identity

1.0e-33

120

60

```
(Z68506) chloroplast inner envelope protein, 110 kD
NCBI Description
                   (IEP110) [Pisum sativum]
                  220120
Seq. No.
Seq. ID
                  LIB3149-042-Q1-K1-A11
                  {\tt BLASTX}
Method
                  q508304
NCBI GI
                  286
BLAST score
                  3.0e-26
E value
                  70
Match length
                  76
% identity
                  (L22305) corC [Medicago sativa]
NCBI Description
                  220121
Seq. No.
                  LIB3149-042-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  g4567202
NCBI GI
BLAST score
                   559
                   1.0e-57
E value
                   116
Match length
% identity
                   94
                   (AC007168) putative myo-inositol 1-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
                   220122
Seq. No.
Seq. ID
                   LIB3149-042-Q1-K1-A5
Method
                   BLASTX
                   g1076511
NCBI GI
                   380
BLAST score
                   9.0e-37
E value
Match length
                   116
% identity
                   68
                   H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                   >gi 758250 emb_CAA59799_ (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
                   220123
Seq. No.
Seq. ID
                   LIB3149-042-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   q141614
                   172
BLAST score
                   1.0e-12
E value
Match length
                   63
                   65
% identity
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                   >gi 82662 pir B22831 22K zein precursor (clone M1) - maize
                   >gi 22527 emb CAA24722 (V01475) reading frame zein [Zea
                   mays] >qi 224510 prf 1107201D zein M1 [Zea mays]
                   220124
Seq. No.
                   LIB3149-042-Q1-K1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q464621
BLAST score
                   355
```

31013



60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir_ S28586

ribosomal protein ML16 - common ice plant

>gi 19539_emb_CAA49175 (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 220125

NCBI Description

Seq. ID LIB3149-042-Q1-K1-B11

Method BLASTX
NCBI GI g4056506
BLAST score 236
E value 3.0e-20
Match length 62
% identity 74

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 220126

Seq. ID LIB3149-042-Q1-K1-B3

Method BLASTX
NCBI GI g1397319
BLAST score 149
E value 1.0e-09
Match length 112
% identity 31

NCBI Description (U61953) No definition line found [Caenorhabditis elegans]

Seq. No. 220127

Seq. ID LIB3149-042-Q1-K1-B4

Method BLASTX
NCBI GI g3860315
BLAST score 454
E value 3.0e-45
Match length 99
% identity 85

NCBI Description (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]

Seq. No. 220128

Seq. ID LIB3149-042-Q1-K1-B5

Method BLASTX
NCBI GI g3860315
BLAST score 433
E value 6.0e-43
Match length 104
% identity 79

NCBI Description (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]

Seq. No. 220129

Seq. ID LIB3149-042-Q1-K1-B7

Method BLASTX
NCBI GI 94417280
BLAST score 381
E value 9.0e-37
Match length 95
% identity 80

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 220130

Seq. ID LIB3149-042-Q1-K1-B9



56

84

Match length

% identity

```
Method
                  BLASTX
                  q2497752
NCBI GI
BLAST score
                  173
                  9.0e-13
E value
Match length
                  51
% identity
                  63
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >qi 1321911 emb CAA65475 (X96714) lipid transfer protein
                  [Prunus dulcis]
Seq. No.
                  220131
Seq. ID
                  LIB3149-042-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2507281
BLAST score
                  352
                  1.0e-33
E value
Match length
                  65
% identity
                  100
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >qi 1668706 emb CAA66048
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
                  220132
Seq. No.
Seq. ID
                  LIB3149-042-Q1-K1-C4
Method
                  BLASTX
                  g1172995
NCBI GI
BLAST score
                  206
                  3.0e-16
E value
                  79
Match length
% identity
                  56
                  60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir S52084 ribosomal
NCBI Description
                  protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
                  ribosomal protein L22 [Rattus norvegicus]
                  >gi 1093952 prf 2105193A ribosomal protein L22 [Rattus
                  norvegicus]
                  220133
Seq. No.
                  LIB3149-042-Q1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3024126
BLAST score
                  687
                  1.0e-72
E value
Match length
                  132
                  97
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
Seq. No.
                   220134
                  LIB3149-042-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                   g133867
NCBI GI
                   242
BLAST score
E value
                   1.0e-20
```

31015

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir_S16577 ribosomal



220135

protein S11 - maize >gi 22470 emb CAA39438 (X55967) ribosomal protein S11 [Zea mays]

Seq. No. Seq. ID LIB3149-042-Q1-K1-C8 BLASTX Method q3046705 NCBI GI BLAST score 201 9.0e-16 E value Match length 59 71 % identity

(AL022198) ribosomal protein S11 - like (partial) NCBI Description

[Arabidopsis thaliana]

220136 Seq. No.

Seq. ID LIB3149-042-Q1-K1-C9

Method BLASTX NCBI GI g1922251 BLAST score 284 9.0e-26 E value 58 Match length % identity

(Y12072) farnesyl pyrophosphate synthase [Gossypium NCBI Description

arboreum]

220137 Seq. No.

Seq. ID LIB3149-042-Q1-K1-D11

Method BLASTX NCBI GI q3128228 BLAST score 441 3.0e-44E value Match length 86 94 % identity

(AC004077) putative ribosomal protein L18A [Arabidopsis NCBI Description

thaliana] >gi 3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

220138 Seq. No.

Seq. ID LIB3149-042-Q1-K1-D12

Method BLASTX NCBI GI q399414 441 BLAST score 3.0e-44E value Match length 87 98 % identity

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_322865_pir__JC1454 translation elongation factor eEF-1

alpha chain - wheat $>gi_170776$ (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum]

>gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha

[Hordeum vulgare]

220139 Seq. No.

LIB3149-042-Q1-K1-D7 Seq. ID

BLASTX Method g3421123 NCBI GI 379 BLAST score



E value 1.0e-36 Match length 84 83

NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis

thaliana]

Seq. No. 220140

Seq. ID LIB3149-042-Q1-K1-D8

Method BLASTX
NCBI GI g131770
BLAST score 349
E value 5.0e-33
Match length 97

% identity 65

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir __R3D024

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 220141

Seq. ID LIB3149-042-Q1-K1-E1

Method BLASTX
NCBI GI g464707
BLAST score 155
E value 3.0e-13
Match length 58
% identity 71

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910 emb_CAB39647.1 (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 220142

Seq. ID LIB3149-042-Q1-K1-E11

Method BLASTX
NCBI GI g2558962
BLAST score 156
E value 1.0e-10
Match length 62
% identity 53

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 220143

Seq. ID LIB3149-042-Q1-K1-E4

Method BLASTX

g586076 NCBI GI 733 BLAST score 5.0e-78 E value 144 Match length 96 % identity TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta NCBI Description tubulin 1 [Lupinus albus] 220144 Seq. No. LIB3149-042-Q1-K1-E6 Seq. ID BLASTX Method q3451473 NCBI GI BLAST score 179 5.0e-13 E value Match length 112 39 % identity (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces NCBI Description pombe] 220145 Seq. No. LIB3149-042-Q1-K1-E7 Seq. ID BLASTX Method g3894172 NCBI GI BLAST score 313 6.0e-29 E value Match length 117 47 % identity (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis NCBI Description thaliana] 220146 Seq. No. LIB3149-042-Q1-K1-E8 Seq. ID BLASTX Method g2244929 NCBI GI 150 BLAST score 1.0e-09 E value Match length 75 43 % identity

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 220147

Seq. ID LIB3149-042-Q1-K1-F1

Method BLASTX
NCBI GI 9729882
BLAST score 143
E value 6.0e-09
Match length 25
% identity 92

NCBI Description CASEIN KINASE II BETA' CHAIN (CK II)

>gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta
chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984)
casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
>gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 220148



```
LIB3149-042-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g4101589
NCBI GI
BLAST score
                  247
                  2.0e-21
E value
                  76
Match length
                  61
% identity
                  (AF005050) aspartyl aminopeptidase [Homo sapiens]
NCBI Description
                  220149
Seq. No.
                  LIB3149-042-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  g4127456
NCBI GI
BLAST score
                  210
                   5.0e-17
E value
Match length
                  70
                   66
% identity
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
                   220150
Seq. No.
                   LIB3149-042-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g2065531
NCBI GI
BLAST score
                   396
                   2.0e-45
E value
Match length
                   117
                   75
% identity
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                   220151
Seq. No.
                   LIB3149-042-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g2632254
NCBI GI
BLAST score
                   503
                   3.0e-51
E value
                   105
Match length
                   87
% identity
                  (Y12465) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   220152
Seq. No.
                   LIB3149-042-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g1841870
NCBI GI
                   294
BLAST score
                   1.0e-26
E value
                   78
Match length
                   73
% identity
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
                   220153
Seq. No.
                   LIB3149-042-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1841870
                   318
BLAST score
                   2.0e-29
E value
```

31019

95

69

Match length

% identity

220159

```
(U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
Seq. No.
                   220154
                   LIB3149-042-Q1-K1-F9
Seq. ID
Method
                   BLASTN
                   g1418705
NCBI GI
BLAST score
                   76
                   8.0e-35
E value
                   178
Match length
                   96
 % identity
                   G.hirsutum metallothionein-like gene
NCBI Description
 Seq. No.
                   220155
                   LIB3149-042-Q1-K1-G10
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g2581785
BLAST score
                   358
                   2.0e-34
E value
                   86
Match length
                   77
 % identity
                   (U94999) class 2 non-symbiotic hemoglobin [Arabidopsis
 NCBI Description
                   thaliana]
                   220156
 Seq. No.
                   LIB3149-042-Q1-K1-G2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g322750
 BLAST score
                   640
                   4.0e-67
 E value
 Match length
                   128
                   95
 % identity
                   ubiquitin / ribosomal protein CEP52 - wood tobacco
 NCBI Description
                   >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
                   220157
 Seq. No.
                   LIB3149-042-Q1-K1-G4
 Seq. ID
 Method
                   BLASTX
                   g1703380
 NCBI GI ,
                    448
 BLAST score
                    1.0e-44
 E value
                    87
 Match length
                    98
 % identity
 NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                   ADP-ribosylation factor [Oryza sativa]
                    220158
 Seq. No.
 Seq. ID
                    LIB3149-042-Q1-K1-G5
                    BLASTX
 Method
 NCBI GI
                    q2431769
                    208
 BLAST score
                    1.0e-16
 E value
 Match length
                    55
 % identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
```



```
Seq. ID
                   LIB3149-042-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3894387
BLAST score
                   208
                   2.0e-16
E value
                   135
Match length
                   5
 % identity
                   (AF053995) Hcr2-OB [Lycopersicon esculentum]
NCBI Description
                   220160
 Seq. No.
                   LIB3149-042-Q1-K1-G7
 Seq. ID
                   BLASTX
 Method
                   g3413167
 NCBI GI
 BLAST score
                   354
                   1.0e-33
 E value
                   71
 Match length
 % identity
                    96
                   (AJ010225) elongation factor 1-alpha [Cicer arietinum]
 NCBI Description
                    220161
 Seq. No.
 Seq. ID
                   LIB3149-042-Q1-K1-G8
                    BLASTX
 Method
 NCBI GI
                    g3319882
 BLAST score
                    265
                    3.0e-23
 E value
                    62
 Match length
                    82
 % identity
                    (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
 NCBI Description
                    arietinum]
                    220162
 Seq. No.
                    LIB3149-042-Q1-K1-H11
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3128228
                    334
 BLAST score
                    1.0e-31
 E value
                    70
 Match length
                    90
 % identity
                    (AC004077) putative ribosomal protein L18A [Arabidopsis
 NCBI Description
                    thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                    L18A [Arabidopsis thaliana]
                    220163
 Seq. No.
                    LIB3149-042-Q1-K1-H3
 Seq. ID
                    BLASTX
 Method
                    g1754522
 NCBI GI
                    170
 BLAST score
                    4.0e-21
 E value
                    106.
 Match length
                    52
 % identity
                   (D89984) ornithine decarboxylase [Nicotiana tabacum]
 NCBI Description
                    220164
 Seq. No.
                    LIB3149-042-Q1-K1-H5
Seq. ID
```

31021

BLASTX

432

g464707

Method

NCBI GI BLAST score



E value 6.0e-43 Match length 107 % identity 83 NCBI Description 40S RIB

40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seg. No. 220165

Seq. ID LIB3149-042-Q1-K1-H6

Method BLASTX
NCBI GI g464707
BLAST score 239
E value 4.0e-20
Match length 78
% identity 62

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 220166

Seq. ID LIB3149-042-Q1-K1-H8

Method BLASTX NCBI GI g3024020

BLAST score 602 E value 1.0e-62 Match length 130 % identity 87

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 220167

Seq. ID LIB3149-043-Q1-K1-A1

Method BLASTN
NCBI GI g642263
BLAST score 187
E value 1.0e-101
Match length 347
% identity 88

NCBI Description R.enysii ITS2 and 28S rRNA gene (partial)

Seq. No. 220168

Seq. ID LIB3149-043-Q1-K1-A2

Method BLASTX
NCBI GI g1350707
BLAST score 121
E value 1.0e-12
Match length 52
% identity 70

NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal

protein 17K - mouse >gi_404766 (L08651) ribosomal protein

[Mus musculus]

Seq. No. 220169

Seq. ID LIB3149-043-Q1-K1-A3

Method BLASTX
NCBI GI g124224
BLAST score 610
E value 1.0e-63
Match length 122
% identity 93

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 220170

Seq. ID LIB3149-043-Q1-K1-A6

Method BLASTX
NCBI GI g126959
BLAST score 297
E value 4.0e-27
Match length 83
% identity 75

NCBI Description TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7-5A (RT-TIP)

>gi_82192_pir__JQ1011 TobRB7-5A protein - common tobacco
>gi_100371_pir__S13719 probable membrane channel protein common tobacco >gi_20011_emb_CAA38634_ (X54855) possible

membrane channel protein [Nicotiana tabacum]

Seq. No. 220171

Seq. ID LIB3149-043-Q1-K1-A8

Method BLASTX
NCBI GI g3873845
BLAST score 150
E value 1.0e-09
Match length 54
% identity 48

NCBI Description (Z82256) similar to 60S ribosomal protein L29; cDNA EST yk493f9.3 comes from this gene [Caenorhabditis elegans]

```
220172
Seq. No.
                  LIB3149-043-Q1-K1-B2
Seq. ID
                  BLASTN
Method
                  g2687434
NCBI GI
BLAST score
                  237
                  1.0e-131
E value
                  277
Match length
                  96
% identity
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                  partial sequence
                  220173
Seq. No.
                  LIB3149-043-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  q4432840
NCBI GI
                  321
BLAST score
                  8.0e-30
E value
                  106
Match length
                  61
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220174
Seq. No.
Seq. ID
                  LIB3149-043-Q1-K1-B7
                  BLASTX
Method
                  g2829871
NCBI GI
                  259
BLAST score
                  5.0e-39
E value
                  103
Match length
                  72
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   220175
Seq. No.
Seq. ID
                  LIB3149-043-Q1-K1-C1
Method
                  BLASTX
                  q3694872
NCBI GI
BLAST score
                   474
                   9.0e-48
E value
                   116
Match length
                   76
% identity
NCBI Description (AF092547) profilin [Ricinus communis]
                   220176
Seq. No.
Seq. ID
                   LIB3149-043-Q1-K1-C10
                   BLASTX
Method
NCBI GI
                   q730526
BLAST score
                   475
                   6.0e-48
E value
Match length
                   97
                   88
% identity
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                   >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein
                   [Arabidopsis thaliana]
Seq. No.
                   220177
                   LIB3149-043-Q1-K1-C11
Seq. ID
```

```
BLASTX
Method
NCBI GI
                  g1917019
                  508
BLAST score
                  1.0e-51
E value
Match length
                  128
                  77
% identity
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                  220178
Seq. No.
                  LIB3149-043-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g2529665
NCBI GI
BLAST score
                   628
                   9.0e-66
E value
                   129
Match length
% identity
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                   thaliana]
                   220179
Seq. No.
                   LIB3149-043-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3128177
BLAST score
                   335
                   1.0e-31
E value
                   82
Match length
% identity
                   80
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                   220180
Seq. No.
                   LIB3149-043-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g2827552
NCBI GI
BLAST score
                   482
                   1.0e-48
E value
                   108
Match length
                   41
% identity
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   220181
                   LIB3149-043-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2894603
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   74
Match length
                   16
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
```

Seq. ID LIB3149-043-Q1-K1-C5

Method BLASTX
NCBI GI g2119353
BLAST score 287
E value 8.0e-26
Match length 115
% identity 50



NCBI Description calmodulin - moss (Physcomitrella patens)

Seq. No. 220183

Seq. ID LIB3149-043-Q1-K1-C6

Method BLASTX
NCBI GI g514322
BLAST score 416
E value 6.0e-41
Match length 122
% identity 63

NCBI Description (L34772) RNA polymerase subunit [Arabidopsis thaliana]

>qi 1586549 prf 2204246A RNA polymerase [Arabidopsis

thaliana]

Seq. No. 220184

Seq. ID LIB3149-043-Q1-K1-C9

Method BLASTX
NCBI GI g1352821
BLAST score 626
E value 2.0e-65
Match length 119
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 220185

Seq. ID LIB3149-043-Q1-K1-D1

Method BLASTX
NCBI GI g3834309
BLAST score 283
E value 2.0e-25
Match length 89
% identity 54

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb_L16983

Daucus carota and a member of S locus glycoprotein family

PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb W43262 come from this gene. [Arabidopsis thaliana]

Seq. No. 220186

Seq. ID LIB3149-043-Q1-K1-D4

Method BLASTX
NCBI GI g4039014
BLAST score 478
E value 3.0e-48
Match length 127
% identity 66

NCBI Description (AF037338) cleft lip and palate transmembrane protein 1

[Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate

transmembrane protein 1 [Homo sapiens]

>gi 4502897 ref NP 001285.1 pCLPTM1_ cleft lip and palate

associated transmembrane protein

Seq. No. 220187

Seq. ID LIB3149-043-Q1-K1-D6



```
BLASTX
Method
                  g2494620
NCBI GI
                  277
BLAST score
                  1.0e-24
E value
Match length
                  71
                  68
% identity
                  SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN >gi_975319
NCBI Description
                   (U31902) succinate dehydrogenase iron-sulfur protein
                  subunit [Paracoccus denitrificans]
                  220188
Seq. No.
                  LIB3149-043-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g2996166
NCBI GI
                  339
BLAST score
                  7.0e-32
E value
                  66
Match length
                  91
% identity
                  (AF051757) putative 60S ribosomal protein L15 [Picea
NCBI Description
                  mariana] >gi 2996168 (AF051758) putative 60S ribosomal
                  protein L15 [Picea mariana] >gi_2996170 (AF051759) putative
                   60S ribosomal protein L15 [Picea mariana]
                  220189
Seq. No.
                  LIB3149-043-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g1335861
NCBI GI
BLAST score
                  55
                  4.0e-22
E value
                  212
Match length
                   84
% identity
NCBI Description Glycine max clathrin heavy chain mRNA, complete cds
                   220190
Seq. No.
                  LIB3149-043-Q1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1296816
BLAST score
                   566
                   1.0e-58
E value
                   111
Match length
                   99
% identity
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]
                   220191
Seq. No.
                   LIB3149-043-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g133812
BLAST score
                   323
                   5.0e - 30
E value
                   74
Match length
                   86
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S16 >gi 71000_pir R3IS16
```

ribosomal protein S16 - white mustard chloroplast >gi_12217_emb_CAA31944_ (X13609) 16S ribosomal protein

[Sinapis alba]

Seq. No. 220192



Seq. ID LIB3149-043-Q1-K1-F12

Method BLASTX
NCBI GI g1174621
BLAST score 191
E value 2.0e-14
Match length 86
% identity 49

NCBI Description T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)

(CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing

cytosolic chaperonin (CCT) theta chain - mouse

>gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit
of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No. 220193

Seq. ID LIB3149-043-Q1-K1-F3

Method BLASTX
NCBI GI g2118220
BLAST score 412
E value 2.0e-40
Match length 117
% identity 75

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>qi 3096941 emb CAA18851.1_ (AL023094) vacuolar

H+-Transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]

Seq. No. 220194

Seq. ID LIB3149-043-Q1-K1-F4

Method BLASTX
NCBI GI g3122060
BLAST score 300
E-value 3.0e-27
Match length 60
% identity 97

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_2598657_emb_CAA10847_ (AJ222579) elongation factor

1-alpha (EF1-a) [Vicia faba]

Seq. No. 220195

Seq. ID LIB3149-043-Q1-K1-F5

Method BLASTX
NCBI GI g4567251
BLAST score 155
E value 3.0e-10
Match length 32
% identity 78

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 220196

Seq. ID LIB3149-043-Q1-K1-F6

Method BLASTX NCBI GI g2911058

NCBI GI

BLAST score E value

Match length

% identity

654

98

8.0e-69 129

```
BLAST score
                  206
                  3.0e-16
E value
                  88
Match length
                  45
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                  220197
Seq. No.
                  LIB3149-043-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g113029
NCBI GI
                  384
BLAST score
                  3.0e-37
E value
Match length
                  73
                  100
% identity
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi_68209_pir__WZCNIU isocitrate lyase (EC 4.1.3.1) -
                   upland cotton >gi 18486_emb_CAA36381_ (X52136) isocitrate
                  lyase (AA 1-576) [Gossypium hirsutum]
                   220198
Seq. No.
                  LIB3149-043-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q557472
BLAST score
                   211
                   7.0e-17
E value
Match length
                   126
                   37
% identity
NCBI Description (U15178) arabinosidase [Bacteroides ovatus]
                   220199
Seq. No.
                   LIB3149-043-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g3450889
NCBI GI
BLAST score
                   340
                   5.0e-32
E value
                   97
Match length
                   73
% identity
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
                   220200
Seq. No.
                   LIB3149-043-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g3450889
NCBI GI
                   149
BLAST score
                   9.0e-10
E value
                   72
Match length
                   53
% identity
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
                   220201
Seq. No.
                   LIB3149-043-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   q2662341
```



NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 220202

Seq. ID LIB3149-043-Q1-K1-G8

Method BLASTN
NCBI GI g1654275
BLAST score 156
E value 8.0e-83
Match length 156
% identity 100

NCBI Description Cienfuegosia tripartita 5.8S ribosomal RNA gene and

internal transcribed spacer 1 and

Seq. No. 220203

Seq. ID LIB3149-043-Q1-K1-H11

Method BLASTX
NCBI GI g464707
BLAST score 514
E value 2.0e-52
Match length 117
% identity 85

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi 434906 emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 220204

Seq. ID LIB3149-043-Q1-K1-H12

Method BLASTX
NCBI GI g1076414
BLAST score 277
E value 1.0e-24
Match length 118
% identity 51

NCBI Description subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis

thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)

subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 220205

Seq. ID LIB3149-043-Q1-K1-H4

Method BLASTX NCBI GI g3157933 BLAST score 514



```
E value
                  2.0e-52
Match length
                  120
% identity
                  79
                  (AC002131) Contains similarity to box helicases gb U29097
NCBI Description
                  from C. elegans and to the ENBP1 gene product gb_X95995
                  from Vicia sativa. [Arabidopsis thaliana]
                  220206
Seq. No.
Seq. ID
                  LIB3149-043-Q1-K1-H5
                  BLASTX
Method
NCBI GI
                  q3687243
BLAST score
                  241
                  2.0e-20
E value
Match length
                  61
% identity
                  77
                  (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  220207
Seq. ID
                  LIB3149-043-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  486
E value
                  4.0e-49
                  128
Match length
% identity
                  75
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi 4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  220208
Seq. ID
                  LIB3149-043-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2827082
BLAST score
                  521
E value
                  3.0e-53
Match length
                  120
                   79
% identity
NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]
Seq. No.
                   220209
                  LIB3149-044-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3212116
BLAST score
                  267
E value
                   2.0e-23
                  107
Match length
                   49
% identity
NCBI Description (Y17393) prefoldin subunit 2 [Mus musculus]
Seq. No.
                   220210
Seq. ID
                  LIB3149-044-Q1-K1-A10
```

BLASTX Method NCBI GI g4371282 BLAST score 497 E value 2.0e-50 Match length 110



```
% identity
                  (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                  thaliana]
                  220211
Seq. No.
                  LIB3149-044-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q2648032
NCBI GI
BLAST score
                  628
E value
                  1.0e-65
Match length
                  141
                  79
% identity
NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]
                  220212
Seq. No.
                  LIB3149-044-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  q2500195
NCBI GI
                  319
BLAST score
E value
                  2.0e-29
                  65
Match length
                  95
% identity
NCBI Description RAC-LIKE GTP BINDING PROTEIN RHO1 >gi 974780 emb CAA89050
                  (Z49191) small G protein [Beta vulgaris]
                  220213
Seq. No.
                  LIB3149-044-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q547886
                  300
BLAST score
E value
                  2.0e-27
                  118
Match length
                   58
% identity
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                   (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi_542102_pir__S42939 malate dehydrogenase
                   (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40)
                  precursor - Flaveria pringlei >gi_1084444_pir__S52016
                  malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)
                   (EC 1.1.1.40) - Flaveria pringlei >gi_459441_emb_CAA54986_
                   (X78069) malate dehydrogenase (oxaloacetate
                   decarboxylating) (NADP+) [Flaveria pringlei]
                   220214
Seq. No.
Seq. ID
                  LIB3149-044-Q1-K1-A3
Method
                   BLASTX
                   q4454033
NCBI GI
BLAST score
                   186
                   5.0e-14
E value
                  54
Match length
                   59
% identity
NCBI Description (AL035394) putative potassium transport protein
                   [Arabidopsis thaliana]
```

Seq. ID LIB3149-044-Q1-K1-A4

Method BLASTX



```
q3893081
NCBI GI
BLAST score
                  523
                  2.0e-53
E value
Match length
                  138
                  70
% identity
NCBI Description (AJ012747) MLH1 protein [Arabidopsis thaliana]
                  220216
Seq. No.
Seq. ID
                  LIB3149-044-Q1-K1-A5
                  BLASTX
Method
NCBI GI
                  q4508079
                  156
BLAST score
                  7.0e-11
E value
                  74
Match length
                  45
% identity
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]
                  220217
Seq. No.
                  LIB3149-044-Q1-K1-A6
Seq. ID
Method
                  BLASTX
                  q1518540
NCBI GI
                  590
BLAST score
                  3.0e-61
E value
Match length
                  127
% identity
                   91
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  220218
                  LIB3149-044-Q1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g547886
BLAST score
                  505
                   3.0e-51
E value
                  137
Match length
                   74
% identity
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                   (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                   >qi 542102 pir S42939 malate dehydrogenase
                   (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40)
                   precursor - Flaveria pringlei >gi_1084444_pir__S52016
                   malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)
                   (EC 1.1.1.40) - Flaveria pringlei >gi_459441_emb_CAA54986_
                   (X78069) malate dehydrogenase (oxaloacetate
                   decarboxylating) (NADP+) [Flaveria pringlei]
Seq. No.
                   220219
                   LIB3149-044-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g2119937
NCBI GI
                   701
BLAST score
                   3.0e-74
E value
                   140
Match length
```

98 % identity

NCBI Description translation initiation factor eIF-4A.13 - common tobacco

(fragment)

Seq. No. 220220

Seq. ID

220225

LIB3149-044-Q1-K1-C7



```
LIB3149-044-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3924597
BLAST score
                  212
E value
                  6.0e-17
Match length
                  133
                  37
% identity
NCBI Description
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  220221
                  LIB3149-044-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  396
E value
                  2.0e-38
Match length
                  84
                  88
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  220222
                  LIB3149-044-Q1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4206210
BLAST score
                  462
E value
                   3.0e-46
Match length
                  141
                   64
% identity
                  (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
                   >gi 4263043 gb AAD15312_ (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
                   220223
Seq. No.
Seq. ID
                   LIB3149-044-Q1-K1-C12
Method
                   BLASTX
NCBI GI
                   q169989
BLAST score
                   506
E value
                   2.0e-51
Match length
                   111
% identity
                   88
                  (L12157) NADPH-specific isocitrate dehydrogenase [Glycine
NCBI Description
                   max]
                   220224
Seq. No.
                   LIB3149-044-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829899
BLAST score
                   299
                   3.0e-27
E value
Match length
                   124
% identity
                   47
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449 2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
```



Method BLASTN
NCBI GI g3241927
BLAST score 52
E value 3.0e-20
Match length 112
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 220226

Seq. ID LIB3149-044-Q1-K1-C9

Method BLASTX
NCBI GI g1362078
BLAST score 231
E value 2.0e-19
Match length 62
% identity 63

NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)

- common nasturtium >gi_311835_emb_CAA48324 (X68254)

cellulase [Tropaeolum majus]

Seq. No. 220227

Seq. ID LIB3149-044-Q1-K1-D2

Method BLASTN NCBI GI g974781 BLAST score 33

E value 5.0e-09 Match length 120 % identity 86

NCBI Description C.blumei kinetoplast met gene for cobalamine-independent

methionine synthase

Seq. No. 220228

Seq. ID LIB3149-044-Q1-K1-D3

Method BLASTX
NCBI GI g730645
BLAST score 440
E value 1.0e-43
Match length 114
% identity 79

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788,gb ATTS0365 come from this gene. [Arabidopsis

thaliama]

Seq. No. 220229

Seq. ID LIB3149-044-Q1-K1-D7

Method BLASTX
NCBI GI g464621
BLAST score 375
E value 4.0e-36
Match length 83
% identity 88

```
60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir__S28586
NCBI Description
                    ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                    220230
Seq. No.
                    LIB3149-044-Q1-K1-D8
Seq. ID
                    BLASTX
Method
                    g218288
NCBI GI
                    281
BLAST score
                    5.0e-25
E value
                    136
Match length
                    29
% identity
                    (D11111) chloroplast 33 kd ribonucleoprotein (cp33)
NCBI Description
                    [Nicotiana sylvestris] >gi_311952_emb_CAA41253_ (X58356) 33
                    kd chloroplast ribonucleoprotein [Nicotiana sylvestris]
```

220231 Seq. No. LIB3149-044-Q1-K1-E11 Seq. ID BLASTX Method g1905910 NCBI GI BLAST score 422 1.0e-41 E value Match length 14454 % identity (AD000092) putative human phenylalanine tRNA synthetase

NCBI Description (AD000092) putative human phenylalanine tRNA synthetase [Homo sapiens]

 Seq. No.
 220232

 Seq. ID
 LIB3149-044-Q1-K1-E2

 Method
 BLASTX

 NCBI GI
 g1351983

 BLAST score
 207

 E value
 1.0e-16

 Match length
 88

(glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus >gi_2147133_pir__S69182 asparagine synthase

(glutamine-hydrolysing) (EC 6.3.5.4) 1 - Lotus japonicus >gi_897771 emb_CAA61589 (X89409) asparagine synthase (glutamine-hydrolysing) [Lotus japonicus]

Seq. No. 220233

Seq. ID LIB3149-044-Q1-K1-E3

Method BLASTX
NCBI GI g1170373
BLAST score 290
E value 2.0e-47
Match length 103
% identity 96

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]



220234

```
LIB3149-044-Q1-K1-E6
Seq. ID
                  BLASTN
Method
                  q2264314
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
                  134
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
                  220235
Seq. No.
                  LIB3149-044-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2970051
                  446
BLAST score
                  2.0e-44
E value
                  95
Match length
                  89
% identity
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
Seq. No.
                  220236
                  LIB3149-044-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  q3882183
NCBI GI
                  192
BLAST score
E value
                  1.0e-14
                  58
Match length
                   31
% identity
                  (AB018274) KIAA0731 protein [Homo sapiens]
NCBI Description
                   220237
Seq. No.
                   LIB3149-044-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g4572674
NCBI GI
                   279
BLAST score
E value
                   9.0e-25
                   73
Match length
                   73
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                   220238
Seq. No.
                   LIB3149-044-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g1362086
NCBI GI
                   540
BLAST score
                   1.0e-55
E value
                   108
Match length
                   94
% identity
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471_emb_CAA58474_ (X83499) methionine synthase
```

[Catharanthus roseus]



```
220239
Seq. No.
                  LIB3149-044-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  q1076746
NCBI GI
                  313
BLAST score
                  9.0e-29
E value
                  80
Match length
                  80
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                  220240
Seq. No.
Seq. ID
                  LIB3149-044-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                   g542179
BLAST score
                   695
                   1.0e-73
E value
Match length
                   139
                   97
% identity
                   alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha
NCBI Description
                   chain - maize (fragment) >gi_393401_emb_CAA52158 (X73980)
                   alpha tubulin [Zea mays]
                   220241
Seq. No.
                   LIB3149-044-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3893081
BLAST score
                   493
                   6.0e-50
E value
                   134
Match length
                   69
% identity
                  (AJ012747) MLH1 protein [Arabidopsis thaliana]
NCBI Description
                   220242
Seq. No.
                   LIB3149-044-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   q3821280
NCBI GI
                   455
BLAST score
                   2.0e-45
E value
                   117
Match length
                   77
% identity
                   (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
                   220243
Seq. No.
Seq. ID
                   LIB3149-044-Q1-K1-G3
                   BLASTX
Method
NCBI GI
                   q477280
BLAST score
                   552
                   7.0e-57
E value
Match length
                   128
% identity
                   81
NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K
```

protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I,



P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

Seq. No. 220244

Seq. ID LIB3149-044-Q1-K1-G6

Method BLASTX
NCBI GI g2842689
BLAST score 233
E value 2.0e-19
Match length 141
% identity 38

NCBI Description HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I

>gi 1638851_emb_CAB03598_ (Z81312) unknown

[Schizosaccharomyces pombe]

Seq. No. 220245

Seq. ID LIB3149-044-Q1-K1-H2

Method BLASTX
NCBI GI g2244910
BLAST score 143
E value 6.0e-09
Match length 141
% identity 35

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 220246

Seq. ID LIB3149-044-Q1-K1-H7

Method BLASTX
NCBI GI g2961358
BLAST score 614
E value 4.0e-64
Match length 137
% identity 86

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 220247

Seq. ID LIB3149-044-Q1-K1-H9

Method BLASTX
NCBI GI g1709970
BLAST score 473
E value 1.0e-47
Match length 126
% identity 75

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 220248

Seq. ID LIB3149-046-Q1-K1-A1

Method BLASTX
NCBI GI g3608485
BLAST score 531
E value 2.0e-54
Match length 113
% identity 88

NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No. 220249

Method

NCBI GI

BLASTX

g3123264



```
LIB3149-046-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  a444791
BLAST score
                  249
                  2.0e-21
E value
                  112
Match length
                  14
% identity
NCBI Description ubiquitin [Bos taurus]
Seq. No.
                  220250
                  LIB3149-046-Q1-K1-A11
Seq. ID
Method
                  BLASTN
                  g438110
NCBI GI
BLAST score
                  35
                  2.0e-10
E value
Match length
                  55
                  91
% identity
NCBI Description L.albus ubiquitin extension protein
                  220251
Seq. No.
                  LIB3149-046-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g541546
BLAST score
                  334
                  2.0e-31
E value
Match length
                  67
                  20
% identity
                  ubiquitin precursor - Volvox carteri
NCBI Description
                  >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox
                  carteri]
                  220252
Seq. No.
                  LIB3149-046-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827002
BLAST score
                  221
E value
                  4.0e-18
Match length
                  82
% identity
                  51
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                  220253
Seq. ID
                  LIB3149-046-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2119045
BLAST score
                  537
                   4.0e-55
E value
Match length
                  130
                  78
% identity
                  small nuclear ribonucleoprotein U1A - potato
NCBI Description
                  >gi 1050840 emb CAA90282 (Z49990) UlsnRNP-specific
                  protein, U1A [Solanum tuberosum]
                  220254
Seq. No.
Seq. ID
                  LIB3149-046-Q1-K1-B11
```

Seq. No.



```
BLAST score
E value
                  5.0e-47
Match length
                  118
% identity
                  76
                  60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279
NCBI Description
                   (297337) hypothetical protein [Arabidopsis thaliana]
                  220255
Seq. No.
Seq. ID
                  LIB3149-046-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q730547
BLAST score
                  249
                  3.0e-28
E value
Match length
                  85
% identity
                  75
NCBI Description 60S RIBOSOMAL PROTEIN L27
                  220256
Seq. No.
                  LIB3149-046-Q1-K1-B3
                  BLASTX
```

Seq. ID Method NCBI GI q4097547 BLAST score 282 E value 2.0e-25 Match length 67 45 % identity

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

220257

220258

Seq. ID LIB3149-046-Q1-K1-B5 Method BLASTX NCBI GI g2262100 BLAST score 534 E value 1.0e-54 Match length 122 % identity 80

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. ID LIB3149-046-Q1-K1-B7 Method BLASTX NCBI GI g4097547 BLAST score 214 E value 2.0e-17 89 Match length % identity 31

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

220259 Seq. No.

Seq. ID LIB3149-046-Q1-K1-C4

Method BLASTX g4490705 NCBI GI BLAST score 466 E value 8.0e-47Match length 111 84 % identity

NCBI Description (AL035680) ribosomal protein L14-like protein [Arabidopsis

thaliana]



```
Seq. No.
                  220260
                  LIB3149-046-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4530585
BLAST score
                  357
                  5.0e - 34
E value
                  85
Match length
                  74
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
Seq. No.
                  220261
                  LIB3149-046-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1084415
BLAST score
                  320
                  1.0e-29
E value
Match length
                  95
                   62
% identity
                  RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
NCBI Description
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
                  220262
Seq. No.
                  LIB3149-046-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1222552
                   153
BLAST score
                   3.0e-10
E value
Match length
                  50
% identity
                   64
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
                   220263
Seq. No.
Seq. ID
                   LIB3149-046-Q1-K1-D1
Method
                   BLASTX
NCBI GI
                   q3643606
BLAST score
                   253
E value
                   1.0e-21
Match length
                   119
% identity
                   41
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   220264
                   LIB3149-046-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3914430
BLAST score
                   550
E value
                   1.0e-56
Match length
                   123
                   86
% identity
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
```

subunit [Spinacia oleracea]

CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi 2285800 dbj BAA21650 (D78172) 26S proteasome beta



```
LIB3149-046-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  g1052973
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
                  46
Match length
                  76
% identity
                  (U37838) fructokinase [Beta vulgaris]
NCBI Description
                  220266
Seq. No.
                  LIB3149-046-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g4314361
NCBI GI
                  216
BLAST score
                  2.0e-17
E value
Match length
                  44
                   95
% identity
                  (AC006340) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220267
Seq. No.
                  LIB3149-046-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                   g322854
NCBI GI
                   180
BLAST score
                   3.0e-13
E value
                   78
Match length
                   44
% identity
                  pollen-specific protein - rice >gi_20310_emb_CAA78897_
NCBI Description
                   (Z16402) pollen specific gene [Oryza sativa]
                   220268
Seq. No.
                   LIB3149-046-Q1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3128192
                   442
BLAST score
                   6.0e-44
E value
Match length
                   109
% identity
                   72
                  (AC004521) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   220269
Seq. No.
                   LIB3149-046-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g2407800
NCBI GI
                   532
BLAST score
                   2.0e-54
E value
Match length
                   133
% identity
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
                   220270
Seq. No.
                   LIB3149-046-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g1169840
NCBI GI
                   356
BLAST score
```

31043

7.0e-34

71

E value Match length



% identity GIBBERELLIN-REGULATED PROTEIN 4 PRECURSOR NCBI Description >gi 2129591 pir S71442 GAST1 protein homolog (clone GASA4) - Arabidopsis thaliana >gi 950099 (U15683) gibberellin-regulated [Arabidopsis thaliana] 220271 Seq. No. LIB3149-046-Q1-K1-D7 Seq. ID Method BLASTX NCBI GI q585973 BLAST score 550 1.0e-56 E value Match length 130 85 % identity FRUCTOKINASE > gi 626018 pir S39997 fructokinase (EC NCBI Description 2.7.1.4) - potato >gi 297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum] Seq. No. 220272 LIB3149-046-Q1-K1-D8 Seq. ID Method BLASTX NCBI GI q2997591 BLAST score 502 6.0e-51 E value Match length 136 76 % identity NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum] Seq. No. 220273 LIB3149-046-Q1-K1-E11 Seq. ID Method BLASTX NCBI GI g1931655 BLAST score 602 E value 1.0e-62 129 Match length 86 % identity NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana] Seq. No. 220274 LIB3149-046-Q1-K1-E12 Seq. ID BLASTX Method NCBI GI g2911073 BLAST score 418 E value 4.0e-41Match length 128 % identity 67 NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 220275

Seq. ID LIB3149-046-Q1-K1-E4

Method BLASTX
NCBI GI g218157
BLAST score 358
E value 4.0e-34
Match length 78



```
% identity
                  (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
                  220276
Seq. No.
                  LIB3149-046-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  q730583
NCBI GI
                  188
BLAST score
E value
                  3.0e-14
                  111
Match length
% identity
                  41
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
NCBI Description
                  (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
                  220277
Seq. No.
                  LIB3149-046-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263791
BLAST score
                  276
                  2.0e-24
E value
                  59
Match length
                  90
% identity
NCBI Description
                  (AC006068) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  220278
Seq. No.
                  LIB3149-046-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  394
                   3.0e-38
E value
Match length
                  129
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  220279
Seq. ID
                  LIB3149-046-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                   q2780194
BLAST score
                   676
E value
                   2.0e-71
Match length
                  140
% identity
                   63
NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]
Seq. No.
                   220280
                  LIB3149-046-Q1-K1-F10
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4539545
BLAST score 632
E value 3.0e-66
Match length 129
% identity 94

NCBI Description (Y16644) PRCI [Nicotiana tabacum]

Seq. No. 220281



```
LIB3149-046-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3142300
BLAST score
                  494
                  4.0e-50
E value
Match length
                  121
                  69
% identity
NCBI Description
                  (AC002411) Contains similarity to pre-mRNA processing
                  protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
                  and gb_T88158, gb_N38703 and gb_AA651043 come from this
                  gene. [Arabidopsis thaliana]
                  220282
Seq. No.
                  LIB3149-046-Q1-K1-F12
Seq. ID
Method
                  BLASTX
                  g3832512
NCBI GI
                  156
BLAST score
E value
                  3.0e-11
                  94
Match length
                  44
% identity
                 (AF097922) granule-bound glycogen (starch) synthase
NCBI Description
                  [Astragalus membranaceus]
                  220283
Seq. No.
                  LIB3149-046-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  189
                  2.0e-14
E value
Match length
                  120
                  41
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
                  [Arabidopsis thaliana]
Seq. No.
                  220284
Seq. ID
                  LIB3149-046-01-K1-F4
Method
                  BLASTX
NCBI GI
                  q121083
BLAST score
                  701
E value
                  3.0e-74
```

Match length 139 % identity 92

NCBI Description GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE

DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi_282926_pir__A42109 glycine dehydrogenase

(decarboxylating) (EC 1.4.4.2) component P precursor garden pea >gi_20741_emb_CAA42443_ (X59773) component of

aminomethyltransferase [Pisum sativum]

Seq. No. 220285

Seq. ID LIB3149-046-Q1-K1-F5

Method BLASTX



```
NCBI GI
                  q2213595
BLAST score
                  290
E value
                  4.0e-26
Match length
                  126
% identity
                   48
                 (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
                  220286
Seq. No.
Seq. ID
                  LIB3149-046-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2493129
BLAST score
                  667
                  3.0e-70
E value
Match length
                  136
% identity
                   99
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi 459198 (U07052) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
Seq. No.
                  220287
                  LIB3149-046-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519264
BLAST score
                  252
                  1.0e-21
E value
Match length
                  118
                  52
% identity
NCBI Description (AB024277) vacuolar H+-ATPase B subunit [Citrus unshiu]
                  220288
Seq. No.
Seq. ID
                  LIB3149-046-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                   g134672
BLAST score
                  554
E value
                   5.0e-57
Match length
                  132
                   78
% identity
                  SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_82145_pir__S03639
NCBI Description
                  superoxide dismutase (EC 1.15.1.1) (Mn) precursor -
                  curled-leaved tobacco >gi 19693 emb CAA32643 (X14482)
                  manganese superoxide dismutase preprotein (AA -24 to 204)
                   [Nicotiana plumbaginifolia]
                  220289
Seq. No.
Seq. ID
                  LIB3149-046-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2832623
BLAST score
                  388
E value
                  1.0e-37
                  111
% identity
                  (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
```

Match length

thaliana]

Seq. No. 220290

Seq. ID LIB3149-046-Q1-K1-G2

Method BLASTX



89

% identity

```
q134672
NCBI GI
BLAST score
                  559
                  1.0e-57
E value
                  132
Match length
                  79
% identity
                  SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_82145 pir__S03639
NCBI Description
                  superoxide dismutase (EC 1.15.1.1) (Mn) precursor -
                  curled-leaved tobacco >gi_19693_emb_CAA32643_ (X14482)
                  manganese superoxide dismutase preprotein (AA -24 to 204)
                   [Nicotiana plumbaginifolia]
                  220291
Seq. No.
                  LIB3149-046-Q1-K1-G3
Seq. ID
Method
                  BLASTX
                  q3643608
NCBI GI
                  171
BLAST score
                   4.0e-12
E value
                  89
Match length
                   53
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  220292
Seq. No.
                  LIB3149-046-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                   g1076746
NCBI GI
                   325
BLAST score
E value
                   3.0e-30
                   88
Match length
                   73
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   220293
Seq. No.
                   LIB3149-046-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q114682
BLAST score
                   251
                   1.0e-21
E value
Match length
                   60
                   80
% identity
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                   >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                   3.6.1.34) \overline{\text{gamma}} chain precursor, mitochondrial - sweet
                   potato >gi_168270 (J05397) F-1-ATPase delta subunit
                   precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                   220294
                   LIB3149-046-Q1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1732358
BLAST score
                   44
                   2.0e-15
E value
                   8.0
Match length
```

NCBI Description Malus domestica elongation factor 1 alpha (EF-lalpha) mRNA,



partial cds

```
220295
Seq. No.
Seq. ID
                  LIB3149-046-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g124226
                  262
BLAST score
                  7.0e-23
E value
Match length
                  58
                  90
% identity
NCBI Description
                  INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                  >gi_100278_pir__S21059 translation initiation factor
                  eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
                  plumbaginifolia]
                  220296
Seq. No.
                  LIB3149-047-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210451
                  363
BLAST score
                  1.0e-34
E value
Match length
                  88
                  76
% identity
NCBI Description (AB016472) ARR2 protein [Arabidopsis thaliana]
Seq. No.
                  220297
                  LIB3149-047-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350736
BLAST score
                   173
                   2.0e-12
E value
Match length
                   35
                   91
% identity
NCBI Description
                 60S RIBOSOMAL PROTEIN L37 >gi 629673 pir S44313 ribosomal
                   protein L37 - tomato >gi 483586 emb CAA55674 (X79074)
                   ribosomal protein L37 [Lycopersicon esculentum]
Seq. No.
                   220298
                   LIB3149-047-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3281868
BLAST score
                   238
E value
                   5.0e-20
                   53
Match length
% identity
                   91
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                   220299
Seq. No.
                   LIB3149-047-Q1-K1-A5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4006940
BLAST score
                   34
                   2.0e-09
E value
                  70
Match length
                   87
% identity
```

NCBI Description Arabidopsis thaliana mRNA for voltage-dependent

BLAST score

275



anion-selective channel protein

```
220300
Seq. No.
Seq. ID
                   LIB3149-047-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   q3024629
                   154
BLAST score
                   4.0e-10
E value
Match length
                   118
% identity
                   31
NCBI Description
                   GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA)
                   >gi_423252_pir__S32369 gamma-SNAP protein - bovine
>gi_298669_bbs_127528 gamma soluble NSF attachment protein,
                   gamma SNAP=N-ethyl-maleimide-sensitive fusion protein
                   attachment protein [cattle, brain, Peptide, 328 aa]
                   >gi_445846_prf__1910317C NSF attachment protein
                   (SNAP):ISOTYPE=gamma [Bos taurus]
Seq. No.
                   220301
Seq. ID
                   LIB3149-047-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   q730449
BLAST score
                   501
E value
                   7.0e-51
Match length
                   118
% identity
                   78
                   60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
NCBI Description
                   >gi_480647_pir__S37132 ribosomal protein L13.A - rape
                   >gi_398918_emb_CAA80341_ (Z22618) cold induced protein
                   (BnC24A) [Brassica napus]
                   220302
Seq. No.
Seq. ID
                   LIB3149-047-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2213620
BLAST score
                   410
E value
                   2.0e-40
Match length
                   93
% identity
                   88
NCBI Description (AC000103) F21J9.13 [Arabidopsis thaliana]
Seq. No.
                   220303
Seq. ID
                   LIB3149-047-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1778145
BLAST score
                   294
E value
                   1.0e-26
Match length
                   66
% identity
                   80
NCBI Description
                  (U66402) phosphate/phosphoenolpyruvate translocator
                   precursor [Nicotiana tabacum]
Seq. No.
                   220304
Seq. ID
                   LIB3149-047-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g1710551
```



E value 2.0e-24
Match length 51
% identity 98
NCRI Description 608 PIR

NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_

(X95458) ribosomal protein L39 [Zea mays]

Seq. No. 220305

Seq. ID LIB3149-047-Q1-K1-B5

Method BLASTX
NCBI GI g3877252
BLAST score 175
E value 1.0e-12
Match length 74
% identity 50

NCBI Description (Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No. 220306

Seq. ID LIB3149-047-Q1-K1-B7

Method BLASTX
NCBI GI g3860255
BLAST score 305
E value 7.0e-28
Match length 140
% identity 48

NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No. 220307

Seq. ID LIB3149-047-Q1-K1-C11

Method BLASTX
NCBI GI g2832641
BLAST score 260
E value 7.0e-23
Match length 78
% identity 65

NCBI Description (AL021710) glycolate oxidase - like protein [Arabidopsis

thaliana]

Seq. No. 220308

Seq. ID LIB3149-047-Q1-K1-C2

Method BLASTX
NCBI GI g3924597
BLAST score 248
E value 4.0e-21
Match length 106
% identity 49

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 220309

Seq. ID LIB3149-047-Q1-K1-C3

Method BLASTX
NCBI GI 94099914
BLAST score 279
E value 8.0e-25
Match length 79
% identity 71

NCBI Description (U91857) ethylene-responsive element binding protein

homolog [Stylosanthes hamata]

Seq. ID

220315

LIB3149-047-Q1-K1-E1



```
Seq. No.
                  220310
Seq. ID
                  LIB3149-047-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1710587
BLAST score
                  469
E value
                  3.0e-47
Match length
                  110
% identity
                  86
NCBI Description
                  60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic
                  ribosomal protein PO [Glycine max]
Seq. No.
                  220311
Seq. ID
                  LIB3149-047-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4510421
BLAST score
                  263
E value
                  6.0e-23
Match length
                  104
% identity
                  52
NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]
Seq. No.
                  220312
Seq. ID
                  LIB3149-047-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2764941
BLAST score
                  415
E value
                  9.0e-41
Match length
                  101
                  70
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  220313
Seq. No.
Seq. ID
                  LIB3149-047-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3135269
BLAST score
                  342
E value
                  3.0e - 32
Match length
                  122
% identity
                  65
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]
Seq. No.
                  220314
Seq. ID
                  LIB3149-047-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3482918
BLAST score
                  390
E value
                  4.0e-38
Match length
                  90
% identity
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  q3341685
BLAST score
                   321
                  4.0e-35
E value
Match length
                  117
                   72
% identity
                  (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220316
Seq. No.
                  LIB3149-047-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g1173209
NCBI GI
BLAST score
                   363
E value
                   6.0e-35
                   92
Match length
                   82
% identity
                  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
NCBI Description
                   protein S16 protein - upland cotton
                   >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
Seq. No.
                   220317
                  LIB3149-047-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512664
                   511
BLAST score
E value
                   5.0e-52
Match length
                   136
                   68
% identity
                  (AC006931) putative ribose phosphate pyrophosphokinase
NCBI Description
                   [Arabidopsis thaliana]
                   >gi 4544471 gb AAD22378.1_AC006580_10 (AC006580) putative
                   ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
                   220318
Seq. No.
Seq. ID
                   LIB3149-047-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q1449179
BLAST score
                   261
                   9.0e-23
E value
Match length
                   112
% identity
                   49
                   (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                   [Nicotiana tabacum]
                   220319
Seq. No.
Seq. ID
                   LIB3149-047-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   g1449179
BLAST score
                   448
E value
                   1.0e-44
Match length
                   137
```

% identity 67

(D86506) N-ethylmaleimide sensitive fusion protein NCBI Description

[Nicotiana tabacum]

Seq. No. 220320

NCBI Description



```
LIB3149-047-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g4455364
NCBI GI
                  368
BLAST score
                  3.0e - 35
E value
Match length
                  127
                  52
% identity
                  (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  220321
Seq. No.
                  LIB3149-047-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3044218
                  143
BLAST score
                  4.0e-09
E value
                  43
Match length
                  67
% identity
                  (AF057144) signal peptidase [Arabidopsis thaliana]
NCBI Description
                  220322
Seq. No.
                  LIB3149-047-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173073
                  198
BLAST score
                  1.0e-15
E value
Match length
                  75
                  59
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 1076787 pir__S54179
NCBI Description
                   acidic ribosomal protein 60S - maize
                   >gi_2130117_pir__S65781 acidic ribosomal protein P2 - maize
                   >gi 790508 emb CAA60251 (X86553) 60S acidic ribosomal
                   protein [Zea mays]
                   220323
Seq. No.
                  LIB3149-047-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1483218
BLAST score
                   153
                   2.0e-17
E value
                   78
Match length
                   63
% identity
                  (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                   thaliana]
                   220324
Seq. No.
Seq. ID
                   LIB3149-047-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q3024020
BLAST score
                   653
E value
                   1.0e-68
Match length
                   129
% identity
                   94
```

>gi 2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

factor 5A3 [Solanum tuberosum]



```
220325
Seq. No.
Seq. ID
                  LIB3149-047-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                   612
                   7.0e-64
E value
                   130
Match length
                   90
% identity
                  (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                   thaliana]
                   220326
Seq. No.
                  LIB3149-047-Q1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3021355
BLAST score
                   360
                   3.0e - 34
E value
                   79
Match length
                   85
% identity
                  (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
                   220327
Seq. No.
                   LIB3149-047-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2425066
BLAST score
                   376
                   2.0e-36
E value
                   92
Match length
                   75
% identity
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]
                   220328
Seq. No.
                   LIB3149-047-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1619300
BLAST score
                   528
E value
                   5.0e-54
Match length
                   112
                   90
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                   220329
Seq. No.
                   LIB3149-047-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g158146
BLAST score
                   153
E value
                   2.0e-10
Match length
                   62
% identity
NCBI Description (M37610) polytene protein [Drosophila melanogaster]
Seq. No.
                   220330
                   LIB3149-047-Q1-K1-G11
Seq. ID
Method
                   BLASTX
```

g1350680

390

NCBI GI

BLAST score



```
4.0e-38
E value
Match length
                  94
                  78
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L1
                  220331
Seq. No.
                  LIB3149-047-Q1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q322750
BLAST score
                  658
                  3.0e-69
E value
Match length
                  128
                  99
% identity
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                  >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
                  220332
Seq. No.
                  LIB3149-047-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961300
BLAST score
                  556
                  3.0e-57
E value
                  126
Match length
                  86
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                  220333
Seq. No.
                  LIB3149-047-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3193303
BLAST score
                  202
                   9.0e-16
E value
                   100
Match length
                   40
% identity
NCBI Description
                   (AF069298) similar to several proteins containing a tandem
                  repeat region such as Plasmodium falciparum GGM tandem
                   repeat protein (GB:U27807); partial CDS [Arabidopsis
                  thaliana]
Seq. No.
                   220334
Seq. ID
                  LIB3149-047-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                   g2228773
BLAST score
                   195
E value
                   3.0e-15
Match length
                   56
% identity
                   71
                   (AF001454) Dc3 promoter-binding factor-2 [Helianthus
NCBI Description
                   annuus]
```

Seq. No. 220335

Seq. ID LIB3149-048-Q1-K1-A2

Method BLASTX
NCBI GI g113232
BLAST score 126
E value 6.0e-12



```
45
Match length
% identity
NCBI Description ACTIN 2 > gi 100150 pir S07003 actin 2 - carrot
Seq. No.
                   220336
                   LIB3149-048-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4240207
BLAST score
                   170
E value
                   4.0e-12
                   118
Match length
                   33
% identity
                  (AB020666) KIAA0859 protein [Homo sapiens]
NCBI Description
                   220337
Seq. No.
                   LIB3149-048-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1053047
BLAST score
                   582
                   2.0e-60
E value
Match length
                   116
                   100
% identity
                  (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                   histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
Seq. No.
                   220338
                   LIB3149-048-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2765366
BLAST score
                   158
                   1.0e-10
E value
Match length
                   72
% identity
                   46
NCBI Description (Y14038) putative Ole e 1 protein [Betula pendula]
Seq. No.
                   220339
                   LIB3149-048-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2894612
BLAST score
                   361
E value
                   2.0e-34
Match length
                   106
% identity
                   68
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   220340
Seq. ID
                   LIB3149-048-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g1841870
BLAST score
                   360
E value
                   3.0e - 34
                   116
Match length
% identity
```

Seq. No. 220341

NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. ID

Method



```
LIB3149-048-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2114046
BLAST score
                   547
                   3.0e-56
E value
                   120
Match length
                   88
% identity
                  (AB002147) water channel protein [Nicotiana excelsior]
NCBI Description
                   220342
Seq. No.
                   LIB3149-048-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2454182
                   495
BLAST score
                   2.0e-50
E value
Match length
                   108
                   88
% identity
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   220343
                   LIB3149-048-Q1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g586004
BLAST score
                   519
                   5.0e-53
E value
Match length
                   107
                   89
% identity
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
                   (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
                   superoxide dismutase [Ipomoea batatas]
                   220344
Seq. No.
Seq. ID
                   LIB3149-048-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   q2789660
BLAST score
                   342
E value
                   3.0e-32
Match length
                   127
% identity
NCBI Description (AF040102) p105 [Arabidopsis thaliana]
Seq. No.
                   220345
Seq. ID
                   LIB3149-048-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   q1531672
BLAST score
                   136
E value
                   4.0e-12
                   93
Match length
                   51
% identity
NCBI Description (U68461) actin [Striga asiatica]
                   220346
Seq. No.
```

31058

LIB3149-048-Q1-K1-C1

BLASTX

Match length

% identity

45

100

```
g1653142
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
Match length
                  85
                  46
% identity
                  (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
                  220347
Seq. No.
                  LIB3149-048-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g974782
NCBI GI
BLAST score
                   636
                   1.0e-66
E value
                   126
Match length
% identity
                   96
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   220348
Seq. No.
                   LIB3149-048-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g974782
NCBI GI
                   302
BLAST score
                   1.0e-27
E value
                   101
Match length
                   64
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   220349
Seq. No.
                   LIB3149-048-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g2828296
NCBI GI
                   546
BLAST score
                   3.0e-56
E value
                   112
Match length
                   60
% identity
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
                   220350
Seq. No.
                   LIB3149-048-Q1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2765366
BLAST score
                   158
                   1.0e-10
E value
                   72
Match length
                   46
% identity
NCBI Description (Y14038) putative Ole e 1 protein [Betula pendula]
                   220351
Seq. No.
                   LIB3149-048-Q1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g71638
BLAST score
                   244
                   8.0e-21
E value
```



```
actin - soybean >gi 18532 emb CAA23728 (V00450) actin
NCBI Description
                  [Glycine max] >gi 223413 prf _0804316A actin [Glycine max]
                  220352
Seq. No.
                  LIB3149-048-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                  g1703375
NCBI GI
                  660
BLAST score
                  2.0e-69
E value
                  130
Match length
                  99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                  220353
Seq. No.
                  LIB3149-048-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g228316
NCBI GI
                  385
BLAST score
                  3.0e-37
E value
                  123
Match length
                  57
% identity
NCBI Description albumin [Theobroma cacao]
                  220354
Seq. No.
                  LIB3149-048-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g4567283
NCBI GI
                  259
BLAST score
                  2.0e-22
E value
                  66
Match length
                  79
% identity
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]
                  220355
Seq. No.
                  LIB3149-048-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g2653446
NCBI GI
                  164
BLAST score
                   2.0e-11
E value
                   36
Match length
                   94
% identity
NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]
                   220356
Seq. No.
                  LIB3149-048-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4006827
BLAST score
                   620
                   9.0e-65
E value
Match length
                   143
% identity
NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]
```

Seq. No. 220357

Seq. ID LIB3149-048-Q1-K1-E2

Method BLASTX



```
g1495251
NCBI GI
                  167
BLAST score
                  7.0e-12
E value
                  98
Match length
% identity
                  44
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  220358
Seq. No.
                  LIB3149-048-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                  g595957
NCBI GI
                  420
BLAST score
                  2.0e-51
E value
Match length
                  122
                  78
% identity
NCBI Description
                  (U17098) Br FatAl [Brassica rapa]
                  220359
Seq. No.
                  LIB3149-048-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                   g3212869
NCBI GI
BLAST score
                   689
                   7.0e-73
E value
                  143
Match length
                   90
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   220360
                  LIB3149-048-Q1-K1-F1
Seq. ID
                   BLASTX
Method
                   g4454464
NCBI GI
BLAST score
                   438
                   1.0e-43
E value
                   114
Match length
                   69
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   220361
                   LIB3149-048-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   q4091080
NCBI GI
BLAST score
                   380
                   1.0e-36
E value
Match length
                   139
% identity
NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa]
Seq. No.
                   220362
Seq. ID
                   LIB3149-048-Q1-K1-F12
                   BLASTX
Method
NCBI GI
                   g1708995
BLAST score
                   148
E value
                   1.0e-09
Match length
                   49
```

% identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 726030

% identity

NCBI Description

81



(U17240) S-adenosylmethionine synthetase [Actinidia chinensis]

220363 Seq. No. LIB3149-048-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI g4490937 BLAST score 153 E value 4.0e-10 Match length 111 40 % identity NCBI Description (AJ132261) hypothetical helicase K12H4.8-like protein [Homo sapiens] 220364 Seq. No. Seq. ID LIB3149-048-Q1-K1-F4 Method BLASTX NCBI GI q416662 BLAST score 427 E value 2.0e-42 Match length 99 78 % identity 21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__\$16252 trypsin NCBI Description inhibitor homolog - soybean >gi_\(\overline{2}\)1909_\(\overline{e}\)mb_\(\overline{CA}\)A39860 (X56509) 21 kDa seed protein [Theobroma cacao] Seq. No. 220365 Seq. ID LIB3149-048-Q1-K1-F6 Method BLASTX NCBI GI q2662343 BLAST score 174 E value 8.0e-13 Match length 55 % identity 65 NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 220366 Seq. ID LIB3149-048-Q1-K1-F7 Method BLASTX NCBI GI q4512705 BLAST score 349 E value 3.0e - 33Match length 98 % identity 72 NCBI Description (AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana] Seq. No. 220367 Seq. ID LIB3149-048-Q1-K1-F9 Method BLASTX NCBI GI g1408471 BLAST score 523 E value 2.0e-53 Match length 116

31062

(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi 3851707 (AF102173) actin depolymerizing



factor 1 [Arabidopsis thaliana]

```
220368
Seq. No.
Seq. ID
                  LIB3149-048-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  223
E value
                  1.0e-18
Match length
                  45
                  91
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                  220369
                  LIB3149-048-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3834309
BLAST score
                  377
                  3.0e-36
E value
Match length
                  115
% identity
                  56
                  (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
NCBI Description
                  Daucus carota and a member of S locus glycoprotein family
                  PF 00954. ESTs gb_F13813, gb_T21052, gb_R30218 and
                  gb W43262 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  220370
Seq. ID
                  LIB3149-048-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  264
E value
                  4.0e-23
Match length
                  64
% identity
                  80
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275_ (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                  gb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
                  220371
Seq. No.
Seq. ID
                  LIB3149-048-Q1-K1-G8
Method
                  BLASTX
                  g2414622
NCBI GI
BLAST score
                  298
```

4.0e-27 E value

Match length 107 % identity 52

Seq. ID



```
(Z99259) conserved protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  220372
Seq. ID
                  LIB3149-048-Q1-K1-H1
Method
                  BLASTX
                  g3402693
NCBI GI
BLAST score
                  465
E value
                  1.0e-46
                  128
Match length
                  73
% identity
                  (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220373
Seq. No.
                  LIB3149-048-Q1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1621268
                   557
BLAST score
                   2.0e-57
E value
                  140
Match length
                   69
% identity
                  (Z81012) unknown [Ricinus communis]
NCBI Description
                   220374
Seq. No.
                  LIB3149-048-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g3122673
NCBI GI
BLAST score
                   465
                   1.0e-46
E value
                   122
Match length
                   75
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   220375
Seq. No.
                   LIB3149-048-Q1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1946355
BLAST score
                   431
E value
                   1.0e-42
Match length
                   124
% identity
                   66
                   (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                   220376
                   LIB3149-049-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   g2982303
NCBI GI
BLAST score
                   194
E value
                   4.0e-15
Match length
                   48
                   75
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                   220377
```

31064

LIB3149-049-Q1-K1-A12



Method NCBI GI BLASTX

q902584

```
504
BLAST score
                    2.0e-51
E value
Match length
                    102
                    15
% identity
                    (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
NCBI Description
                    mays]
                    220378
Seq. No.
                    LIB3149-049-Q1-K1-A5
Seq. ID
                    BLASTX
Method
NCBI GI
                    q1522681
                    157
BLAST score
                    1.0e-10
E value
Match length
                    114
                    29
% identity
                    (U49240) symplekin [Homo sapiens] >gi_2143262_emb_CAA71861_
NCBI Description
                    (Y10931) symplekin [Homo sapiens]
                    220379
Seq. No.
                    LIB3149-049-Q1-K1-A6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2832681
BLAST score
                    153
                    5.0e-10
E value
Match length
                    32
                    88
% identity
                   (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                    220380
Seq. No.
                    LIB3149-049-Q1-K1-A7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q81452
BLAST score
                    142
E value
                     8.0e-09
Match length
                    29
                     97
% identity
                    tubulin beta chain - red goosefoot (fragment)
NCBI Description
                    >gi_82057_pir__S06045 tubulin beta chain - carrot
(fragment) >gi_829259 emb_CAA34673 (X16700) tubulin like
protein fragment (AA 1-77) [Chenopodium rubrum]
                    >gi 829261_emb_CAA34609 (X16608) tubulin like protein
                     fragment (AA 1-77) [Daucus carota]
                     220381
Seq. No.
Seq. ID
                     LIB3149-049-Q1-K1-A8
Method
                    BLASTX
NCBI GI
                     g3355470
BLAST score
                     431
E value
                     1.0e-42
Match length
                    124
% identity
                     68
                    (AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                     thaliana]
                     220382
Seq. No.
```



LIB3149-049-Q1-K1-B1 Seq. ID Method BLASTX NCBI GI q4539543 612 BLAST score 6.0e-64E value 124 Match length 97 % identity (AJ133422) glyceraldehyde-3-phosphate dehydrogenase NCBI Description [Nicotiana tabacum] 220383 Seq. No. LIB3149-049-Q1-K1-B10 Seq. ID BLASTX Method q1708313 NCBI GI 147 BLAST score 2.0e-09 E value 60 Match length 57 % identity HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 NCBI Description (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana] 220384 Seq. No. LIB3149-049-Q1-K1-B2 Seq. ID Method BLASTX NCBI GI q2583128 511 BLAST score 5.0e-52 E value Match length 128 76 % identity (AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description 220385 Seq. No. LIB3149-049-Q1-K1-B4 Seq. ID Method BLASTX NCBI GI g3249096 BLAST score 624 3.0e-65 E value Match length 134 % identity (AC003114) Match to mRNA for importin alpha-like protein 4 NCBI Description (impa4) gb_Y14616 from A. thaliana. ESTs gb N96440, gb N37503, gb N37498 and gb T42198 come from this gene. [Arabidopsis thaliana] Seq. No. 220386 LIB3149-049-Q1-K1-B5 Seq. ID Method BLASTX NCBI GI g1173218 BLAST score 617

E value 2.0e-64 Match length 122 % identity 98

40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal NCBI Description protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

570

127

g4210330

5.0e-59



```
220387
Seq. No.
Seq. ID
                  LIB3149-049-Q1-K1-B7
Method
                  BLASTX
                  g2795805
NCBI GI
BLAST score
                  384
                  4.0e-37
E value
                  110
Match length
                  66
% identity
NCBI Description
                  (AC003674) putative protein kinase [Arabidopsis thaliana]
                  >gi 3355493 (AC004218) putative protein kinase [Arabidopsis
                  thaliana]
                  220388
Seq. No.
Seq. ID
                  LIB3149-049-Q1-K1-B8
Method
                  BLASTX
                  g3036802
NCBI GI
BLAST score
                  237
                  6.0e-20
E value
                  128
Match length
% identity
                  40
                  (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805864 emb CAA21484 (AL031986) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  220389
Seq. ID
                  LIB3149-049-Q1-K1-B9
Method
                  BLASTX
                  q1708313
NCBI GI
BLAST score
                  145
E value
                  3.0e-09
Match length
                  48
                   71
% identity
NCBI Description
                  HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                  thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                  thaliana]
                  220390
Seq. No.
Seq. ID
                  LIB3149-049-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                   680
E value
                  7.0e-72
Match length
                  132
% identity
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                  220391
Seq. ID
                  LIB3149-049-Q1-K1-C10
```



```
83
% identity
NCBI Description
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
                   [Arabidopsis thaliana]
                  220392
Seq. No.
                  LIB3149-049-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210330
BLAST score
                  214
                  3.0e-17
E value
                  113
Match length
                   47
% identity
                  (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  220393
Seq. ID
                  LIB3149-049-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                   g1222552
BLAST score
                   222
                   2.0e-18
E value
Match length
                  50
% identity
                   82
                 (U49330) pectin methylesterase [Lycopersicon esculentum]
NCBI Description
                  220394
Seq. No.
                  LIB3149-049-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g2829899
NCBÍ GI
BLAST score
                   300
E value
                   3.0e-27
Match length
                  122
                   48
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp_AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   220395
                  LIB3149-049-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g543905
BLAST score
                   715
                   6.0e-76
E value
Match length
                   132
                   96
% identity
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                   220396
Seq. ID
                  LIB3149-049-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q1843527
BLAST score
                   453
E value
                   3.0e-45
Match length
                  118
```

31068

(U73747) annexin [Gossypium hirsutum]

77

% identity

NCBI Description



```
220397
Seq. No.
                  LIB3149-049-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210330
BLAST score
                  614
E value
                  4.0e-64
Match length
                  130
% identity
                  88
                  (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  220398
Seq. ID
                  LIB3149-049-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2224731
BLAST score
                  242
E value
                  1.0e-20
Match length
                  95
% identity
                  57
NCBI Description (AB004932) Aux22d [Vigna radiata]
Seq. No.
                  220399
Seq. ID
                  LIB3149-049-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q1834353
BLAST score
                  165
E value
                  2.0e-18
Match length
                  107
% identity
                   48
NCBI Description (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
Seq. No.
                  220400
Seq. ID
                  LIB3149-049-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                 . g3892052
BLAST score
                  352
E value
                  2.0e-33
Match length
                  86
                  79
% identity
NCBI Description (AC002330) predicted protein of unknown function
                   [Arabidopsis thaliana]
                  220401
Seq. No.
Seq. ID
                  LIB3149-049-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3947719
BLAST score
                  240
                   2.0e-20
E value
Match length
                   51
                   92
% identity
                  (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                   >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
```

Seq. No. 220402

ribosomal protein S28 [Prunus persica]

LIB3149-049-Q1-K1-E1

Seq. ID Method BLASTX NCBI GI a3096949 BLAST score 541 1.0e-55 E value Match length 124 % identity 81

(Y16328) putative cyclic nucleotide-regulated ion channel NCBI Description

[Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No. 220403

Seq. ID LIB3149-049-Q1-K1-E10

Method BLASTX NCBI GI q2505940 BLAST score 574 E value 2.0e-59 Match length 124 87 % identity

NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

220404 Seq. No.

LIB3149-049-Q1-K1-E4 Seq. ID

Method BLASTX NCBI GI q3033544 BLAST score 147 2.0e-09 E value 78 Match length % identity 38

NCBI Description (AF055873) hypothetical protein [Synechococcus PCC7942]

220405 Seq. No.

LIB3149-049-Q1-K1-E5 Seq. ID

Method BLASTX NCBI GI g115486 BLAST score 530 E value 3.0e-54Match length 104 57 % identity

CALMODULIN-2/3/5 >gi 99671 pir S22503 calmodulin -NCBI Description

Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin - leaf mustard >gi_2146726_pir__S71513 calmodulin - Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2 [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183 emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150)

calmodulin [Brassica napus] >gi 899058 (M88307) calmodulin

[Brassica juncea] >gi_1183005_dbj_BAA08283 (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333

(AC005623) calmodulin [Arabidopsis thaliana]

>gi 228407 prf 1803520A calmodulin 2 [Arabidopsis

thaliana]

Seq. No. 220406

Seq. ID LIB3149-049-Q1-K1-E8

Method BLASTX

E value

Match length

% identity

1.0e-46

130

74



```
NCBI GI
                  g1001631
BLAST score
                  238
                  5.0e-20
E value
Match length
                  129
                  40
% identity
NCBI Description
                  (D64002) integral membrane protein [Synechocystis sp.]
                  220407
Seq. No.
Seq. ID
                  LIB3149-049-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2505940
                  569
BLAST score
                  7.0e-59
E value
Match length
                  122
% identity
                  88
                 (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
NCBI Description
                  220408
Seq. No.
                  LIB3149-049-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  671
E value
                  8.0e-71
Match length
                  134
% identity
                  98
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  220409
Seq. No.
                  LIB3149-049-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363482
BLAST score
                  159
E value
                  9.0e-11
Match length
                  84
% identity
                  48
NCBI Description
                  IAA11 protein - Arabidopsis thaliana >gi 972925 (U18413)
                  IAA11 [Arabidopsis thaliana]
Seq. No.
                  220410
Seq. ID
                  LIB3149-049-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1363482
BLAST score
                  286
                  1.0e-25
E value
                  125
Match length
% identity
                  55
                  IAA11 protein - Arabidopsis thaliana >gi_972925 (U18413)
NCBI Description
                  IAA11 [Arabidopsis thaliana]
Seq. No.
                  220411
Seq. ID
                  LIB3149-049-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  g2833388
BLAST score
                  393
```

GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR NCBI Description >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta] 220412 Seq. No. LIB3149-049-Q1-K1-G5 Seq. ID Method BLASTN g2760168 NCBI GI BLAST score 34 E value 1.0e-09 Match length 88 92 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MEE6, complete sequence [Arabidopsis thaliana] 220413 Seq. No. LIB3149-049-Q1-K1-G6 Seq. ID Method BLASTX NCBI GI g3482967 605 BLAST score E value 5.0e-63 137 Match length % identity 80 (AL031369) Protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana] Seq. No. 220414 Seq. ID LIB3149-049-Q1-K1-G7 Method BLASTN NCBI GI q2529657 BLAST score 38 5.0e-12E value Match length 70 % identity 89 Arabidopsis thaliana chromosome II BAC T30B22 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 220415 Seq. No. Seq. ID LIB3149-049-Q1-K1-H10 Method BLASTX NCBI GI q1174448 BLAST score 198 E value 2.0e-15 Match length 61 % identity TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR NCBI Description (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >qi 547391 (L32016) alpha-subunit; putative

[Arabidopsis thaliana] 220416

LIB3149-050-Q1-K1-A11 Seq. ID Method BLASTX

NCBI GI g1351987

Seq. No.



BLAST score 307 E value 3.0e-29 Match length 90 % identity 72

NCBI Description ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)

(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_507946 (L29083) glutamine-dependent asparagine synthetase

[Arabidopsis thaliana]

Seq. No. 220417

Seq. ID LIB3149-050-Q1-K1-A12

Method BLASTX
NCBI GI g4314400
BLAST score 229
E value 3.0e-19
Match length 73
% identity 60

NCBI Description (AC006232) putative selenium-binding protein [Arabidopsis

thaliana]

Seq. No. 220418

Seq. ID LIB3149-050-Q1-K1-A3

Method BLASTX
NCBI GI g1477428
BLAST score 710
E value 2.0e-75
Match length 134
% identity 96

NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 220419

Seq. ID LIB3149-050-Q1-K1-A4

Method BLASTX
NCBI GI g1477428
BLAST score 405
E value 3.0e-46
Match length 110
% identity 85

NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 220420

Seq. ID LIB3149-050-Q1-K1-B11

Method BLASTX
NCBI GI g3128228
BLAST score 416
E value 4.0e-41
Match length 88
% identity 89

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi 3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 220421

Seq. ID LIB3149-050-Q1-K1-B12

Method BLASTX NCBI GI g1053047 BLAST score 354



```
7.0e - 34
 E value
                   85
Match length
                   85
 % identity
                   (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
 NCBI Description
                   histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
                   220422
 Seq. No.
                   LIB3149-050-Q1-K1-B7
 Seq. ID
                   BLASTX
 Method
                   g2943792
 NCBI GI
 BLAST score
                   625
                   2.0e-65
 E value
 Match length
                   128
                   88
 % identity
                  (AB006809) PV72 [Cucurbita sp.]
 NCBI Description
                   220423
 Seq. No.
                   LIB3149-050-Q1-K1-B8
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   g2264305
 BLAST score
                   34
                   1.0e-09
 E value
                   117
 Match length
                   91
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MBK23, complete sequence [Arabidopsis thaliana]
                   220424
 Seq. No.
                   LIB3149-050-Q1-K1-C12
 Seq. ID
 Method
                   BLASTX
                   g3850573
 NCBI GI
 BLAST score
                   353
                   9.0e-34
 E value
                   94
 Match length
                    69
 % identity
 NCBI Description
                   (AC005278) Similar to gi_1652733 glycogen operon protein
                   GlgX from Synechocystis sp. genome gb D90908. ESTs
                    gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from
                    this gene. [Arabidopsis thaliana]
                    220425
 Seq. No.
                   LIB3149-050-Q1-K1-C2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q133785
                    297
 BLAST score
 E value
                    3.0e-27
 Match length
                    77
 % identity
                    82
                   40S RIBOSOMAL PROTEIN S14 >gi 70945 pir R3RT14 ribosomal
 NCBI Description
```

protein S14 - rat >gi_57129_emb_CAA33143_ (X15040) ribosomal protein S14 (AA 1-152) [Rattus norvegicus]

220426 Seq. No.

LIB3149-050-Q1-K1-C3 Seq. ID

Method BLASTN NCBI GI g4325218



BLAST score 35 E value 4.0e-10 Match length 63 % identity 89

NCBI Description Arabidopsis thaliana hydrophobic protein (RCI2B) mRNA,

complete cds

Seq. No. 220427

Seq. ID LIB3149-050-Q1-K1-C4

Method BLASTX
NCBI GI g3928543
BLAST score 174
E value 2.0e-12
Match length 109
% identity 39

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 220428

Seq. ID LIB3149-050-Q1-K1-C6

Method BLASTX
NCBI GI g531389
BLAST score 180
E value 3.0e-13
Match length 87
% identity 41

NCBI Description (U12626) copia-like retrotransposon Hopscotch polyprotein

[Zea mays]

Seq. No. 220429

Seq. ID LIB3149-050-Q1-K1-C7

Method BLASTX
NCBI GI g3183247
BLAST score 311
E value 1.0e-28
Match length 128
% identity 51

NCBI Description PUTATIVE GTP-BINDING PROTEIN W08E3.3

>gi_3880615_emb_CAB07131_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD

protein, putative GTP-binding protein (SW:P38219); cDNA EST

EMBL: D64516 comes from this gene; cDNA EST EMBL: D65777

comes from this gene; cDNA EST EMB

Seq. No. 220430

Seq. ID LIB3149-050-Q1-K1-C8

Method BLASTX
NCBI GI g485742
BLAST score 614
E value 4.0e-64
Match length 131
% identity 90

NCBI Description (L32791) pyrophosphatase [Beta vulgaris]

Seq. No. 220431

Seq. ID LIB3149-050-Q1-K1-C9

Method BLASTX

```
g1402878
NCBI GI
                  270
BLAST score
                  5.0e-24
E value
                  91
Match length
                  59
% identity
NCBI Description (X98130) unknown [Arabidopsis thaliana]
                  220432
Seq. No.
                  LIB3149-050-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  q4115377
NCBI GI
                  316
BLAST score
                  4.0e-47
E value
Match length
                  116
                  82
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  220433
Seq. No.
                  LIB3149-050-Q1-K1-E7
Seq. ID
                  BLASTN
Method
                  g18342
NCBI GI
                  35
BLAST score
                  4.0e-10
E value
                  64
Match length
                  16
% identity
NCBI Description Carrot gene for extensin
Seq. No.
                  220434
                  LIB3149-050-Q1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3913919
BLAST score
                  326
                  1.0e-30
E value
                  77
Match length
                  82
% identity
NCBI Description
                  ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
                  SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                   (VACUOLAR INVERTASE) >gi 2351827 (U92438) soluble acid
                  invertase [Phaseolus vulgaris]
                  220435
Seq. No.
                  LIB3149-050-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2621768
BLAST score
                  149
E value
                  1.0e-09
Match length
                  97
% identity
                  (AE000848) ribonuclease PH [Methanobacterium
NCBI Description
```

thermoautotrophicum]

Seq. No. 220436

LIB3149-050-Q1-K1-F7 Seq. ID

BLASTX Method g2642450 NCBI GI BLAST score 576 1.0e-59 E value



```
Match length
                  131
% identity
                  85
                  (AC002391) putative metal ion transporter (Nramp)
NCBI Description
                  [Arabidopsis thaliana] >gi 3169188 (AC004401) putative
                  metal ion transporter (Nramp) [Arabidopsis thaliana]
                  220437
Seq. No.
Seq. ID
                  LIB3149-050-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  g3337356
BLAST score
                  330
                  4.0e-31
E value
Match length
                  86
                  76
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  220438
Seq. No.
Seq. ID
                  LIB3149-050-Q1-K1-G12
                  BLASTN
Method
NCBI GI
                  q4519188
BLAST score
                  37
                  2.0e-11
E value
Match length
                  89
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21L19, complete sequence
Seq. No.
                  220439
                  LIB3149-050-Q1-K1-G3
Seq. ID
Method
                  BLASTX
                  q2982299
NCBI GI
                  238
BLAST score
                  4.0e-20
E value
                  83
Match length
                  60
% identity
                  (AF051234) transcription factor BTF3 homolog [Picea
NCBI Description
                  mariana]
                  220440
Seq. No.
                  LIB3149-050-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g2414622
NCBI GI
BLAST score
                  246
                  5.0e-21
E value
                  102
Match length
                   50
% identity
                 (Z99259) conserved protein [Schizosaccharomyces pombe]
NCBI Description
                  220441
Seq. No.
                  LIB3149-050-Q1-K1-G7
Seq. ID
```

BLASTX Method NCBI GI a1350680 162 BLAST score 1.0e-11 E value 65 Match length 49 % identity



```
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   220442
 Seq. No.
 Seq. ID
                   LIB3149-050-Q1-K1-H10
 Method
                   BLASTX
 NCBI GI
                   q1222552
                   424
 BLAST score
                   4.0e-42
 E value
                   95
 Match length
                   81
 % identity
                   (U49330) pectin methylesterase [Lycopersicon esculentum]
 NCBI Description
                   220443
 Seq. No.
                   LIB3149-050-Q1-K1-H9
 Seq. ID
                   BLASTN
 Method
                   g4263774
 NCBI GI
                   36
 BLAST score
                   6.0e-11
 E value
                   64
 Match length
                   45
 % identity
 NCBI Description Arabidopsis thaliana chromosome II BAC T20F21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   220444
Seq. No.
                   LIB3149-051-Q1-K1-A5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4455198
 BLAST score
                    225
                    1.0e-18
 E value
                   98
 Match length
                    53
 % identity
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                    220445
 Seq. No.
                   LIB3149-051-Q1-K1-A6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q3319882
                    460
 BLAST score
                    3.0e-46
 E value
                    99
 Match length
                    89
 % identity
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
 NCBI Description
                    arietinum]
                    220446
 Seq. No.
 Seq. ID
                    LIB3149-051-Q1-K1-A7
 Method
                    BLASTX
 NCBI GI
                    q3850568
 BLAST score
                    216
 E value
                    1.0e-17
 Match length
                    67
                    66
 % identity
                    (ACO05278) Similar to hypothetical protein SPAC2F7.14c
 NCBI Description
                    gi 1052797 from Schizosaccharomyces pombe cosmid gb_Z50142.
                    [Arabidopsis thaliana]
```

Seq. No. 220447



BLASTX

Seq. ID Method

LIB3149-051-Q1-K1-B12

```
q4263713
NCBI GI
BLAST score
                  285
                  1.0e-25
E value
Match length
                  69
                  71
% identity
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  220448
Seq. No.
                  LIB3149-051-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  q2760322
NCBI GI
                  137
BLAST score
                   9.0e-09
E value
Match length
                  55
                   53
% identity
                 (AC002130) F1N21.7 [Arabidopsis thaliana]
NCBI Description
                  220449
Seq. No.
                  LIB3149-051-Q1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1222552
                   477
BLAST score
E value
                   3.0e-48
Match length
                  103
% identity
                   83
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
                   220450
Seq. No.
                   LIB3149-051-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                   q3882203
NCBI GI
BLAST score
                   209
                   1.0e-19
E value
Match length
                   80
% identity
                   62
NCBI Description (AB018284) KIAA0741 protein [Homo sapiens]
                   220451
Seq. No.
Seq. ID
                   LIB3149-051-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   387
E value
                   1.0e-37
Match length
                   87
% identity
                   84
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   220452
Seq. ID
                   LIB3149-051-Q1-K1-C10
Method
                   BLASTN
NCBI GI
                   g2687435
BLAST score
                   275
                   1.0e-153
E value
Match length
                   303
```



```
% identity
                  Hamamelis virginiana large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                  220453
Seq. No.
                  LIB3149-051-Q1-K1-C11
Seq. ID
                  BLASTN
Method
                  g1360093
NCBI GI
                  35
BLAST score
                  3.0e-10
E value
                  47
Match length
                  94
% identity
                  N.tabacum mRNA for a putative serine/threonine receptor
NCBI Description
                  kinase
                  220454
Seq. No.
                  LIB3149-051-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  g629597
NCBI GI
                   277
BLAST score
                   1.0e-24
E value
                   62
Match length
                   79
% identity
                  proline-rich protein - rape >gi_545029_bbs_142669 (S68113)
NCBI Description
                   proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                   Peptide, 147 aa] [Brassica napus]
                   220455
Seq. No.
                   LIB3149-051-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g531829
NCBI GI
BLAST score
                   154
                   2.0e-10
E value
                   74
Match length
                   42
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   220456
Seq. No.
                   LIB3149-051-Q1-K1-C7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2558961
BLAST score
                   222
                   1.0e-122
E value
                   234
Match length
% identity
NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds
                   220457
Seq. No.
Seq. ID
                   LIB3149-051-Q1-K1-D10
                   BLASTX
Method
                   q1710546
NCBI GI
BLAST score
                   365
                   4.0e-35
E value
Match length
                   81
                   88
% identity
```

31080

NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative



ribosomal protein [Daucus carota]

```
Seq. No.
                  220458
                  LIB3149-051-Q1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4098126
BLAST score
                  108
                  6.0e-54
E value
Match length
                  197
                  97
% identity
NCBI Description Gossypium hirsutum sucrose synthase mRNA, partial cds
                  220459
Seq. No.
                  LIB3149-051-Q1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4098126
BLAST score
                  35
                  1.0e-10
E value
Match length
                  85
% identity
                  93
NCBI Description Gossypium hirsutum sucrose synthase mRNA, partial cds
Seq. No.
                  220460
Seq. ID
                  LIB3149-051-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q730526
BLAST score
                  194
E value
                   4.0e-15
Match length
                  91
                   48
% identity
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                   >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein
                   [Arabidopsis thaliana]
Seq. No.
                   220461
Seq. ID
                  LIB3149-051-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q1350944
BLAST score
                  391
E value
                   4.0e-38
                  80
Match length
                  96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S17
Seq. No.
                   220462
Seq. ID
                  LIB3149-051-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q3925703
BLAST score
                   425
E value
                   4.0e-42
                  98
Match length
                   88
% identity
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                   220463
Seq. ID
                  LIB3149-051-Q1-K1-E12
```

NCBI GI

BLAST score



```
Method
                    BLASTX
 NCBI GI
                    g1354849
                    197
 BLAST score
                    2.0e-15
 E value
                    102
 Match length
                    60
 % identity
                   (U57350) epoxide hydrolase [Nicotiana tabacum]
 NCBI Description
                    220464
 Seq. No.
                    LIB3149-051-Q1-K1-E4
 Seq. ID
                    BLASTX
 Method
                    g1351987
 NCBI GI
                    352
 BLAST score
                    1.0e-33
 E value
 Match length
                    94
                    73
 % identity
                    ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
 NCBI Description
                    (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 507946
                    (L29083) glutamine-dependent asparagine synthetase
                    [Arabidopsis thaliana]
 Seq. No.
                    220465
                    LIB3149-051-Q1-K1-F10
 Seq. ID
                    BLASTX
 Method
                    g4158232
 NCBI GI
                    532
 BLAST score
                    1.0e-54
 E value
 Match length
                    105
                    90
~ % identity
                   (Y18626) reversibly glycosylated polypeptide [Triticum
 NCBI Description
                    aestivum]
                    220466
 Seq. No.
                    LIB3149-051-Q1-K1-F4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3269284
 BLAST score
                    240
 E value
                    2.0e-20
                    87
 Match length
  % identity
                    59
 NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
                    220467
  Seq. No.
 Seq. ID
                    LIB3149-051-Q1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    g4522012
 BLAST score
                    296
 E value
                    6.0e-27
 Match length
                    79
  % identity
 NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                    220468
                    LIB3149-051-Q1-K1-F7
 Seq. ID
 Method
                    BLASTX
```

31082

g4371285

```
9.0e-44
E value
Match length
                  98
                  85
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  220469
                  LIB3149-051-Q1-K1-F8
Seq. ID
```

BLASTX Method g1877397 NCBI GI BLAST score 336 1.0e-31 E value

73 Match length 85 % identity

NCBI Description (Y11591) shaggy-like kinase [Ricinus communis]

Seq. No. LIB3149-051-Q1-K1-F9 Seq. ID BLASTX Method NCBI GI g3451411 BLAST score 330

5.0e-31E value Match length 102 % identity 62

(Z98761) seryl-tRNA synthetase [Helianthus annuus] NCBI Description

220471 Seq. No.

LIB3149-051-Q1-K1-G1 Seq. ID

220470

Method BLASTX _g1352821 NCBI GI 284 BLAST score 1.0e-25 E value Match length 56 93 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 220472

Seq. ID LIB3149-051-Q1-K1-G11

Method BLASTX NCBI GI q2499945 BLAST score 394 E value 2.0e-38 Match length 102 % identity 75

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi 1076363 pir S46440 orotate

phosphoribosyltransferase (EC 2.4.2.10) /

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)

pyrE-F [Arabidopsis thaliana]

220473 Seq. No.

Seq. ID LIB3149-051-Q1-K1-G2

Match length

% identity

98

36



```
Method
                  BLASTX
NCBI GI
                  g1617272
                  419
BLAST score
                  2.0e-41
E value
                  101
Match length
                  73
% identity
                 (Z72151) AMP-binding protein [Brassica napus]
NCBI Description
                  220474
Seq. No.
                  LIB3149-051-Q1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3037045
BLAST score
                  148
                  1.0e-09
E value
Match length
                  74
% identity
                  43
NCBI Description (AF052621) hypothetical protein COX4AL [Mus musculus]
                  220475
Seq. No.
                  LIB3149-051-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580519
                  377
BLAST score
                  2.0e-36
E value
                  101
Match length
                  71
% identity
NCBI Description (AF036303) scarecrow-like 6 [Arabidopsis thaliana]
                  220476
Seq. No.
                  LIB3149-051-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g4115377
NCBI GI
BLAST score
                  432
                  6.0e-43
E value
Match length
                  111
                  73
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  220477
                  LIB3149-051-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2281090
BLAST score
                  217
                  8.0e-18
E value
Match length
                  112
% identity
                   46
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  220478
Seq. ID
                  LIB3149-051-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                   g4263822
BLAST score
                   153
E value
                   3.0e-10
```

31084

NCBI Description (AC006067) putative receptor protein kinase [Arabidopsis

% identity

69

NCBI Description T complex protein [Cucumis sativus]



thaliana]

```
220479
Seq. No.
                  LIB3149-051-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  q2267567
NCBI GI
                  402
BLAST score
                  2.0e-39
E value
                  89
Match length
                  87
% identity
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                  220480
Seq. No.
                  LIB3149-052-Q1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4193382
                  262
BLAST score
                  4.0e-23
E value
                  50
Match length
                  90
% identity
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
                  220481
Seq. No.
                  LIB3149-053-Q1-K1-A1
Seq. ID
                  BLASTN
Method
                  g2275090
NCBI GI
                  173
BLAST score
E value
                  1.0e-92
Match length
                  193
                   97
% identity
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
Seq. No.
                   220482
                  LIB3149-053-Q1-K1-A11
Sèq. ID
Method
                  BLASTX
NCBI GI
                   q3914535
BLAST score
                   159
E value
                   5.0e-11
Match length
                   39
                   85
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_
                   (AJ223363) ribosomal protein L13a [Lupinus luteus]
Seq. No.
                   220483
Seq. ID
                   LIB3149-053-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   q1587206
BLAST score
                   361
E value
                   2.0e-34
Match length
                   116
```

Method

NCBI GI

BLASTX

g2213425



```
Seq. No.
                  220484
                  LIB3149-053-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  q1587206
NCBI GI
BLAST score
                  623
                  3.0e-65
E value
                  130
Match length
                  94
% identity
NCBI Description T complex protein [Cucumis sativus]
                  220485
Seq. No.
                  LIB3149-053-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g1587206
NCBI GI
BLAST score
                  519
                  6.0e-53
E value
                  132
Match length
                  79
% identity
NCBI Description T complex protein [Cucumis sativus]
                  220486
Seq. No.
                  LIB3149-053-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                  g1703375
NCBI GI
                  210
BLAST score
                  8.0e-28
E value
                  93
Match length
% identity
                  80
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259 (D45420)
                  DcARF1 [Daucus carota]
                  220487
Seq. No.
                  LIB3149-053-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g2500026
NCBI GI
                   556
BLAST score
E value
                   3.0e-57
Match length
                  126
                   83
% identity
                  ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE
NCBI Description
                  LIGASE) >gi_1616657 (U49389) adenylosuccinate synthetase
                   [Arabidopsis thaliana]
                   220488
Seq. No.
                   LIB3149-053-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g643469
BLAST score
                   139
                   9.0e-09
E value
                   40
Match length
% identity
                   65
NCBI Description (U19886) unknown [Lycopersicon esculentum]
                   220489
Seq. No.
                   LIB3149-053-Q1-K1-B2
Seq. ID
```



```
BLAST score 314
E value 4.0e-29
Match length 70
% identity 47
```

NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 220490

Seq. ID LIB3149-053-Q1-K1-B3

Method BLASTX
NCBI GI g399940
BLAST score 628
E value 8.0e-66
Match length 131
% identity 96

NCBI Description MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR

>gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock

protein [Phaseolus vulgaris]

Seq. No. 220491

Seq. ID LIB3149-053-Q1-K1-B5

Method BLASTX
NCBI GI g133424
BLAST score 166
E value 1.0e-11
Match length 46
% identity 72

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_66969_pir__RNNTB

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain -

common tobacco chloroplast >gi_11781_emb_CAA31238_ (X12745) ORF 1070 (AA 1-1070); put. RNA polymerase beta-subunit [Nicotiana tabacum] >gi_11822_emb_CAA77346_ (Z00044) RNA

polymerase beta subunit [Nicotiana tabacum]

Seq. No. 220492

Seq. ID LIB3149-053-Q1-K1-B7

Method BLASTN
NCBI GI g3869069
BLAST score 36
E value 8.0e-11
Match length 226
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 220493

Seq. ID LIB3149-053-Q1-K1-C12

Method BLASTX
NCBI GI g2500355
BLAST score 212
E value 3.0e-17
Match length 56
% identity 79

NCBI Description 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG)

>gi_629704_pir__S44144 ribosomal protein L10.e, cytosolic common tobacco (fragment) >gi_473104_emb_CAA78461_ (Z14083)
HOMOLOGIE with Human WILM's tumor-related protein HUMQM

Seq. No.

[Nicotiana tabacum]

220494 Seq. No. LIB3149-053-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI g417148 363 BLAST score 1.0e-34 E value 129 Match length 55 % identity PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) NCBI Description (G2-4) >gi_99912_pir__A33654 heat shock protein 26A soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max] 220495 Seq. No. LIB3149-053-Q1-K1-C4 Seq. ID Method BLASTX g1420938 NCBI GI BLAST score 277 1.0e-24 E value Match length 80 69 % identity (U61379) Vigna unguiculata ascorbate peroxidase mRNA, NCBI Description complete cds [Vigna unguiculata] Seq. No. 220496 Seq. ID LIB3149-053-Q1-K1-C5 Method BLASTX NCBI GI q2827544 BLAST score 211 E value 7.0e-17 Match length 44 93 % identity NCBI Description (AL021635) HSP associated protein like [Arabidopsis thaliana] Seq. No. 220497 Seq. ID LIB3149-053-Q1-K1-C7 Method BLASTX g2894599 NCBI GI BLAST score 210 E value 9.0e-17 Match length 119 % identity NCBI Description (AL021889) putative protein [Arabidopsis thaliana] Seq. No. 220498 LIB3149-053-Q1-K1-D1 Seq. ID Method BLASTX NCBI GI g4559346 BLAST score 421 E value 2.0e-41 ~ 128 Match length 64 % identity

31088

NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]



```
LIB3149-053-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g136712
NCBI GI
BLAST score
                   585
                   1.0e-60
E value
Match length
                   133
                   80
% identity
                   CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                   (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_81457_pir__S00454
                   plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                   iron-sulfur protein precursor - spinach
                   >gi_21311_emb_CAA29590_ (X06244) Rieske FeS-precursor
[Spinacia oleracea] >gi_226151_prf__1412276A rieske FeS
                   precursor protein [Spinacia oleracea]
                   220500
Seq. No.
                   LIB3149-053-Q1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q136707
BLAST score
                   242
                   2.0e-20
E value
Match length
                   52
                   90
% identity
                  CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                   (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397 pir S26199
                   plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                   iron-sulfur protein precursor - garden pea
                   >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS
                   protein [Pisum sativum]
                   220501
Seq. No.
Seq. ID
                   LIB3149-053-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2499488
BLAST score
                   628
E value
                   9.0e-66
Match length
                   130
% identity
                   95
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                   ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                   pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
                   220502
Seq. No.
Seq. ID
                   LIB3149-053-Q1-K1-D5
Method
                   BLASTX
```

NCBI GI q3335359 BLAST score 235 E value 1.0e-19 Match length 128 % identity

(AC003028) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 220503

LIB3149-053-Q1-K1-D6 Seq. ID



Method BLASTX
NCBI GI g3335359
BLAST score 159
E value 8.0e-11
Match length 128
% identity 36

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 220504

Seq. ID LIB3149-053-Q1-K1-D7

Method BLASTX
NCBI GI g3913633
BLAST score 158
E value 4.0e-13
Match length 88
% identity 60

NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown

protein [Arabidopsis thaliana]

Seq. No. 220505

Seq. ID LIB3149-053-Q1-K1-D8

Method BLASTN NCBI GI g1419087

BLAST score 38
E value 5.0e-12
Match length 78
% identity 87

NCBI Description N.plumbaginifolia mRNA for calreticulin

Seq. No. 220506

Seq. ID LIB3149-053-Q1-K1-E1

Method BLASTN
NCBI GI g683501
BLAST score 40
E value 3.0e-13
Match length 56
% identity 93

NCBI Description A.thaliana mRNA for 65 kDa regulatory subunit of protein

phosphatase 2A

Seq. No. 220507

Seg. ID LIB3149-053-Q1-K1-E10

Method BLASTX
NCBI GI g3687235
BLAST score 140
E value 1.0e-08
Match length 88
% identity 45

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 220508

Seq. ID LIB3149-053-Q1-K1-E3

Method BLASTX NCBI GI g3914535 BLAST score 170 E value 3.0e-12

% identity

65

```
Match length
                  39
                  87
% identity
                  60S RIBOSOMAL PROTEIN L13A >gi 2791948_emb_CAA11283_
NCBI Description
                  (AJ223363) ribosomal protein L13a [Lupinus luteus]
                  220509
Seq. No.
                  LIB3149-053-Q1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3776005
BLAST score
                  442
                  6.0e-44
E value
Match length
                  93
                  94
% identity
                 (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  220510
Seq. No.
                  LIB3149-053-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1922242
BLAST score
                  194
E value
                  7.0e-15
Match length
                  69
                  61
% identity
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  220511
Seq. ID
                  LIB3149-053-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3885515
BLAST score
                  447
                  1.0e-44
E value
Match length
                  103
% identity
                  81
                  (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                  sativa]
Seq. No.
                  220512
                  LIB3149-053-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q531829
BLAST score
                  146
E value
                  1.0e-09
Match length
                  72
                  50
% identity
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                   220513
Seq. ID
                  LIB3149-053-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2894612
BLAST score
                  372
E value
                  8.0e-36
Match length
                  118
```

31091

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]



```
220514
Seq. No.
                  LIB3149-053-Q1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539350
BLAST score
                  357
                  5.0e - 34
E value
                  79
Match length
                  78
% identity
                  (AL035539) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  220515
                  LIB3149-053-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q399785
BLAST score
                  609
                  2.0e-63
E value
Match length
                  132
% identity
                  87
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
NCBI Description
                  (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                  >gi_100331_pir__S21454 glutamate-1-semialdehyde
                  2,1-aminomutase (EC 5.4.3.8) - common tobacco
                  >gi_19873_emb_CAA46786_ (X65973) glutamate-1-semialdehyde
                  2,1-aminomutase [Nicotiana tabacum]
Seq. No.
                  220516
                  LIB3149-053-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  g3702343
NCBI GI
BLAST score
                   323
                  4.0e-30
E value
                  114
Match length
                   57
% identity
NCBI Description
                  (AC005397) putative homeotic gene regulator [Arabidopsis
                  thaliana]
Seq. No.
                   220517
                  LIB3149-053-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g399785
BLAST score
                   591
E value
                   2.0e-61
Match length
                   132
% identity
NCBI Description GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
                   (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                   >gi_100331_pir__S21454 glutamate-1-semialdehyde
                   2,1-aminomutase (EC 5.4.3.8) - common tobacco
                   >gi_19873_emb_CAA46786_ (X65973) glutamate-1-semialdehyde
                   2,1-aminomutase [Nicotiana tabacum]
Seq. No.
                   220518
Seq. ID
                   LIB3149-053-Q1-K1-G3
```

Method BLASTX NCBI GI g1666173 477 BLAST score E value 5.0e-48

220524

```
Match length
                  114
                  83
% identity
                 (Y09106) transcription factor [Nicotiana plumbaginifolia]
NCBI Description
                  220519
Seq. No.
                  LIB3149-053-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4176531
BLAST score
                  171
                  4.0e-12
E value
Match length
                  118
                  39
% identity
                  (AL035263) weak similarity to chick phosphatidylcholine-ste
NCBI Description
                  rol acetyltransferase [Schizosaccharomyces pombe]
                  220520
Seq. No.
                  LIB3149-053-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567304
BLAST score
                  140
                  1.0e-11
E value
                  120
Match length
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                  220521
                  LIB3149-054-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708401
BLAST score
                  412
E value
                  2.0e-40
Match length
                  90
                  90
% identity
NCBI Description ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE
                  DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)
Seq. No.
                   220522
                  LIB3149-054-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707074
BLAST score
                  201
E value
                   9.0e-16
                  117
Match length
                  38
% identity
NCBI Description (U80450) M01E11.2 [Caenorhabditis elegans]
Seq. No.
                   220523
                  LIB3149-054-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2597826
BLAST score
                   372
E value
                   9.0e-36
                  95
Match length
                   73
% identity
NCBI Description (Y14590) class IV chitinase [Arabidopsis thaliana]
```



```
LIB3149-054-Q1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1350680
BLAST score
                  221
                  5.0e-30
E value
                  104
Match length
                  65
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                  220525
Seq. No.
                  LIB3149-054-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406777
BLAST score
                  156
                  2.0e-10
E value
                  79
Match length
                  43
% identity
NCBI Description (AC006532) putative zinc-finger protein [Arabidopsis
                  thaliana]
                  220526
Seq. No.
                  LIB3149-054-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702321
                  491
BLAST score
                  1.0e-49
E value
Match length
                  127
% identity
                  38
NCBI Description (AC005397) putative TGF-beta receptor interacting protein
                  [Arabidopsis thaliana]
Seq. No.
                  220527
                  LIB3149-054-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266989
BLAST score
                  499
E value
                  1.0e-50
Match length
                  118
% identity
                  83
NCBI Description GTP-BINDING PROTEIN SAR1B >gi 322517 pir S28603
                  GTP-binding protein - Arabidopsis thaliana >gi_166734
                  (M95795) GTP-binding protein [Arabidopsis thaliana]
                  220528
Seq. No.
                  LIB3149-054-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334322
BLAST score
                  295
E value
                  8.0e-27
Match length
                  97
                  62
% identity
NCBI Description GTP-BINDING PROTEIN SAR1B >gi 2108347 (U55036) small
                  GTP-binding protein Bsarlb [Brassica rapa]
```

Seq. ID LIB3149-054-Q1-K1-C11

Method BLASTX



```
g1255951
  NCBI GI
   BLAST score
                     290
                     3.0e-26
   E value
                     59
   Match length
                     86
   % identity
                    (X96932) PS60 [Nicotiana tabacum]
  NCBI Description
                     220530
   Seq. No.
                     LIB3149-054-Q1-K1-C12
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g1255951
   BLAST score
                     150
                     4.0e-10
   E value
   Match length
                     56
                     55
   % identity
   NCBI Description (X96932) PS60 [Nicotiana tabacum]
   Seq. No.
                     220531
                     LIB3149-054-Q1-K1-C5
  Seq. ID
                     BLASTX
  Method
                     g3925703
  NCBI GI
  BLAST score
                     408
                     6.0e-40
   E value
                     90
  Match length
                     91
% identity
   NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
   Seq. No.
                     220532
                     LIB3149-054-Q1-K1-C6
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     q132908
   BLAST score
                     155
                     3.0e-10
  E value
                     42
  Match length
                     69
   % identity
                    50S RIBOSOMAL PROTEIN L34 >gi_79021_pir__JQ0732 ribosomal
   NCBI Description
                     protein L34 - Proteus mirabilis >gi_150877 (M58352)
                     ribosomal protein L34 [Proteus mirabilis]
                     220533
   Seq. No.
                     LIB3149-054-Q1-K1-C8
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g1171978
   BLAST score
                     388
   E value
                     1.0e-37
   Match length
                     129
                     25
   % identity
   NCBI Description
                    POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                     (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                     [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                     poly(A)-binding protein [Arabidopsis thaliana]
```

Seq. ID LIB3149-054-Q1-K1-D12

Method BLASTX NCBI GI g2501850 BLAST score 253



```
E value
                  3.0e-32
Match length
                  84
                  87
% identity
                  (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
NCBI Description
                  220535
Seq. No.
                  LIB3149-054-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4098129
BLAST score
                  537
E value
                  3.0e-55
Match length
                  107
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                  220536
Seq. No.
                  LIB3149-054-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  g1362086
NCBI GI
BLAST score
                  588
E value
                  4.0e-61
Match length
                  122
                  90
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  220537
Seq. ID
                  LIB3149-054-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2739379
BLAST score
                  245
E value
                  6.0e-21
Match length
                  86
% identity
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  220538
Seq. ID
                  LIB3149-054-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q266945
BLAST score
                  145
E value
                  3.0e-21
Match length
                  91
% identity
                  61
```

NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)

>gi_100065_pir__S19978 ribosomal protein L9 - garden pea
>gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
>gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9

[Pisum sativum]

Seq. No. 220539

Seq. ID LIB3149-054-Q1-K1-D9



87

Match length % identity

```
Method
                  BLASTX
                  g136707
NCBI GI
                  395
BLAST score
                  2.0e-38
E value
Match length
                  103
                  72
% identity
                  CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                   (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  iron-sulfur protein precursor - garden pea
                  >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS
                  protein [Pisum sativum]
                  220540
Seq. No.
                  LIB3149-054-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                  g2500380
NCBI GI
BLAST score
                  564
                  3.0e-58
E value
                  104
Match length
                  99
% identity
                 60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal
NCBI Description
                  protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal
                  protein L44 isoform a [Gossypium hirsutum] >gi_1553131
                   (U64678) ribosomal protein L44 isoform b [Gossypium
                  hirsutum]
                  220541
Seq. No.
                  LIB3149-054-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3122753
BLAST score
                   185
                   2.0e-14
E value
Match length
                   48
                   73
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb CAB10211.1
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
                   220542
Seq. No.
Seq. ID
                   LIB3149-054-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                   g4432841
BLAST score
                   306
E value
                   5.0e-28
Match length
                   82
% identity
NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   220543
                   LIB3149-054-Q1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g170354
BLAST score
                   431
E value
                   1.0e-42
```

NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]



Seq. ID LIB3149-054-Q1-K1-E5

Method BLASTX
NCBI GI g3947448
BLAST score 298
E value 4.0e-27
Match length 127
% identity 44

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA

EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 220545

Seq. ID LIB3149-054-Q1-K1-E8

Method BLASTX
NCBI GI g1173223
BLAST score 340
E value 3.0e-37
Match length 87
% identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal

protein S11 [Glycine max]

Seq. No. 220546

Seq. ID LIB3149-054-Q1-K1-F11

Method BLASTX
NCBI GI g1350956
BLAST score 527
E value 7.0e-54
Match length 112
% identity 93

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 220547

Seq. ID LIB3149-054-Q1-K1-F6

Method BLASTX
NCBI GI g1399380
BLAST score 594
E value 9.0e-62
Match length 134
% identity 82

NCBI Description (U43683) S-adenosyl-L-methionine:delta24-sterol-C-

methyltransferase [Glycine max]

Seq. No. 220548

Seq. ID LIB3149-054-Q1-K1-F7

Method BLASTX NCBI GI g2780194 BLAST score 538 E value 3.0e-55

```
Match length
% identity
                    (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
                    220549
Seq. No.
                    LIB3149-054-Q1-K1-G1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q133808
                    177
BLAST score
                    5.0e-13
E value
                    44
Match length
                    80
% identity
                    40S RIBOSOMAL PROTEIN S16 >gi_70921_pir__R3YL16 ribosomal
NCBI Description
                    protein S16, cytosolic - large-leaved lupine
>gi_19512_emb_CAA36068_ (X51766) rps16 gene product (AA
                    1-145) [Lupinus polyphyllus]
                    220550
Seq. No.
                    LIB3149-054-Q1-K1-G11
Seq. ID
                    BLASTX
Method
                    g728868
NCBI GI
BLAST score
                    142
                    6.0e-09
E value
                    66
Match length
                    52
% identity
                    ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                    >gi_99824_pir__S16748 proline-rich protein - rape (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                    protein [Brassica napus]
                    220551
Seq. No.
                    LIB3149-054-Q1-K1-G9
Seq. ID
Method
                    BLASTX
                    q3033396
NCBI GI
                    241
BLAST score
E value
                    2.0e-20
Match length
                    74
% identity
                    57
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]
                    220552
Seq. No.
                    LIB3149-054-Q1-K1-H1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3687243
                    245
BLAST score
E value
                    4.0e-21
Match length
                    61
                    79
% identity
                    (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    220553
                    LIB3149-054-Q1-K1-H11
Seq. ID
                    BLASTX
Method
                    g4126399
NCBI GI
BLAST score
                    438
```

31099

1.0e-43

E value



Match length 108 80 % identity NCBI Description

(AB011794) chalcone isomerase [Citrus sinensis]

Seq. No.

220554

LIB3149-054-Q1-K1-H3 Seq. ID

Method BLASTX NCBI GI g3687243 BLAST score 188 E value 3.0e-1457 Match length 68 % identity

NCBI Description (AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No.

220555

LIB3149-054-Q1-K1-H4 Seq. ID

Method BLASTX NCBI GI q3510254 BLAST score 459 E value 6.0e-46109 Match length 83 % identity

(AC005310) putative zinc transporter [Arabidopsis thaliana] NCBI Description

Seq. No.

220556

Seq. ID LIB3149-054-Q1-K1-H6 Method BLASTX

NCBI GI q2286153 563 BLAST score E value 3.0e-58 Match length 119 92 % identity

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 220557

LIB3149-054-Q1-K1-H8 Seq. ID

Method BLASTX NCBI GI q951427 BLAST score 465 E value 1.0e-46 Match length 121 72 % identity

(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus NCBI Description

communis]

Seq. No. 220558

Seq. ID LIB3149-055-Q1-K1-A3

Method BLASTX NCBI GI q3064039 BLAST score 136 E value 1.0e-08 62 Match length

% identity 48

NCBI Description (AF054445) major latex protein homolog [Mesembryanthemum

crystallinum]



```
220559
Seq. No.
                  LIB3149-055-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2583108
                  190
BLAST score
                  1.0e-14
E value
                  59
Match length
                  56
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                  220560
Seq. No.
                  LIB3149-055-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2914700
BLAST score
                  140
E value
                  1.0e-08
Match length
                  78
                   47
% identity
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                  thaliana]
                  220561
Seq. No.
                  LIB3149-055-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979553
BLAST score
                  174
                   5.0e-13
E value
Match length
                  65
% identity
                   51
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
                  220562
Seq. No.
                  LIB3149-055-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3023847
BLAST score
                   315
E value
                   2.0e-29
Match length
                   74
% identity
                   58
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
Seq. No.
                   220563
                  LIB3149-055-Q1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3108024
                  32
BLAST score
E value
                   1.0e-08
Match length
                   43
                   93
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC T1F15 sequence,
                  complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB3149-055-Q1-K1-B5

Method BLASTX



```
NCBI GI
                  g1408471
                  170
BLAST score
                  4.0e-12
E value
Match length
                  39
                  85
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                  thaliana] >gi_3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
                  220565
Seq. No.
Seq. ID
                  LIB3149-055-Q1-K1-B8
                  BLASTX
Method
                  g1708313
NCBI GI
BLAST score
                  161
                  4.0e-11
E value
Match length
                  50
                  74
% identity
                  HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs_163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                   thaliana]
Seq. No.
                   220566
                  LIB3149-055-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q167367
BLAST score
                   164
E value
                   2.0e-11
Match length
                   34
                   94
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   220567
Seq. No.
                   LIB3149-055-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g4056497
NCBI GI
BLAST score
                   296
E value
                   7.0e-27
                   93
Match length
                   69
% identity
NCBI Description (AC005896) putative histone H2B [Arabidopsis thaliana]
                   220568
Seq. No.
                   LIB3149-055-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3264767
BLAST score
                   142
E value
                   2.0e-16
Match length
                   93
% identity
                   52
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                   220569
Seq. No.
                   LIB3149-055-Q1-K1-C5
Seq. ID
```

31102

BLASTX

543

g1200205

Method NCBI GI

BLAST score

```
6.0e-56
E value
Match length
                   109
                   94
% identity
                   (X95753) DAG [Antirrhinum majus]
NCBI Description
                   220570
Seq. No.
                   LIB3149-055-Q1-K1-C6
Seq. ID
                   BLASTN
Method
                   g167366
NCBI GI
BLAST score
                   325
                   0.0e + 00
E value
Match length
                   394
                   96
% identity
NCBI Description Gossypium hirsutum peroxidase mRNA, complete cds
                   220571
Seq. No.
                   LIB3149-055-Q1-K1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2558962
BLAST score
                   293
E value
                   2.0e-26
Match length
                   60
                   98
% identity
                  (AF025667) histone H2B1 [Gossypium hirsutum]
NCBI Descriptión
                   220572
Seq. No.
                   LIB3149-055-Q1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1172995
                   235
BLAST score
                   1.0e-19
E value
                   95
Match length
                   56
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]
                   >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
                   norvegicus]
                    220573
Seq. No.
Seq. ID
                   LIB3149-055-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                    g4263712
BLAST score
                    268
E value
                    6.0e-24
Match length
                   71
% identity
                    66
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
```

thaliana]

Seq. No. 220574

Seq. ID LIB3149-055-Q1-K1-E2

Method BLASTX
NCBI GI g1172995
BLAST score 136
E value 1.0e-08
Match length 48



% identity 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal NCBI Description protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus] 220575 Seq. No. LIB3149-055-Q1-K1-E4 Seq. ID BLASTX Method NCBI GI q728867 BLAST score 191 1.0e-14 E value Match length 88 42 % identity ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR NCBI Description >gi_99694_pir__S21961 proline-rich protein APG -Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana] Seq. No. 220576 LIB3149-055-Q1-K1-E5 Seq. ID BLASTX Method NCBI GI g2239085 BLAST score 222 3.0e-18E value Match length 92 % identity 50 (Z84384) anthranilate N-hydroxycinnamoyl/benzoyltransferase NCBI Description [Dianthus caryophyllus] 220577 Seq. No. LIB3149-055-Q1-K1-E7 Seq. ID Method BLASTX g166878 NCBI GI 196 BLAST score 1.0e-19 E value Match length 94 57 % identity (M95796) St12p protein [Arabidopsis thaliana] NCBI Description 220578 Seq. No. LIB3149-055-Q1-K1-F12 Seq. ID BLASTX Method g1173187 NCBI GI 364 BLAST score 5.0e-35 E value Match length 82 90 % identity 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673 NCBI Description ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 (U19940) putative 40S ribosomal

Seq. No. 220579

Seq. ID LIB3149-055-Q1-K1-F2

Method BLASTX

31104

protein s12 [Fragaria x ananassa]



```
g4512698
NCBI GI
BLAST score
                  197
                  3.0e-15
E value
                  107
Match length
                  41
% identity
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  220580
Seq. No.
                  LIB3149-055-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g2244734
NCBI GI
BLAST score
                  267
E value
                  2.0e-23
                  59
Match length
                  92
% identity
NCBI Description
                 (D88414) actin [Gossypium hirsutum]
                  220581
Seq. No.
                  LIB3149-055-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2369714
BLAST score
                  264
                  5.0e-23
E value
                  72
Match length
% identity
                  74
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
Seq. No.
                  220582
                  LIB3149-055-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173187
                   370
BLAST score
E value
                   1.0e-35
                   75
Match length
                   97
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi 643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
                   220583
Seq. No.
Seq. ID
                   LIB3149-055-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g2244811
BLAST score
                   194
                   4.0e-17
E value
Match length
                   113
% identity
NCBI Description (Z97336) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                   220584
```

Seq. ID LIB3149-055-Q1-K1-G7

Method BLASTX
NCBI GI g3924597
BLAST score 146
E value 2.0e-09
Match length 57



```
% identity
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                  220585
Seq. No.
                  LIB3149-055-Q1-K1-H1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q559547
                  97
BLAST score
                  3.0e-47
E value
Match length
                  153
                  91
% identity
                  Transformation vector pPRV100B, plastid targeting segment
NCBI Description
                  220586
Seq. No.
                  LIB3149-056-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  q2494261
NCBI GI
                  406
BLAST score
                  1.0e-39
E value
                  84
Match length
                  93
% identity
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                  >gi_99903_pir__S21567 translation elongation factor Tu
                  precursor - soybean chloroplast >gi_18776_emb_CAA46864_
                   (X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A
                  elongation factor Tu [Glycine max]
                  220587
Seq. No.
                  LIB3149-056-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710838
BLAST score
                  281
E value
                   1.0e-25
                   63
Match length
                  86
% identity
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                   HYDROLASE) (ADOHCYASE) >gi 535584 (L36119)
                   adenosylhomocysteinase [Medicago sativa]
                   220588
Seq. No.
                   LIB3149-056-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g81811
BLAST score
                   396
                   1.0e-38
E value
Match length
                   98
% identity
                   79
                  ribosomal protein S11 - soybean (fragment) >gi_170054
NCBI Description
                   (M31024) ribosomal protein S11 [Glycine max]
Seq. No.
                   220589
Seq. ID
                   LIB3149-056-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   g3335341
```

Method BLASTX
NCBI GI g3335341
BLAST score 200
E value 9.0e-16
Match length 71



```
% identity
                   (AC004512) T8F5.10 [Arabidopsis thaliana]
NCBI Description
                   220590
Seq. No.
                   LIB3149-056-Q1-K1-C9
Seq. ID
                   BLASTN
Method
                   g20419
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   95
Match length
                   15
% identity
NCBI Description P.amygdalus mRNA for extensin
                   220591
Seq. No.
                   LIB3149-056-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   g1170660
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
Match length
                   56
                   73
% identity
                   MEVALONATE KINASE (MK) >gi_541880_pir__S42088 mevalonate
NCBI Description
                   kinase (EC 2.7.1.36) - Arabidopsis thaliana
                   >gi_456614_emb_CAA54820_ (X77793) mevalonate kinase
                    [Arabidopsis thaliana]
                   220592
Seq. No.
                   LIB3149-056-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g3287826
NCBI GI
                   360
BLAST score
                   1.0e-34
E value
                   79
Match length
                    87
% identity
                   (+)-DELTA-CADINENE SYNTHASE ISOZYME C2 (D-CADINENE
NCBI Description
                    SYNTHASE) >gi_2879841_emb_CAA76223.1_ (Y16432)
                    (+)-delta-cadinene synthase [Gossypium arboreum]
                    220593
Seq. No.
                    LIB3149-056-Q1-K1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                    q3287824
BLAST score
                    171
                    9.0e-13
E value
                    38
Match length
                    82
% identity
                   (+)-DELTA-CADINENE SYNTHASE ISOZYME XC1 (D-CADINENE
NCBI Description
                    SYNTHASE) >gi_2147015_pir__S68365 (+)-delta-cadinene synthase isozyme XC1 - Gossypium arboreum >gi_1045312
                    (U23206) (+)-delta-cadinene synthase isozyme XC1 [Gossypium
                    arboreum]
```

Seq. ID LIB3149-056-Q1-K1-E7

Method BLASTX NCBI GI g3024516 BLAST score 341



2.0e-32 E value Match length 70 97 % identity RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong NCBI Description similarity to A. thaliana ara- $\overline{2}$ (gb_ATHARA2). ESTs gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene. [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related small GTPase [Arabidopsis thaliana] 220595 Seq. No. Seq. ID LIB3149-056-Q1-K1-E8 BLASTX Method g1076510 NCBI GI 607 BLAST score 9.0e-64 E value 142 Match length % identity 85 peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean NCBI Description >gi 829119 emb CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris] 220596 Seq. No. LIB3149-056-Q1-K1-F9 Seq. ID Method BLASTX g2739366 NCBI GI 244 BLAST score 1.0e-20 E value Match length 125 % identity 42 (AC002505) SF16 like protein [Arabidopsis thaliana] NCBI Description 220597 Seq. No. LIB3149-056-Q1-K1-G5 Seq. ID BLASTX Method g3461848 NCBI GI 137 BLAST score 1.0e-08 E value Match Tength 34 85 % identity (AC005315) putative ATPase [Arabidopsis thaliana] NCBI Description 220598 Seq. No. LIB3149-056-Q1-K1-G9 Seq. ID BLASTX Method NCBI GI g3080421 272 BLAST score 6.0e-24 E value Match length 128 46 % identity (AL022604) putative protein [Arabidopsis thaliana] NCBI Description 220599 Seq. No.

Seq. ID LIB3149-056-Q1-K1-H9

Method BLASTX
NCBI GI g4567207
BLAST score 216
E value 8.0e-18

Seq. ID

220605

LIB3149-057-Q1-K1-B11



```
Match length
                  79
                  57
% identity
NCBI Description
                  (AC007168) unknown protein [Arabidopsis thaliana]
                  220600
Seq. No.
                  LIB3149-057-Q1-K1-A1
Seq. ID
Method
                  BLASTX
                  g3107931
NCBI GI
BLAST score
                  385
E value
                  1.0e-37
                  88
Match length
                  84
% identity
                  (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
                  220601
Seq. No.
                  LIB3149-057-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q585963
BLAST score
                  170
                  4.0e-12
E value
Match length
                  49
                  73
% identity
                  PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
NCBI Description
                  220602
Seq. No.
                  LIB3149-057-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                  g3549660
NCBI GI
                   380
BLAST score
                   8.0e-37
E value
Match length
                  107
% identity
                   66
                  (AL031394) carbonate dehydratase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   220603
Seq. ID
                   LIB3149-057-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   q1841870
BLAST score
                   332
E value
                   3.0e-31
Match length
                   81
% identity
                   79
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
Seq. No.
                   220604
Seq. ID
                   LIB3149-057-Q1-K1-B10
Method
                   BLASTN
NCBI GI
                   q1518539
BLAST score
                   44
E value
                   1.0e-15
                  76
Match length
                   89
% identity
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
```

Seq. ID

220610

LIB3149-057-Q1-K1-D1



```
BLASTX
Method
NCBI GI
                  g1351017
                  232
BLAST score
                  2.0e-19
E value
                  46
Match length
                  93
% identity
                  40S RIBOSOMAL PROTEIN S9 (S4) >gi 629697 pir S45375
NCBI Description
                  ribosomal protein S4 - common tobacco (fragment)
                  >gi 443960 emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4
                  [Nicotiana tabacum]
                  220606
Seq. No.
                  LIB3149-057-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  q1669597
NCBI GI
BLAST score
                  359
                  2.0e-34
E value
                  97
Match length
                  75
% identity
                  (D88745) AR192 [Arabidopsis thaliana]
NCBI Description
                  220607
Seq. No.
                  LIB3149-057-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g3287832
NCBI GI
                  601
BLAST score
                  1.0e-62
E value
Match length
                  114
                  98
% identity
                  (+)-DELTA-CADINENE SYNTHASE (D-CADINENE SYNTHASE)
NCBI Description
                  >gi 1843647 (U88318) (+)-delta-cadinene synthase [Gossypium
                  hirsutum]
                  220608
Seq. No.
                  LIB3149-057-Q1-K1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2687437
                   60
BLAST score
                   4.0e-25
E value
                   60
Match length
                   100
% identity
NCBI Description
                  Jepsonia parryi large subunit 26S ribosomal RNA gene,
                  partial sequence
                   220609
Seq. No.
                   LIB3149-057-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1703380
BLAST score
                   264
                   2.0e-23
E value
Match length
                   85
                   66
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1132483 dbj BAA04607 (D17760)
NCBI Description
                   ADP-ribosylation factor [Oryza sativa]
```

BLAST score

E value Match length 371 8.0e-36



```
BLASTN
Method
                  g2351065
NCBI GI
                  35
BLAST score
                  3.0e-10
E value
                  147
Match length
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHF15, complete sequence [Arabidopsis thaliana]
                  220611
Seq. No.
                  LIB3149-057-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  q1173234
NCBI GI
BLAST score
                  327
                  2.0e-30
E value
Match length
                  72
                  89
% identity
                  40S RIBOSOMAL PROTEIN S25 >gi_481909 pir__S40089 ribosomal
NCBI Description
                  protein S25 - tomato >gi 435679 emb CAA54132 (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                  >gi 1584836 prf__2123431A ribosomal protein S25
                   [Lycopersicon esculentum]
                  220612
Seq. No.
                  LIB3149-057-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g409574
NCBI GI
                  38
BLAST score
                   4.0e-12
E value
                   50
Match length
                   94
% identity
                  Atriplex nummularia glyceraldehyde-3-phosphate
NCBI Description
                   dehydrogenase (GAPDH) mRNA, complete cds.
                   >gi_414606_emb_X75597_ANDAP3DH A.nummularia mRNA for
                   glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                   220613
                   LIB3149-057-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q119354
BLAST score
                   146
E value
                   2.0e-09
Match length
                   32
                   91
% identity
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 82082 pir_ JQ1185
                   phosphopyruvate hydratase (EC 4.2.1.11) - tomato
                   >gi 19281 emb CAA41115_ (X58108) enolase [Lycopersicon
                   esculentum]
Seq. No.
                   220614
                   LIB3149-057-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   g3925703
NCBI GI
```

Seq. ID

220620

LIB3149-057-Q1-K1-G10

```
% identity
                   (X95905) 14-3-3 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   220615
                  LIB3149-057-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2795807
BLAST score
                   187
E value
                   4.0e-14
                   81
Match length
% identity
                   49
                   (AC003674) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   220616
Seq. No.
                   LIB3149-057-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q2119360
NCBI GI
                   455
BLAST score
                   1.0e-45
E value
Match length
                   89
% identity
                   64
                   calmodulin (clone PCM2) - potato (fragment) >gi_687698
NCBI Description
                   (U20291) calmodulin [Solanum tuberosum] >gi 687702 (U20293)
                   calmodulin [Solanum tuberosum]
Seq. No.
                   220617
                   LIB3149-057-01-K1-F7
Seq. ID
Method
                   BLASTX
                   q2326231
NCBI GI
BLAST score
                   620
E value
                   7.0e-65
                   125
Match length
                   93
% identity
NCBI Description
                  (AF012889) tousled-like kinase 4 [Zea mays]
Seq. No.
                   220618
                   LIB3149-057-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158474
BLAST score
                   481
E value
                   1.0e-48
Match length
                   106
% identity
                   89
                  (AF067184) aquaporin 1 [Samanea saman]
NCBI Description
Seq. No.
                   220619
                   LIB3149-057-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g3158474
NCBI GI
BLAST score
                   198
                   1.0e-15
E value
                   72
Match length
                   62
% identity
                  (AF067184) aquaporin 1 [Samanea saman]
NCBI Description
```

NCBI GI

BLAST score



```
Method
                  BLASTX
                  q3122785
NCBI GI
BLAST score
                  458
                  7.0e-46
E value
                  102
Match length
                  88
% identity
                  40S RIBOSOMAL PROTEIN S14 >qi 2565340 (AF026079) ribosomal
NCBI Description
                  protein S14 [Lupinus luteus]
                  220621
Seq. No.
                  LIB3149-057-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1694976
BLAST score
                  458
                  4.0e-46
E value
Match length
                  103
% identity
                  85
                  (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                  thaliana]
                  220622
Seq. No.
Seq. ID
                  LIB3149-057-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                   g3915189
                   193
BLAST score
                   6.0e-15
E value
                  79
Match length
% identity
                   53
                  UBIQUITIN-CONJUGATING ENZYME X (UBIQUITIN-PROTEIN LIGASE)
NCBI Description
                   (UBIQUITIN CARRIER PROTEIN)
                   220623
Seq. No.
                   LIB3149-057-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g225267
NCBI GI
                   247
BLAST score
                   3.0e-21
E value
                   108
Match length
                   52
% identity
NCBI Description ORF 1244 [Nicotiana tabacum]
Seq. No.
                   220624
                   LIB3149-057-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g3201613
NCBI GI
                   457
BLAST score
                   9.0e-46
E value
                   121
Match length
                   70
% identity
NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]
                   220625
Seq. No.
                   LIB3149-057-Q1-K1-H1
Seq. ID
Method
                   BLASTX
```

31113

q3549691

% identity

69



2.0e-51 E value 102 Match length 81 % identity (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum] NCBI Description 220626 Seq. No. LIB3149-057-Q1-K1-H7 Seq. ID BLASTX Method g2160694 NCBI GI 282 BLAST score 3.0e-25 E value 94 Match length 55 % identity (U73528) B' regulatory subunit of PP2A [Arabidopsis NCBI Description thaliana] 220627 Seq. No. LIB3149-059-Q1-K1-A12 Seq. ID BLASTX Method q3334320 NCBI GI 634 BLAST score 2.0e-66 E value 123 Match length 98 % identity 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) NCBI Description ribosome-associated protein p40 [Glycine max] 220628 Seq. No. LIB3149-059-Q1-K1-A2 Seq. ID BLASTX Method q3914535 NCBI GI 389 BLAST score 1.0e-37 E value 93 Match length 86 % identity 60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb_CAA11283_ NCBI Description (AJ223363) ribosomal protein Lī3a [Lupīnus luteus] 220629 Seq. No. LIB3149-059-Q1-K1-A3 Seq. ID Method BLASTX NCBI GI q3747050 434 BLAST score 4.0e-43 E value Match length 100 85 % identity (AF093540) ribosomal protein L26 [Zea mays] NCBI Description Seq. No. 220630 LIB3149-059-Q1-K1-B11 Seq. ID BLASTX Method NCBI GI q2493046 BLAST score 374 E value 5.0e-36 Match length 109

31114

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR



220631

>gi_82297_pir__A41740 H+-transporting ATP synthase (EC
3.6.1.34) delta' chain precursor - sweet potato
>gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
delta subunit [Ipomoea batatas]

Seq. ID LIB3149-059-Q1-K1-B2
Method BLASTX
NCBI GI g3269289
BLAST score 368
E value 2.0e-35
Match length 113
% identity 67

Seq. No.

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 220632

Seq. ID LIB3149-059-Q1-K1-B4

Method BLASTX
NCBI GI g515377
BLAST score 209
E value 8.0e-17
Match length 45
% identity 93

NCBI Description (X79715) histone H4 [Lolium temulentum]

Seq. No. 220633

Seq. ID LIB3149-059-Q1-K1-B5

Method BLASTX
NCBI GI g4193382
BLAST score 209
E value 1.0e-16
Match length 39
% identity 100

NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana]

>qi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis

thaliana]

Seq. No. 220634

Seq. ID LIB3149-059-Q1-K1-B7

Method BLASTX
NCBI GI g2648032
BLAST score 391
E value 5.0e-38
Match length 119
% identity 65

NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 220635

Seq. ID LIB3149-059-Q1-K1-B9

Method BLASTX
NCBI GI g4056462
BLAST score 532
E value 1.0e-54
Match length 121
% identity 79

NCBI Description (AC005990) Strong similarity to gb_Y09876 aldehyde

dehydrogenase (NAD+) from Nicotiana tabacum and a member of



the aldehyde dehydrogenase family PF_00171. ESTs gb_F15117, gb_R83958 and gb_586262 come from this gene. [Arabidopsis thaliana]

220636 Seq. No. LIB3149-059-Q1-K1-C1 Seq. ID Method BLASTX q3212879 NCBI GI BLAST score 424 7.0e-42E value Match length 103 79 % identity (AC004005) putative ribosomal protein L7 [Arabidopsis NCBI Description thaliana] 220637 Seq. No. Seq. ID LIB3149-059-Q1-K1-C11 BLASTX Method NCBI GI g2132388 BLAST score 166 1.0e-11 E value 112 Match length 37 % identity PHO85 protein - yeast (Saccharomyces cerevisiae) NCBI Description >gi 1163103 (U43503) Lph16p [Saccharomyces cerevisiae] Seq. No. 220638 Seq. ID LIB3149-059-Q1-K1-C3 Method BLASTX NCBI GI q4455235 BLAST score 225 2.0e-18 E value 68 Match length % identity 65 (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA NCBI Description SUBUNIT-like [Arabidopsis thaliana] 220639 Seq. No. LIB3149-059-Q1-K1-D10 Seq. ID BLASTN Method g18506 NCBI GI BLAST score 161 1.0e-85 E value Match length 215 94 % identity NCBI Description Cotton mRNA for malate synthase (EC 4.1.3.2) 220640 Seq. No. LIB3149-059-Q1-K1-D12 Seq. ID Method BLASTX NCBI GI q913227 218 BLAST score 1.0e-17 E value 77 Match length 56 % identity

31116

NCBI Description transcription factor XlDP-1 [Xenopus laevis, embryos,

Peptide, 409 aa]

```
220641
Seq. No.
                  LIB3149-059-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g3892055
NCBI GI
BLAST score
                  212
                  5.0e-17
E value
                  90
Match length
                  52
% identity
                  (AC002330) putative transport protein [Arabidopsis
NCBI Description
                  thaliana]
                  220642
Seq. No.
                  LIB3149-059-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2492514
                  547
BLAST score
                  3.0e-56
E value
                  125
Match length
                  86
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
                  220643
Seq. No.
                  LIB3149-059-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4510428
NCBI GI
                   264
BLAST score
                   5.0e-23
E value
Match length
                  133
                   47
% identity
                  (AC006929) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   220644
Seq. ID
                  LIB3149-059-Q1-K1-E12
                   BLASTX
Method
NCBI GI
                   g2347054
BLAST score
                   218
E value
                   8.0e-18
Match length
                   82
                   52
% identity
NCBI Description (X96791) arginine decarboxylase [Vitis vinifera]
                   220645
Seq. No.
Seq. ID
                   LIB3149-059-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1350720
BLAST score
                   390
```

NCBI Description 60S RIBOSOMAL PROTEIN L32 Seq. No. 220646

E value

Match length

% identity

Seq. ID LIB3149-059-Q1-K1-E4

99

74

6.0e-38

Method

NCBI GI

BLAST score

BLASTX

g495731 513



```
BLASTX
Method
NCBI GI
                  g1346675
BLAST score
                  560
                  7.0e-58
E value
Match length
                  118
                  92
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
NCBI Description
                  >gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                  bidentis]
                  220647
Seq. No.
                  LIB3149-059-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  g3901014
NCBI GI
BLAST score
                  234
                  8.0e-20
E value
                  55
Match length
                  76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
                  220648
Seq. No.
                  LIB3149-059-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  g3461822
NCBI GI
                  285
BLAST score
E value
                   2.0e-25
Match length
                  72
                   68
% identity
                  (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   220649
Seq. No.
                  LIB3149-059-Q1-K1-F10
Seq. ID
                   BLASTN
Method
                   q2618602
NCBI GI
BLAST score
                   37
E value
                   2.0e-11
Match length
                   77
                   87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   220650
                   LIB3149-059-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3650030
BLAST score
                   240
E value
                   3.0e-20
                   79
Match length
% identity
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]
                   220651
Seq. No.
                   LIB3149-059-Q1-K1-F12
Seq. ID
```



```
2.0e-52
E value
Match length
                  104
% identity
                 (L16790) small ras-related protein [Arabidopsis thaliana]
NCBI Description
                  220652
Seq. No.
                  LIB3149-059-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4263720
BLAST score
                  195
                  4.0e-15
E value
                  86
Match length
                  47
% identity
                  (AC006223) putative cysteine proteinase inhibitor
NCBI Description
                   [Arabidopsis thaliana]
                  220653
Seq. No.
Seq. ID
                  LIB3149-059-Q1-K1-F6
Method
                  BLASTX
                  g3914394
NCBI GI
BLAST score
                   604
                   6.0e-63
E value
                  128
Match length
                   89
% identity
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >gi 2118335 pir__S60473 phosphoglycerate mutase (EC
                   5.4.2.1) - common ice plant >gi 602426 (U16021)
                   phosphoglyceromutase [Mesembryanthemum crystallinum]
                   220654
Seq. No.
                   LIB3149-059-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   q974782
NCBI GI
BLAST score
                   632
                   3.0e-66
E value
Match length
                   126
                   95
% identity
NCBI Description
                   (Z49150) cobalamine-independent methionine synthase
                   [Solenostemon scutellarioides]
                   220655
Seq. No.
                   LIB3149-059-Q1-K1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2500518
                   307
BLAST score
                   5.0e-49
E value
                   107
Match length
                   96
% identity
                   EUKARYOTIC INITIATION FACTOR 4A-11 (EIF-4A-11)
NCBI Description
                   >gi 485987 emb CAA55737 (X79136) NeIF-4A11 [Nicotiana
                   tabacum]
                   220656
Seq. No.
                   LIB3149-059-Q1-K1-G1
Seq. ID
```

BLASTX

g3024426

Method

NCBI GI



```
BLAST score
                  476
                  3.0e-52
E value
                  117
Match length
                  92
% identity
                  PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
NCBI Description
                  (PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi_1084302_pir__S55478
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice
                  plant >gi 854265_emb_CAA57872_ (X82489)
                  pyruvate, orthophosphate dikinase [Mesembryanthemum
                  crystallinum]
                  220657
Seq. No.
                  LIB3149-059-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2746719
BLAST score
                  242
                  1.0e-20
E value
Match length
                  59
                  88
% identity
                  (AF038386) histone H2B [Capsicum annuum]
NCBI Description
                  220658
Seq. No.
                  LIB3149-059-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  g3334200
NCBI GI
BLAST score
                   624
                   3.0e-65
E value
Match length
                   140
% identity
                   84
                  GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE
NCBI Description
                   DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
                   >gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor
                   [Solanum tuberosum]
                   220659
Seq. No.
                   LIB3149-059-Q1-K1-G2
Seq. ID
Method
                   BLASTX
                   g1362093
NCBI GI
                   271
BLAST score
E value
                   6.0e-24
                   94
Match length
                   62
% identity
                   hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi_924632 (U20595) unknown [Solanum lycopersicum]
                   220660
Seq. No.
                   LIB3149-059-Q1-K1-G6
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI 94103152
BLAST score 180
E value 3.0e-13
Match length 75
% identity 49

NCBI Description (AF020716) histidyl-tRNA synthetase [Triticum aestivum]

Seq. No. 220661

Seq. ID LIB3149-059-Q1-K1-G8



Method BLASTX q133867 NCBI GI BLAST score 544 5.0e-56 E value 110 Match length 92 % identity 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal NCBI Description protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays] 220662 Seq. No. LIB3149-059-Q1-K1-G9 Seq. ID Method BLASTX q2497752 NCBI GI BLAST score 276 2.0e-24 E value 94 Match length % identity 56 NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description >qi 1321911 emb CAA65475 (X96714) lipid transfer protein [Prunus dulcis] Seq. No. 220663 LIB3149-059-Q1-K1-H1 Seq. ID Method BLASTX NCBI GI g2435518 BLAST score 255 E value 2.0e-22 Match length 62 84 % identity (AF024504) contains similarity to C3HC4-type zinc fingers NCBI Description [Arabidopsis thaliana] 220664 Seq. No. LIB3149-059-Q1-K1-H11 Seq. ID BLASTX Method g2827992 NCBI GI BLAST score 268 1.0e-23 E value 102 Match length 53 % identity NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum] 220665 Seq. No. LIB3149-059-Q1-K1-H8 Seq. ID BLASTX Method NCBI GI q4263771 BLAST score 330 E value 9.0e-31119 Match length 55 % identity (AC006218) putative nonspecific lipid-transfer protein NCBI Description

precursor [Arabidopsis thaliana]

Seq. No. 220666

Seq. ID LIB3149-059-Q1-K1-H9

Method BLASTX

BLAST score

E value Match length 619 1.0e-64

122



```
g2982331
NCBI GI
                  477
BLAST score
                  3.0e-48
E value
Match length
                  103
                  92
% identity
NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]
                  220667
Seq. No.
                  LIB3149-060-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2623300
BLAST score
                  241
                  2.0e-20
E value
Match length
                  60
                  80
% identity
                  (AC002409) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  220668
Seq. No.
                  LIB3149-060-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g3915665
NCBI GI
BLAST score
                  378
                  2.0e-36
E value
                  137
Match length
                   51
% identity
                  ELONGATION FACTOR G (EF-G) >gi_2688449 (AE001155)
NCBI Description
                   translation elongation factor G (fus-1) [Borrelia
                  burgdorferi]
                   220669
Seq. No.
                  LIB3149-060-Q1-K1-A7
Seq. ID
Method
                   BLASTX
                   g2832682
NCBI GI
                   210
BLAST score
                   1.0e-16
E value
Match length
                   119
% identity
                   46
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]
                   220670
Seq. No.
                   LIB3149-060-Q1-K1-B11
Seq. ID
Method
                   BLASTX
                   q4103963
NCBI GI
                   141
BLAST score
                   1.0e-08
E value
Match length
                   31
% identity
NCBI Description (AF030035) calmodulin [Phaseolus vulgaris]
                   220671
Seq. No.
Seq. ID
                   LIB3149-060-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3687239
```

% identity

81



```
% identity
                  (AC005169) putative clathrin coat assembly protein
NCBI Description
                  [Arabidopsis thaliana]
                  220672
Seq. No.
                  LIB3149-060-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g2495365
NCBI GI
                  348
BLAST score
                  5.0e - 33
E value
                  86
Match length
                  79
% identity
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127 prf__1908431B
NCBI Description
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  220673
Seq. No.
                  LIB3149-060-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  q2961300
NCBI GI
                  546
BLAST score
                   4.0e-56
E value
                  125
Match length
                   85
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                   220674
Seq. No.
                   LIB3149-060-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g548852
                   361
BLAST score
                   2.0e-34
E value
                   82
Match length
                   80
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                   protein S21 - rice >gi_303839_dbj_BAA02158 (D12633) 40S
                   subunit ribosomal protein [Oryza sativa]
                   220675
Seq. No.
                   LIB3149-060-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g167367
NCBI GI
                   255
BLAST score
                   5.0e-22
E value
                   49
Match length
                   100
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   220676
Seq. No.
                   LIB3149-060-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   q2499931
NCBI GI
                   263
 BLAST score
 E value
                   6.0e-23
                   63
Match length
```

>gi 2129534_pir__S71272 adenine phosphoribosyltransferase

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)



(EC 2.4.2.7) - Arabidopsis thaliana >gi_1321681_emb_CAA65609_ (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]

220677 Seq. No. LIB3149-060-Q1-K1-C9 Seq. ID Method BLASTX g4006886 NCBI GI BLAST score 367 4.0e-35 E value Match length 119 % identity 61 (Z99708) putative protein [Arabidopsis thaliana] NCBI Description 220678 Seq. No. LIB3149-060-Q1-K1-D1 Seq. ID

Method BLASTX
NCBI GI g3063396
BLAST score 423
E value 7.0e-42
Match length 93
% identity 85

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 220679

Seq. ID LIB3149-060-Q1-K1-D11

Method BLASTX
NCBI GI g2979553
BLAST score 297
E value 6.0e-27
Match length 130
% identity 45

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 220680

Seq. ID LIB3149-060-Q1-K1-D2

Method BLASTX
NCBI GI g2495365
BLAST score 414
E value 1.0e-40
Match length 118
% identity 75

NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B

heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No. 220681

Seq. ID LIB3149-060-Q1-K1-D3

Method BLASTX
NCBI GI g1710587
BLAST score 317
E value 1.0e-33
Match length 122
% identity 66

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic

ribosomal protein PO [Glycine max]

Seq. No. 220682



```
Seq. ID
                  LIB3149-060-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1173198
BLAST score
                  434
                  4.0e-43
E value
                  91
Match length
                  92
% identity
                  40S RIBOSOMAL PROTEIN S13 >gi 480095_pir__S36423 ribosomal
NCBI Description
                  protein S13.e - garden pea >gi 396639_emb_CAA80974_
                  (Z25509) ribosomal protein S13 [Pisum sativum]
                  220683
Seq. No.
                  LIB3149-060-Q1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1710587
BLAST score
                  237
                  5.0e-20
E value
Match length
                  83
                  59
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic
NCBI Description
                  ribosomal protein PO [Glycine max]
Seq. No.
                  220684
                  LIB3149-060-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  g70753
NCBI GI
BLAST score
                  482
E value
                  1.0e-48
Match length
                  117
                  84
% identity
                  histone H3 - garden pea >gi 82610 pir S00373 histone H3 -
NCBI Description
                  wheat
                  220685
Seq. No.
                  LIB3149-060-Q1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3377941
BLAST score
                   150
E value
                   1.0e-09
                   88
Match length
                   42
% identity
                  (AL021960) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   220686
Seq. No.
                   LIB3149-060-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g461729
BLAST score
                   394
                   3.0e - 38
E value
                   94
Match length
                   74
% identity
                  10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)
NCBI Description
                   >gi 2146744 pir__S65597 probable chaperonin, 10K -
```

[Arabidopsis thaliana]

Arabidopsis thaliana >gi_166662 (L02843) 10 kDa chaperonin



```
220687
Seq. No.
                  LIB3149-060-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g82200
NCBI GI
                  375
BLAST score
                  4.0e-36
E value
Match length
                  137
% identity
                  55
                  hypothetical protein 1244 - common tobacco chloroplast
NCBI Description
                  220688
Seq. No.
                  LIB3149-060-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  g2459412
NCBI GI
BLAST score
                  235
                  9.0e-20
E value
                  91
Match length
% identity
                  49
                  (ACO02332) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                  220689
Seq. No.
                  LIB3149-060-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2605932
BLAST score
                  519
                  6.0e-53
E value
                  133
Match length
% identity
                  76
                  (AF029898) aspartate aminotransferase [Lotus corniculatus]
NCBI Description
                  220690
Seq. No.
                  LIB3149-060-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  g3047084
NCBI GI
                   564
BLAST score
                   3.0e-58
E value
                  128
                              d.
Match length
% identity
                   82
                  (AF058914) similar to aminoacyl-tRNA synthetases
NCBI Description
                   [Arabidopsis thaliana]
                   220691
Seq. No.
                  LIB3149-060-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2833390
NCBI GI
                   624
BLAST score
                   3.0e-65
E value
Match length
                   129
                   88
% identity
                  GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSII)
NCBI Description
                   (GRANULE-BOUND STARCH SYNTHASE II) >gi 887649 emb CAA61241
                   (X87988) glycogen (starch) synthase [Solanum tuberosum]
                   220692
Seq. No.
                   LIB3149-060-Q1-K1-F2
Seq. ID
```

BLASTX

g1336084

Method NCBI GI

NCBI Description



```
BLAST score
E value
                   5.0e-52
                   116
Match length
% identity
                   79
NCBI Description
                  (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
                   (GDH2) mRNA, complete cds. [Arabidopsis thaliana]
Seq. No.
                   220693
Seq. ID
                   LIB3149-060-Q1-K1-F5
Method
                   BLASTX
                   g2982432
NCBI GI
BLAST score
                   335
                   2.0e-31
E value
Match length
                   76
% identity
                   80
NCBI Description (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                   220694
                   LIB3149-060-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g549732
                   189
BLAST score
                   3.0e-14
E value
                   78
Match length
% identity
                   47
NCBI Description HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION
                   >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast
(Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_
                   (Z26877) unknown [Saccharomyces cerevisiae]
                   >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w
                   [Saccharomyces cerevisiae] >gi 1582545 prf 2118404F ORF
                   [Saccharomyces cerevisiae]
Seq. No.
                   220695
Seq. ID
                   LIB3149-060-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g1351271
BLAST score
                   178
E value
                   5.0e-13
Match length
                   43
% identity
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                   >gi 1084309 pir S52032 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - spinach >gi 806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                   220696
                   LIB3149-060-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1694976
BLAST score
                   221
                   3.0e-24
E value
Match length
                   92
                   62
% identity
```

>gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis

(Y09482) HMG1 [Arabidopsis thaliana]

% identity

93



thaliana]

```
220697
Seq. No.
                  LIB3149-060-Q1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q322639
                  229
BLAST score
                  5.0e-19
E value
                  68
Match length
                  56
% identity
                  beta-1,3-glucanase homolog (clone A20) - rape (fragment)
NCBI Description
                  >gi 17734_emb_CAA49515_ (X69889) beta-1,3-glucanase
                  homologue [Brassica napus]
Seq. No.
                  220698
                  LIB3149-060-Q1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3116020
                  165
BLAST score
                  1.0e-11
E value
                  46
Match length
                  76
% identity
                  (Y15383) FtsZ protein [Pisum sativum]
NCBI Description
                  220699
Seq. No.
                  LIB3149-060-Q1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3287696
BLAST score
                  512
                  4.0e-52
E value
                  131
Match length
                  71
% identity
                  (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb_D86180 from Pisum sativum. This ORF may be
                  part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
Seq. No.
                   220700
                  LIB3149-060-Q1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076524
                   269
BLAST score
                   9.0e-24
E value
                   78
Match length
                   59
% identity
                  chloroplast outer envelope protein OEP86 precursor - garden
NCBI Description
                   pea >gi_599958_emb_CAA83453_ (Z31581) chloroplast outer
                   envelope protein 86 [Pisum sativum]
                   220701
Seq. No.
                   LIB3149-061-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q312179
BLAST score
                   306
                   4.0e-28
E value
Match length
                   61
```



(X73151) glyceraldehyde 3-phosphate dehydrogenase NCBI Description (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi 1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] 220702 Seq. No. LIB3149-061-Q1-K1-A3 Seq. ID Method BLASTX NCBI GI q120669 BLAST score 453 3.0e-45E value 87 Match length 97 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >qi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora] Seq. No. 220703 LIB3149-061-Q1-K1-A5 Seq. ID Method BLASTX g3367647 NCBI GI BLAST score 536 6.0e-55 E value Match length 131 78 % identity (Y17298) enolase [Cunninghamella elegans] NCBI Description 220704 Seq. No. LIB3149-061-Q1-K1-B3 Seq. ID Method BLASTX g2462834 NCBI GI 234 BLAST score E value 1.0e-19 Match length 87 53 % identity (AF000657) hypothetical protein [Arabidopsis thaliana] NCBI Description 220705 Seq. No. Seq. ID LIB3149-061-Q1-K1-B5 Method BLASTX NCBI GI g2499476 BLAST score 178 5.0e-13 E value Match length 102 % identity 43

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR

>gi_1498198_emb_CAA63909_ (X94218) 2-Cys peroxiredoxin bas1
[Arabidopsis thaliana] >gi_1783308_emb_CAA71503_ (Y10478)

2-Cys peroxiredoxin [Arabidopsis thaliana]

220706 Seq. No.

LIB3149-061-Q1-K1-B7 Seq. ID

BLASTX Method NCBI GI g3493172



```
BLAST score 685
E value 2.0e-72
Match length 133
% identity 50
NCBI Description (U89609
```

NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Seq. No. 220707

Seq. ID LIB3149-061-Q1-K1-B9

Method BLASTX
NCBI GI g4204294
BLAST score 330
E value 8.0e-31
Match length 105
% identity 67

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 220708

Seq. ID LIB3149-061-Q1-K1-C3

Method BLASTX
NCBI GI g3850821
BLAST score 258
E value 1.0e-22
Match length 103
% identity 50

NCBI Description (Y18350) U2 snRNP auxiliary factor, large subunit

[Nicotiana plumbaginifolia]

Seq. No. 220709

Seq. ID LIB3149-061-Q1-K1-C7

Method BLASTX
NCBI GI g1754997
BLAST score 146
E value 3.0e-09
Match length 31
% identity 94

NCBI Description (U48690) calmodulin TaCaM2-1 [Triticum aestivum]

Seq. No. 220710

Seq. ID LIB3149-061-Q1-K1-E11

Method BLASTX
NCBI GI g1172556
BLAST score 275
E value 2.0e-24
Match length 60
% identity 87

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 220711

Seq. ID LIB3149-061-Q1-K1-F11

Method BLASTX NCBI GI g4454032



```
BLAST score
                  282
                  2.0e-25
E value
                  81
Match length
% identity
                   69
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
                  220712
Seq. No.
                  LIB3149-061-Q1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1477428
BLAST score
                   631
                   4.0e-66
E value
Match length
                   135
                   88
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
Seq. No.
                   220713
                   LIB3149-062-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   g3122053
NCBI GI
                   117
BLAST score
                   3.0e-10
E value
                   71
Match length
                   58
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_1235582_emb_CAA65391_ (X96555) elongation factor
                   1-alpha [Pisum sativum]
Seq. No.
                   220714
                   LIB3149-062-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   q1350983
NCBI GI
BLAST score
                   381
                   3.0e-54
E value
Match length
                   132
                   81
% identity
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
Seq. No.
                   220715
                   LIB3149-062-Q1-K1-A12
Seq. ID
Method
                   BLASTX
                   g2088652
NCBI GI
                   442
BLAST score
                   2.0e-44
E value
                   115
Match length
                   77
% identity
                   (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2351376 (U54561) translation
                   initiation factor eIF2 p47 subunit homolog [Arabidopsis
                   thaliana]
                   220716
Seq. No.
                   LIB3149-062-Q1-K1-A6
```

Seq. ID

BLASTX Method g4539335 NCBI GI 373 BLAST score 2.0e-47 E value



```
Match length
                  136
                  62
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                  220717
Seq. No.
                  LIB3149-062-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  g421843
NCBI GI
                  317
BLAST score
                  7.0e-36
E value
Match length
                  125
                  60
% identity
                  protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
NCBI Description
                  >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein
                  kinase [Arabidopsis thaliana]
                  220718
Seq. No.
                  LIB3149-062-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g2662343
NCBI GI
                  508
BLAST score
                  7.0e-67
E value
                  133
Match length
                  98
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  220719
Seq. No.
                  LIB3149-062-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  q3785989
NCBI GI
                  229
BLAST score
                  7.0e - 37
E value
                  132
Match length
                   67
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                  220720
Seq. No.
                  LIB3149-062-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3334405
                   437
BLAST score
                   2.0e-50
E value
                   118
Match length
% identity
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
                   >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                   220721
Seq. No.
                   LIB3149-062-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454464
```

Method BLASTX
NCBI GI 94454464
BLAST score 273
E value 3.0e-24
Match length 64

% identity 73

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]



```
220722
Seq. No.
                  LIB3149-062-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                   g3738285
NCBI GI
                   192
BLAST score
                   3.0e-15
E value
                   99
Match length
                   43
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   220723
Seq. No.
                   LIB3149-062-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   g2369714
NCBI GI
                   497
BLAST score
                   2.0e-50
E value
                   136
Match length
                   72
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   220724
Seq. No.
                   LIB3149-062-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g100226
NCBI GI
                   129
BLAST score
                   9.0e-12
E value
                   84
Match length
                   48
% identity
                   hypothetical protein - tomato >gi_19275 emb CAA78112_
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   220725
 Seq. No.
                   LIB3149-062-Q1-K1-D9
Seq. ID
Method
                   BLASTX
:NCBI GI
                  . q585876
                   123
BLAST score
                   2.0e-14
E value
                   67
Match length
                   67
 % identity
                   60S RIBOSOMAL PROTEIN L23A (L25) >gi 1084424 pir S48026
 NCBI Description
                   ribosomal protein L25 - common tobacco >gi_310935 (L18908)
                   60S ribosomal protein L25 [Nicotiana tabacum]
                   220726
 Seq. No.
                   LIB3149-062-Q1-K1-E11
 Seq. ID
 Method
                   BLASTX
                   q886116
 NCBI GI
                    197
 BLAST score
                    5.0e-25
 E value
 Match length
                    69
                    77
 % identity
                    (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473
 NCBI Description
                    (AF051338) xyloglucan endotransglycosylase related protein
```

[Arabidopsis thaliana]

```
220727
Seq. No.
                  LIB3149-062-Q1-K1-E6
Seq. ID
Method
                  BLASTX
                  g3075398
NCBI GI
                  163
BLAST score
                  1.0e-22
E value
                  137
Match length
                  41
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  220728
                  LIB3149-062-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113029
BLAST score
                  502
                  2.0e-71
E value
Match length
                  137
                  99
% identity
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi_68209_pir__WZCNIU isocitrate lyase (EC 4.1.3.1) -
                  upland cotton >gi_18486_emb_CAA36381_ (X52136) isocitrate
                  lyase (AA 1-576) [Gossypium hirsutum]
                   220729
Seq. No.
                  LIB3149-062-Q1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2661840
                   295
BLAST score
                   1.0e-26
E value
                   118
Match length
                   55
% identity
                  (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
                   220730
Seq. No.
                   LIB3149-062-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g3892058
NCBI GI
                   194
BLAST score
                   8.0e-15
E value
                   98
Match length
                   43
% identity
                  (AC002330) putative glutamate-/aspartate-binding peptide
NCBI Description
                   [Arabidopsis thaliana]
                   220731
Seq. No.
                   LIB3149-062-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g1498053
NCBI GI
BLAST score
                   323
                   3.0e-46
E value
                   133
Match length
```

% identity

NCBI Description

Seq. ID LIB3149-062-Q1-K1-G5

75

(U64436) ribosomal protein S8 [Zea mays]



```
Method
                  BLASTX
                  g2827992
NCBI GI
BLAST score
                  330
                  2.0e-44
E value
                  137
Match length
% identity
                   60
                   (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
                  220733
Seq. No.
                  LIB3149-062-Q1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2213862
                   207
BLAST score
                   6.0e-20
E value
Match length
                  126
% identity
                   45
                  (AF003086) PfSNF2L [Plasmodium falciparum]
NCBI Description
                   220734
Seq. No.
                   LIB3149-062-Q1-K1-G8
Seq. ID
                   BLASTX
Method
                   g2664214
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
                   91
Match length
                   53
% identity
                  (AJ222646) G2484-1 [Arabidopsis thaliana]
NCBI Description
                   220735
Seq. No.
                   LIB3149-062-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g4204303
NCBI GI
                   292
BLAST score
                   3.0e-45
E value
                   128
Match length
                   68
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   220736
Seq. No.
                   LIB3149-062-Q1-K1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2980767
                   305
BLAST score
                   7.0e-28
E value
                   111
Match length
                   63
% identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   220737
Seq. No.
                   LIB3149-062-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1174448
                   260
BLAST score
                   6.0e-24
E value
```

31135

98

62

Match length

% identity

% identity

82



```
TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                  (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                  (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative
                  [Arabidopsis thaliana]
                  220738
Seq. No.
                  LIB3149-062-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g294060
BLAST score
                  169
E value
                  7.0e-12
Match length
                  96
                  40
% identity
NCBI Description (L06467) major latex protein [Papaver somniferum]
                  220739
Seq. No.
                  LIB3149-062-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g886116
BLAST score
                  340
E value
                  2.0e-50
Match length
                  138
% identity
                  68
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
NCBI Description
                   (AF051338) xyloglucan endotransglycosylase related protein
                   [Arabidopsis thaliana]
                  220740
Seq. No.
                  LIB3149-063-Q1-K1-A1
Seq. ID
Method
                  BLASTX
                  q3183640
NCBI GI
                  329
BLAST score
                   4.0e-31
E value
Match length
                  66
% identity
NCBI Description (AJ005869) transmembrane channel protein [Cicer arietinum]
                   220741
Seq. No.
Seq. ID
                  LIB3149-063-Q1-K1-A12
                  BLASTX
Method
                   g3402703
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
Match length
                   92
% identity
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
                   220742
Seq. No.
Seq. ID
                   LIB3149-063-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g3183640
                   295
BLAST score
                   1.0e-26
E value
Match length
                   68
```

NCBI Description (AJ005869) transmembrane channel protein [Cicer arietinum]



```
220743
Seq. No.
                  LIB3149-063-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                   g466160
NCBI GI
                   364
BLAST score
                   9.0e-35
E value
                   84
Match length
                   83
% identity
                   HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi_289769 (L14429) putative [Caenorhabditis
                   elegans]
                   220744
Seq. No.
                   LIB3149-063-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g466160
NCBI GI
                   287
BLAST score
                   1.0e-25
E value
                   82
Match length
                   71
% identity
                   HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi_289769 (L14429) putative [Caenorhabditis
                   elegans]
Seq. No.
                   220745
                   LIB3149-063-Q1-K1-A7
Seq. ID
                   BLASTN
Method
                   g2558943
NCBI GI
                   38
BLAST score
                   6.0e-12
E value
                   65
Match length
                   92
% identity
NCBI Description Gossypium hirsutum histone 3 mRNA, complete cds
                   220746
Seq. No.
                   LIB3149-063-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   q1174592
NCBI GI
                   729
BLAST score
                   1.0e-77
E value
                   137
Match length
                   100
% identity
                   TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                    - garden pea >gi_525332 (\overline{U}12589) \overline{a}lpha-tubulin [Pisum
                   sativum]
                    220747
 Seq. No.
                   LIB3149-063-Q1-K1-B1
 Seq. ID
                   BLASTX
Method
NCBI GI
                    q4193382
 BLAST score
                    386
                    2.0e-37
E value
Match length
                    86
 % identity
```

NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana]



>gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis
thaliana]

 Seq. No.
 220748

 Seq. ID
 LIB3149-063-Q1-K1-B11

 Method
 BLASTX

 NCBI GI
 g3024017

 BLAST score
 552

 E value
 6.0e-57

E value 6.00 Match length 112 % identity 94

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation

initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 220749

Seq. ID LIB3149-063-Q1-K1-B12

Method BLASTX
NCBI GI 94371293
BLAST score 253
E value 9.0e-22
Match length 96
% identity 64

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 220750

Seq. ID LIB3149-063-Q1-K1-B2

Method BLASTX
NCBI GI g2065531
BLAST score 429
E value 2.0e-42
Match length 118

% identity 64

NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 220751

Seq. ID LIB3149-063-Q1-K1-B4

Method BLASTX
NCBI GI g2244750
BLAST score 599
E value 2.0e-62
Match length 137
% identity 82

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 220752

Seq. ID LIB3149-063-Q1-K1-B5

Method BLASTX
NCBI GI g2244750
BLAST score 444
E value 3.0e-44
Match length 108
% identity 80

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase



[Arabidopsis thaliana]

```
220753
Seq. No.
                  LIB3149-063-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  q4204265
NCBI GI
                  156
BLAST score
                  2.0e-10
E value
                  49
Match length
                   65
% identity
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
                  220754
Seq. No.
                  LIB3149-063-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                   g1762945
NCBI GI
                   323
BLAST score
                   5.0e-30
E value
                   120
Match length
                   53
% identity
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
                   220755
Seq. No.
                   LIB3149-063-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4218120
                   357
BLAST score
                   5.0e - 34
E value
                   106
Match length
                   66
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   220756
Seq. No.
                   LIB3149-063-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   g2244970
NCBI GI
                   430
BLAST score
                   1.0e-42
E value
                   117
Match length
                   65
 % identity
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall
                   protein [Arabidopsis thaliana]
 Seq. No.
                   220757
                   LIB3149-063-Q1-K1-D1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2828296
                   323
 BLAST score
                   4.0e-30
 E value
 Match length
                   67
                   88
 % identity
                   (AL021687) RNase L inhibitor [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   220758
```



```
LIB3149-063-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  g3377797
NCBI GI
BLAST score
                  497
                  2.0e-50
E value
                  125
Match length
                  76
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  220759
Seq. No.
                  LIB3149-063-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g1419088
NCBI GI
BLAST score
                   666
                  3.0e-70
E value
                  127
Match length
                   94
% identity
                  (Z71395) calreticulin [Nicotiana plumbaginifolia]
NCBI Description
                   220760
Seq. No.
                   LIB3149-063-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   q4432857
NCBI GI
BLAST score
                   181
                   3.0e-18
E value
                   115
Match length
                   46
% identity
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   220761
Seq. No.
                   LIB3149-063-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g1710546
NCBI GI
BLAST score
                   116
                   2.0e-14
E value
                   100
Match length
                   48
% identity
                   60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
NCBI Description
                   ribosomal protein [Daucus carota]
                   220762
Seq. No.
                   LIB3149-063-Q1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q531829
                   166
BLAST score
                   4.0e-12
E value
                   46
Match length
                   72
 % identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
```

Seq. ID LIB3149-063-Q1-K1-E11



```
BLASTX
Method
                    g3021485
NCBI GI
BLAST score
                    261
                    8.0e-23
E value
                    63
Match length
                    83
% identity
                   (AJ224932) histone H2B-3 [Lycopersicon esculentum]
NCBI Description
                    220764
Seq. No.
                    LIB3149-063-Q1-K1-E2
Seq. ID
                    BLASTX
Method
                    g3142291
NCBI GI
                    445
BLAST score
                    2.0e-44
E value
Match length
                    112
                    70
% identity
                    (AC002411) Contains similarity to adenylate cyclase
NCBI Description
                    gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes
                    from this gene. [Arabidopsis thaliana]
                    220765
Seq. No.
                    LIB3149-063-Q1-K1-E4
Seq. ID
                    BLASTX
Method
                    g1174592
NCBI GI
                    341
BLAST score
                    3.0e - 32
E value
                    116
Match length
% identity
                    60
                    TUBULIN ALPHA-1 CHAIN >gi_2119270 pir _S60233 alpha-tubulin
NCBI Description
                    - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                    sativum]
                    220766
Seq. No.
                    LIB3149-063-Q1-K1-E6
Seq. ID
                    BLASTX
Method
                    g266972
NCBI GI
BLAST score
                    204
                    5.0e-16
E value
                    54
Match length
                     65
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S29 >gi_631884 pir_S30298 ribosomal
                    protein S29 - rat >gi_1362934_pir__ S55919 ribosomal protein
S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal
                    protein S29 [Rattus norvegicus] >gi_550027 (U14973)
                     ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610)
                     homologous to antisense sequence of krev-1, anti oncogene
                     [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29
                     [Bos taurus] >gi_1\overline{0}96945_prf__2113200H ribosomal protein
                     S29 [Homo sapiens] >gi 4506717_ref_NP_001023.1_pRPS29_
                     ribosomal protein S29
                     220767
```

LIB3149-063-Q1-K1-E7 Seq. ID

BLASTX Method g120669 NCBI GI BLAST score 454



```
2.0e-45
E value
Match length
                  105
                  81
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   220768
Seq. No.
                  LIB3149-063-Q1-K1-E8
Seq. ID
                   BLASTX
Method
                   g2459429
NCBI GI
                   470
BLAST score
                   3.0e-47
E value
Match length
                   112
                   73
% identity
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   220769
Seq. No.
                   LIB3149-063-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g1174448
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
                   113
Match length
                   56
% identity
                   TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative
                   [Arabidopsis thaliana]
                   220770
Seq. No.
                   LIB3149-063-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g1399380
NCBI GI
                   662
BLAST score
                   9.0e-70
E value
                   131
Match length
                   92
% identity
                   (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                   methyltransferase [Glycine max]
                   220771
Seq. No.
                   LIB3149-063-Q1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3560474
BLAST score
                   259
                   1.0e-22
E value
                   96
Match length
                   52
 % identity
                   (U81312) S-adenosyl-methionine-sterol-C- methyltransferase
NCBI Description
                   [Nicotiana tabacum]
```

Seq. ID LIB3149-063-Q1-K1-F2

Method BLASTX

E value

Match length



```
NCBI GI
                  q1431629
                   459
BLAST score
                   5.0e-46
E value
                  122
Match length
                   68
% identity
                   (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  220773
Seq. No.
                  LIB3149-063-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q1172977
NCBI GI
                   531
BLAST score
                   2.0e-54
E value
                   122
Match length
                   84
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
                   220774
Seq. No.
                   LIB3149-063-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g3004560
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
                   47
Match length
                   66
% identity
                   (AC003673) putative ATP binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   220775
Seq. No.
                   LIB3149-063-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g4027891
NCBI GI
                   339
BLAST score
                   7.0e-32
E value
                   117
Match length
                   62
% identity
                   (AF049350) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                   220776
Seq. No.
                   LIB3149-063-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g4204293
NCBI GI
                   493
BLAST score
                   6.0e-50
E value
                   115
Match length
                   81
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                   220777
 Seq. No.
                   LIB3149-063-Q1-K1-G3
 Seq. ID
                   BLASTX
Method
                   g1928981
 NCBI GI
                   392
 BLAST score
                    4.0e-38
```

Match length

% identity



```
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
Seq. No.
                  220778
                  LIB3149-063-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g1173234
NCBI GI
BLAST score
                  327
                  2.0e-30
E value
                  72
Match length
                  89
% identity
                  40S RIBOSOMAL PROTEIN S25 >gi 481909_pir__S40089 ribosomal
NCBI Description
                  protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714)
                  ribosomal protein S25 [Lycopersicon esculentum]
                  >gi_1584836_prf__2123431A ribosomal protein S25
                   [Lycopersicon esculentum]
                  220779
Seq. No.
                  LIB3149-063-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g1052973
NCBI GI
                  342
BLAST score
                  3.0e-32
E value
Match length
                  87
                  76
% identity
NCBI Description (U37838) fructokinase [Beta vulgaris]
                  220780
Seq. No.
                  LIB3149-063-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                   q3885339
NCBI GI
                   239
BLAST score
                   5.0e-23
E value
                   110
Match length
                   54
% identity
NCBI Description (AC005623) putative bzip protein [Arabidopsis thaliana]
                   220781
Seq. No.
                   LIB3149-063-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4056420
BLAST score
                   307
E value
                   4.0e-28
Match length
                   81
                   73
% identity
NCBI Description (AC005322) ESTs gb_T144077 and gb_T43352 come from this
                   gene. [Arabidopsis thaliana]
                   220782
Seq. No.
                   LIB3149-063-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   g20559
NCBI GI
BLAST score
                   64.7
                   6.0e-68
E value
                   140
```

```
(X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]
NCBI Description
                  220783
Seq. No.
                  LIB3149-063-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4415934
BLAST score
                  261
                  1.0e-22
E value
                  87
Match length
                   55
% identity
                   (AC006418) putative auxin response factor 1 [Arabidopsis
NCBI Description
                  thaliana]
                   220784
Seq. No.
                  LIB3149-063-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3645985
BLAST score
                   438
E value
                   2.0e-43
Match length
                   77
% identity
                   96
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method score=23.36;
                   1-evidence_end; 2-evidence=predicted by match;
                   2-match_accession=AA141041;
                   2-match_description=CK01110.3prime CK Drosophila
                   melanogaster
Seq. No.
                   220785-
                   LIB3149-063-Q1-K1-H9
                   BLASTX
                   q1477428
                   565
                   2.0e-58
```

Seq. ID Method NCBI GI BLAST score

E value 126 Match length % identity 89

(X99623) alpha-tubulin 1 [Hordeum vulgare] NCBI Description

220786 Seq. No.

LIB3149-064-Q1-K1-A11 Seq. ID

Method BLASTX NCBI GI g3647355 BLAST score 329 1.0e-30 E value Match length 134 % identity

NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w),

> Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No. 220787

Seq. ID LIB3149-064-Q1-K1-A12

Method BLASTX NCBI GI g4115377 BLAST score 611 E value 1.0e-63



```
Match length
                  143
% identity
                  80
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220788
Seq. No.
                  LIB3149-064-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  g3426051
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
                  105
Match length
                  55
% identity
                  (AC005168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  220789
Seq. No.
                  LIB3149-064-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4539417
                   498
BLAST score
                   2.0e-50
E value
                   111
Match length
                   79
% identity
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                   220790
Seq. No.
                   LIB3149-064-Q1-K1-B11
Seq. ID
                   BLASTN
Method
                   g2826742
NCBI GI
                   170
BLAST score
                   5.0e-91
E value
                   194
Match length
                   96
% identity
                   Gossypium arboreum ribosomal protein L16 (rpl16) gene,
NCBI Description
                   chloroplast gene encoding chloroplast protein, partial cds,
                   and intron sequence
                   220791
Seq. No.
                   LIB3149-064-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   q544134
NCBI GI
                   160
BLAST score
                   5.0e-11
E value
Match length
                   64
                   50
% identity
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
NCBI Description
                   >gi_99720_pir__S22863 hypothetical protein - Arabidopsis
                   thaliana >gi_421844_pir__A46260 RecA functional analog
                   DRT100 - Arabidopsis thaliana (fragment)
                   220792
 Seq. No.
                   LIB3149-064-Q1-K1-B2
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   g2341034
                   560
 BLAST score
                   9.0e-58
 E value
```

114

97

Match length

% identity



```
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
                  220793
Seq. No.
                  LIB3149-064-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g2688820
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
                  85
Match length
                  42
% identity
                  (U93271) enoyl-CoA hydratase [Prunus armeniaca]
NCBI Description
                  220794
Seq. No.
                  LIB3149-064-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g3600052
NCBI GI
                  116
BLAST score
                  6.0e-14
E value
                  100
Match length
                   43
% identity
                  (AF080120) contains similarity to glycosyl hydrolases
NCBI Description
                   family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03)
                   [Arabidopsis thaliana]
                   220795
Seq. No.
                   LIB3149-064-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g974782
                   589
BLAST score
                   3.0e-61
E value
                   129
Match length
                   90
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   220796
Seq. No.
                   LIB3149-064-Q1-K1-B9
Seq. ID
Method
                   BLASTX
                   q218157
NCBI GI
                   459
BLAST score
E value
                   5.0e-46
                   116
Match length
                   80
% identity
                  (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
                   220797
Seq. No.
                   LIB3149-064-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1856971
                   554
BLAST score
                   5.0e-57
E value
                   117
Match length
% identity
                   89
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
```

periwinkle cells. [Catharanthus roseus]

during the cell cycle in the synchronous culture of



64

NCBI Description (Y11124) invertase [Cichorium intybus]

% identity

```
220798
Seq. No.
                  LIB3149-064-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  q2501433
NCBI GI
                  359
BLAST score
                  3.0e - 34
E value
                  87
Match length
                  72
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-EPF5) >gi_181916
                   (M91670) ubiquitin carrier protein [Homo sapiens]
                   220799
Seq. No.
                  LIB3149-064-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g1856971
NCBI GI
                   304
BLAST score
                   1.0e-27
E value
                   136
Match length
                   56
% identity
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
                   220800
Seq. No.
                   LIB3149-064-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g1706319
NCBI GI
                   282
BLAST score
                   4.0e-25
E value
                   103
Match length
                   53
% identity
                   HISTIDINE DECARBOXYLASE (HDC) (TOM92)
NCBI Description
                   >gi_481829_pir__S39554 histidine decarboxylase (EC
                   4.1.1.22) - tomato >gi_416534_emb CAA50719 (X71900)
                   histidine decarboxylase [Lycopersicon esculentum]
                   220801
Seq. No.
                   LIB3149-064-Q1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3395440
BLAST score
                   231
                   3.0e-19
E value
                   105
Match length
                   46
 % identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   220802
                   LIB3149-064-Q1-K1-C7
 Seq. ID
                   BLASTX
 Method
                   g4127660
 NCBI GI
                   462
 BLAST score
 E value
                   3.0e-46
                   138
 Match length
```



```
220803
Seq. No.
                  LIB3149-064-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                  g232031
NCBI GI
                  278
BLAST score
                  1.0e-24
E value
                  95
Match length
                   58
% identity
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir__$29224
NCBI Description
                  translation elongation factor eEF-1 beta chain - rice
                  >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                  220804
Seq. No.
                  LIB3149-064-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                   g3152660
NCBI GI
BLAST score
                   204
                   5.0e-16
E value
                   119
Match length
% identity
                   33
                  (AF064603) GA17 protein [Homo sapiens]
NCBI Description
                   220805
Seq. No.
                  LIB3149-064-Q1-K1-D11
Seq. ID
                   BLASTN
Method
                   g2501849
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   56
Match length
                   91
% identity
                   Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA,
NCBI Description
                   complete cds
                   220806
Seq. No.
                   LIB3149-064-Q1-K1-D12
Seq. ID
Method
                   BLASTN
                   g531251
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
                   34
Match length
                   100
% identity
                   Apple mitochondrial atp9 gene for F0-ATPase subunit 9
NCBI Description
                   (complete cds) and nad5 gene for NADH dehydrogehase subunit
                   5 (exon a and b)
                   220807
Seq. No.
                   LIB3149-064-Q1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236238
                   263
BLAST score
                   7.0e-23
E value
                   143
Match length
                   46
% identity
                   (ACO04684) putative ARF1 GTPase activating protein
NCBI Description
```

(AB017876) Aspl [Arabidopsis thaliana]

[Arabidopsis thaliana] >gi 4519792 dbj_BAA75744.1_

BLAST score

Match length

E value

357 8.0e-42

117



```
220808
Seq. No.
                   LIB3149-064-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g1173256
NCBI GI
                   664
BLAST score
                   6.0e-70
E value
                   128
Match length
                   99
% identity
                   40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   220809
Seq. No.
                   LIB3149-064-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g1856971
NCBI GI
                   443
BLAST score
                   5.0e-44
E value
                   95
Match length
                   88
% identity
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
                   220810
Seq. No.
                   LIB3149-064-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g3377820
NCBI GI
                    393
BLAST score
                    4.0e-38
E value
                    98
Match length
                    77
% identity
                   (AF076275) contains similarity to coatomer zeta chains
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    220811
                    LIB3149-064-Q1-K1-F11
Seq. ID
                    BLASTX
Method
NCBI GI
                    q629483
                    357
BLAST score
                    6.0e-34
E value
                    125
Match length
                    58
% identity
                    gene 1-Sc3 protein - European white birch
NCBI Description
                    >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula] >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                    pendula]
Seq. No.
                    220812
                    LIB3149-064-Q1-K1-F2
Seq. ID
Method
                    BLASTX
                    g2088654
NCBI GI
```



```
% identity
                  (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                  [Arabidopsis thaliana]
                  220813
Seq. No.
                  LIB3149-064-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g1673344
NCBI GI
                  166
BLAST score
                  2.0e-11
E value
                  53
Match length
                  55
% identity
                 (D64002) hypothetical protein [Synechocystis sp.]
NCBI Description
                  220814
Seq. No.
                  LIB3149-064-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  q1256830
NCBI GI
                  578
BLAST score
                  7.0e-60
E value
                  141
Match length
                  77
% identity
                  (U52970) cysteine endopeptidase 1 [Phaseolus vulgaris]
NCBI Description
                  >gi 2959418_emb_CAA12118_ (AJ224766) cysteine protease
                   [Phaseolus vulgaris]
                   220815
Seq. No.
                  LIB3149-064-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                   g1684857
NCBI GI
                   572
BLAST score
                   4.0e-59
E value
                   116
Match length
                   39
% identity
NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]
                   220816
Seq. No.
                   LIB3149-064-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   q4455174
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
                   52
Match length
% identity
                   62
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                   220817
Seq. No.
                   LIB3149-064-Q1-K1-H10
Seq. ID
Method
                   BLASTX
                   g4406780
NCBI GI
BLAST score
                   543
                   9.0e-56
E value
Match length
                   125
```



```
Seq. No.
                  220818
Seq. ID
                  LIB3149-064-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q4406780
BLAST score
                  141
E value
                  3.0e-09
Match length
                  52
                  58
% identity
NCBI Description (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
                  220819
Seq. No.
                  LIB3149-064-01-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2507222
                  404
BLAST score
                  2.0e-39
E value
                  105
Match length
% identity
                  69
NCBI Description
                  KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi 1709236 (U09505)
                  kinase associated protein phosphatase [Arabidopsis
                  thaliana]
Seq. No.
                  220820
                  LIB3165-001-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  g3914603
NCBI GI
                  734
BLAST score
                  4.0e-78
E value
Match length
                  151
% identity
                  89
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Oryza sativa]
Seq. No.
                  220821
                  LIB3165-001-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131385
BLAST score
                  484
E value
                  7.0e-49
Match length
                  122
% identity
                  83
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
Seq. No.
                  220822
Seq. ID
                  LIB3165-001-Q1-K1-A3
Method
                  BLASTX
                  g131397
NCBI GI
```

Method BLASTX
NCBI GI g131397
BLAST score 376
E value 3.0e-36
Match length 133
% identity 62

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD



SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)

>gi_81480_pir__S00008 photosystem II oxygen-evolving
complex protein 3 precursor - spinach

>gi_755802_emb_CAA29056_(X05512) 16 kDa protein of the
photosynthetic oxygen- evolving protein (OEC) [Spinacia
oleracea] >gi_225597_prf__1307179B luminal protein 16kD
[Spinacia oleracea]

 Seq. No.
 220823

 Seq. ID
 LIB3165-001-Q1-K1-A6

 Method
 BLASTX

 NCBI GI
 g4406530

 BLAST score
 423

 100 41

BLAST score 423 E value 1.0e-41 Match length 118 % identity 75

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 220824

Seq. ID LIB3165-001-Q1-K1-A7

Method BLASTX
NCBI GI g100616
BLAST score 294
E value 1.0e-26
Match length 67
% identity 84

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 220825

Seq. ID LIB3165-001-Q1-K1-A8

Method BLASTX
NCBI GI g100616
BLAST score 294
E value 1.0e-26
Match length 67
% identity 84

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 220826

Seq. ID LIB3165-001-Q1-K1-B12

Method BLASTX
NCBI GI g1352821
BLAST score 729
E value 2.0e-77
Match length 145
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain



precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

220827 Seq. No. LIB3165-001-Q1-K1-B2 Seq. ID BLASTX Method g136707 NCBI GI 443 BLAST score 4.0e-44E value 123 Match length 69 % identity CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR NCBI Description (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

220828 Seq. No. LIB3165-001-Q1-K1-B3 Seq. ID BLASTX Method g3183088 NCBI GI 205 BLAST score 4.0e-16 E value 70 Match length 56 % identity

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__ S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer

like protein [Vigna unguiculata]

220829 Seq. No. LIB3165-001-Q1-K1-B4 Seq. ID BLASTX Method g100454 NCBI GI 648 BLAST score E value 4.0e-68 Match length 138 89 % identity

NCBI Description photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein

of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 220830

Seq. ID LIB3165-001-Q1-K1-B5

Method BLASTX
NCBI GI g1352821
BLAST score 593
E value 1.0e-61
Match length 111
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SÚBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
220831
Seq. No.
                  LIB3165-001-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4126403
BLAST score
                  503
                  5.0e-51
E value
                  144
Match length
                  64
% identity
                  (AB011796) flavonol synthase [Citrus unshiu]
NCBI Description
                  220832
Seq. No.
                  LIB3165-001-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  q1172664
NCBI GI
                  265
BLAST score
                  4.0e-23
E value
                  56
Match length
                  93
% identity
                 PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi 419791 pir S31165 photosystem I chain III precursor -
                  Flaveria trinervia >gi_298482_bbs_127083 photosystem I
                  reaction center subunit III, PSI-RC PsaF [Flaveria
                  trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                   I subunit III [Flaveria trinervia]
                  220833
Seq. No.
                  LIB3165-001-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g100196
NCBI GI
                   584
BLAST score
E value
                  1.0e-60
                   127
Match length
                   83
% identity
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.
                   220834
                  LIB3165-001-Q1-K1-C10
Seq. ID
Method
                   BLASTX
                   q3600059
NCBI GI
                   354
BLAST score
                   1.0e-33
E value
Match length
                   79
% identity
                  (AF080120) contains similarity to WB domains, G-beta
NCBI Description
                   repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                   [Arabidopsis thaliana]
Seq. No.
                   220835
                   LIB3165-001-Q1-K1-C11
Seq. ID
Method
                   BLASTN
```

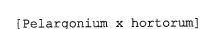
Method BLASTN
NCBI GI g4049332
BLAST score 40
E value 4.0e-13
Match length 64
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4



(ESSAII project)

```
Seq. No.
                  220836
                  LIB3165-001-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  q120661
NCBI GI
                  547
BLAST score
                  2.0e-56
E value
                  115
Match length
                  93
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                  220837
                  LIB3165-001-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g4027897
NCBI GI
                  351
BLAST score
                  2.0e-33
E value
                  72
Match length
                  88
% identity
                  (AF049353) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                   220838
Seq. No.
                  LIB3165-001-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4204267
BLAST score
                   220
                  8.0e-18
E value ~
                  131
Match length
                   45
% identity
                  (AC005223) 55585 [Arabidopsis thaliana]
NCBI Description
                   220839
Seq. No.
                   LIB3165-001-Q1-K1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q266936
BLAST score
                   432
                   1.0e-42
E value
                   120
Match length
                   76
% identity
NCBI Description 50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)
                   >gi 282960 pir A42840 ribosomal protein L27 - common
                   tobacco >gi 170306 (M98473) ribosomal protein L27
                   [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein
                   L27 [Nicotiana tabacum]
                   220840
 Seq. No.
                   LIB3165-001-Q1-K1-C8
 Seq. ID
                   BLASTX
Method
                   g1527191
NCBI GI
 BLAST score
                   431
                   1.0e-42
 E value
                   97
Match length
 % identity
 NCBI Description (U67861) 1-aminocyclopropane-1-carboxylate oxidase
```



```
220841
 Seq. No.
                   LIB3165-001-Q1-K1-C9
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g4006858
 BLAST score
                    362
                    2.0e-34
 E value
                    95
 Match length
                    66
 % identity
                   (Z99707) cold acclimation protein homolog [Arabidopsis
 NCBI Description
                    thaliana]
                    220842
 Seq. No.
                   LIB3165-001-Q1-K1-D10
 Seq. ID
 Method
                    BLASTX
                    g430947
 NCBI GI
 BLAST score
                    431
                    1.0e-42
 E value
                    105
 Match length
                    81
 % identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
 NCBI Description
                    [Arabidopsis thaliana]
                    220843
 Seq. No.
                    LIB3165-001-Q1-K1-D11
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g226263
                    232
 BLAST score
                    1.0e-19
 E value
                    43
 Match length
                    100
 % identity
 NCBI Description chlorophyll a/b binding protein [Glycine max]
                    220844
 Seq. No.
                    LIB3165-001-Q1-K1-D12
 Seq. ID
".Method
                    BLASTX
 NCBI GI
                  - g1532118
 BLAST score
                    241
                    2.0e-20
 E value
                    127
 Match length
 % identity
 NCBI Description (U36268) beta-prime-adaptin [Homo sapiens]
                    220845
 Seq. No.
                    LIB3165-001-Q1-K1-D3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1352821
 BLAST score
                    626
                    2.0e-65
 E value
 Match length
                    117
                    97
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                    ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                    precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
```

ribulose bisphosphate carboxylase [Gossypium hirsutum]



75

% identity

```
220846
Seq. No.
                  LIB3165-001-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  q1352821
NCBI GI
                  612
BLAST score
                  8.0e-64
E value
                  114
Match length
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  220847
Seq. No.
                  LIB3165-001-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g2190992
NCBI GI
BLAST score
                  229
                  6.0e-19
E value
Match length
                  79
                  58
% identity
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                  tauschii]
                   220848
Seq. No.
Seq. ID
                  LIB3165-001-Q1-K1-D7
Method
                  BLASTX
                  q2754849
NCBI GI
                  209
BLAST score
                  1.0e-17
E value
                  55
Match length
% identity
                   89
                  (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
                   220849
Seq. No.
                   LIB3165-001-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   g3747111
NCBI GI
                   369
BLAST score
                   3.0e - 35
E value
                   114
Match length
                   61
% identity
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
                   220850
Seq. No.
                   LIB3165-001-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4406530
BLAST score
                   409
E value
                   5.0e-40
Match length
                   115
```

NCBI Description (AF126870) rubisco activase [Vigna radiata]



```
220851
Seq. No.
                  LIB3165-001-Q1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2815246
BLAST score
                  225
                  2.0e-18
E value
                  55
Match length
                  73
% identity
                 (X95709) class I type 2 metallothionein [Cicer arietinum]
NCBI Description
                  220852
Seq. No.
                  LIB3165-001-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  g18058
NCBI GI
                  108
BLAST score
                   3.0e-54
E value
                  136
Match length
                   95
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                   220853
Seq. No.
                  LIB3165-001-Q1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3426051
BLAST score
                   159
                   1.0e-10
E value
Match length
                   63
% identity
                   56
NCBI Description (AC005168) hypothetical protein [Arabidopsis thaliana]
                   220854
Seq. No.
                   LIB3165-001-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3790567
                   180
BLAST score
E value
                   4.0e-13
Match length
                   115
% identity
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   220855
                   LIB3165-001-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   637
E value
                   9.0e-67
Match length
                   120
                   97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
```

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 220856

LIB3165-001-Q1-K1-F1 Seq. ID



Method BLASTX
NCBI GI g166834
BLAST score 307
E value 4.0e-28
Match length 71
% identity 79
NCBI Description (M86720
activas
Rubisco

(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 220857 Seq. ID LIB3165-001-Q1-K1-F2

Method BLASTX
NCBI GI g557084
BLAST score 159
E value 1.0e-10
Match length 103
% identity 3

NCBI Description (L35601) ankyrin [Drosophila melanogaster]

>gi 1092123_prf__2022340A ankyrin [Drosophila melanogaster]

Seq. No. 220858

Seq. ID LIB3165-001-Q1-K1-F5

Method BLASTX
NCBI GI g441457
BLAST score 591
E value 2.0e-61
Match length 112
% identity 98

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No. 220859

Seq. ID LIB3165-001-Q1-K1-F9

Method BLASTX
NCBI GI g2496789
BLAST score 500
E value 1.0e-50
Match length 148
% identity 68

NCBI Description 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP

REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183_ (D64000)

hypothetical protein [Synechocystis sp.]

Seq. No. 220860

Seq. ID LIB3165-001-Q1-K1-G4

Method BLASTX
NCBI GI g2702281
BLAST score 407
E value 5.0e-40
Match length 101
% identity 56

NCBI Description (AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No. 220861

Seq. ID LIB3165-001-Q1-K1-G5



```
Method
                  BLASTX
NCBI GI
                  q1354515
                  303
BLAST score
                  1.0e-27
E value
Match length
                  136
                  53
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  220862
Seq. No.
                  LIB3165-001-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                   g4512018
NCBI GI
                   614
BLAST score
                   4.0e-64
E value
Match length
                   131
                   84
% identity
                  (AF106660) mRNA binding protein precursor [Lycopersicon
NCBI Description
                   esculentum]
                   220863
Seq. No.
                   LIB3165-001-Q1-K1-G8
Seq. ID
Method
                   BLASTX
                   g1928981
NCBI GI
                   580
BLAST score
                   4.0e-60
E value
Match length
                   123
% identity
                   93
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   220864
Seq. No.
                   LIB3165-001-Q1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q131225
BLAST score
                   390
E value
                   5.0e-52
                   149
Match length
                   71
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi 167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
                   220865
Seq. No.
                   LIB3165-001-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q166834
BLAST score
                   378
                   2.0e-36
E value
                   88
Match length
```

80 % identity

(M86720) ribulose bisphosphate carboxylase/oxygenase NCBI Description

activase [Arabidopsis thaliana] >gi 2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 220866

```
LIB3165-001-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g4406530
NCBI GI
                  360
BLAST score
                  3.0e - 34
E value
Match length
                  98
                  76
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  220867
Seq. No.
                  LIB3165-001-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                  g3914472
NCBI GI
BLAST score
                  291
                  2.0e-26
E value
Match length
                  97
                  62
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                  >gi_322764_pir__S32021 photosystem II 10K protein - common
                   tobacco >gi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana
                   tabacum]
                  220868
Seq. No.
                  LIB3165-001-Q1-K1-H2
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g125578
BLAST score
                  444
                  4.0e-44
E value
                  116
Match length
                  74
% identity
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi 167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                   220869
Seq. No.
                  LIB3165-001-Q1-K1-H4
Seq. ID,
Method
                  BLASTX
                   q400890
NCBI GI
                   229
BLAST score
E value
                   5.0e-19
Match length
                  110
                   48
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
```

>gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

220870 Seq. No.

% identity

Seq. ID LIB3165-002-Q1-K1-A1

Method BLASTX NCBI GI q4406530 BLAST score 347 E value 8.0e-33 Match length 92 77

Method

BLASTX



```
(AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  220871
Seq. No.
                  LIB3165-002-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g3901268
NCBI GI
                  224
BLAST score
                  2.0e-18
E value
                  132
Match length
                  35
% identity
                  (AF060173) SV2 related protein [Rattus norvegicus]
NCBI Description
                  220872
Seq. No.
                  LIB3165-002-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g505482
NCBI GI
                   457
BLAST score
                   1.0e-45
E value
                   114
Match length
                   82
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                   photosystem II [Nicotiana tabacum]
                   220873
Seq. No.
                   LIB3165-002-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g4210948
NCBI GI
BLAST score
                   495
                   4.0e-50
E value
                   99
Match length
                   93
% identity
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
                   220874
Seq. No.
                   LIB3165-002-Q1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3869088
                   574
BLAST score
                   2.0e-59
E value
                   110
Match length
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                   220875
Seq. No.
                   LIB3165-002-Q1-K1-A8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4519194
BLAST score
                   41
E value
                   1.0e-13
                   193
Match length
                   80
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHM17, complete sequence
                   220876
Seq. No.
                   LIB3165-002-Q1-K1-A9
Seq. ID
```

BLAST score

Match length

E value

441

104

8.0e-44



```
NCBI GI
                  g3738261
BLAST score
                  563
                  4.0e-58
E value
                  130
Match length
                  86
% identity
                  (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                  nigra]
                  220877
Seq. No.
                  LIB3165-002-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g4510345
NCBI GI
BLAST score
                  161
                  5.0e-11
E value
                  53
Match length
% identity
                   53
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  220878
Seq. No.
                  LIB3165-002-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545262
                   239
BLAST score
                   4.0e-20
E value
                  44
Match length
% identity
                  100
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
                   220879
Seq. No.
                  LIB3165-002-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2864617
BLAST score
                   251
                   2.0e-21
E value
                 . 121
Match length
% identity
                   46
NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like
                   protein [Arabidopsis thaliana]
Seq. No.
                   220880
Seq. ID
                   LIB3165-002-Q1-K1-B6
Method
                   BLASTX
                   q2765081
NCBI GI
BLAST score
                   455
                   2.0e-45
E value
Match length
                   128
% identity
NCBI Description (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                   220881
Seq. ID
                   LIB3165-002-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g4185515
```

Match length

% identity

129

NCBI Description (U73747) annexin [Gossypium hirsutum]



```
% identity
                  (AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  220882
                  LIB3165-002-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  g2244905
NCBI GI
                  364
BLAST score
                  8.0e-35
E value
                  121
Match length
% identity
                  57
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  220883
Seq. No.
                  LIB3165-002-Q1-K1-B9
Seq. ID
Method
                  BLASTX
                  g3643192
NCBI GI
BLAST score
                  268
E value
                  1.0e-23
Match length
                  122
% identity
                  51
NCBI Description (AF087435) unknown [Arabidopsis thaliana]
Seq. No.
                  220884
                  LIB3165-002-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  682
                  4.0e-72
E value
Match length
                  128
                  99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  220885
                  LIB3165-002-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1781348
BLAST score
                   609
E value
                   2.0e-63
Match length
                  122
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                   220886
Seq. ID
                  LIB3165-002-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q1843527
BLAST score
                   654
E value
                   8.0e-69
```



Seq. No. 220887 LIB3165-002-Q1-K1-C12 Seq. ID Method BLASTX q68200 NCBI GI 528 BLAST score 5.0e-54 E value Match length 131 82 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea] 220888 Seq. No. LIB3165-002-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI q505482 209 BLAST score 1.0e-23 E value 102 Match length 69 % identity (X64349) 33 kDa polypeptide of water-oxidizing complex of NCBI Description photosystem II [Nicotiana tabacum] Seq. No. 220889 LIB3165-002-Q1-K1-C6 Seq. ID BLASTX Method NCBI GI q1750404 BLAST score 209 E value 1.0e-16 56 Match length 62 % identity (U80953) Similar to 40S ribosomal protein S29; coded for by NCBI Description C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk107e8.5; coded for by C. elegans cDNA CEESF55F; coded for by C. elegans cDNA yk107e8.3; Seq. No. 220890 LIB3165-002-Q1-K1-C8 Seq. ID BLASTX Method g418854 NCBI GI 538 BLAST score E value 3.0e-55 109 Match length 18 % identity ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ NCBI Description (X64344) polyubiquitin [Petroselinum crispum] >gi 288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum] 220891 Seq. No.

Seq. ID LIB3165-002-Q1-K1-D1

Method BLASTX
NCBI GI g1352821
BLAST score 570
E value 6.0e-59
Match length 108



% identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 220892 Seq. No. LIB3165-002-Q1-K1-D11 Seq. ID Method BLASTN NCBI GI g3821780 33 BLAST score 6.0e-09 E value 33 Match length 58 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 220893 LIB3165-002-Q1-K1-D12 Seq. ID BLASTX Method NCBI GI g4263710 BLAST score 364 8.0e-35 E value 74 Match length 59 % identity (AC006223) putative pur-alpha transcriptional activator NCBI Description protein [Arabidopsis thaliana] 220894 Seq. No. LIB3165-002-Q1-K1-D2 Seq. ID Method BLASTX g1170567 NCBI GI BLAST score 512 E value 4.0e-52 Match length 102 90 % identity NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi] 220895 Seq. No. Seq. ID LIB3165-002-Q1-K1-D3 Method BLASTX NCBI GI g3157952 BLAST score 245 8.0e-21 E value Match length 100 % identity 55 NCBI Description (AC002131) F12F1.11 [Arabidopsis thaliana] 220896

Seq. No.

Seq. ID LIB3165-002-Q1-K1-D5

Method BLASTX NCBI GI g1655536 BLAST score 256 E value 4.0e-22 Match length 88



% identity 56

(Y09095) chloride channel [Arabidopsis thaliana] NCBI Description

>gi 1742957 emb CAA96059 (Z71447) CLC-c chloride channel

protein [Arabidopsis thaliana]

220897 Seq. No.

LIB3165-002-Q1-K1-D6 Seq. ID

BLASTX Method g1352821 NCBI GI 553 BLAST score 6.0e-57 E value Match length 105 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

220898 Seq. No.

LIB3165-002-Q1-K1-D8 Seq. ID

Method BLASTX NCBI GI g2618686 209 BLAST score 1.0e-16 E value Match length . 118 42 % identity

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

220899 Seq. No.

LIB3165-002-Q1-K1-E1 Seq. ID

BLASTX Method g3913018 NCBI GI BLAST score 624 3.0e-65 E value 125 Match length 94 % identity

FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

220900 Seq. No.

Seq. ID LIB3165-002-Q1-K1-E10

Method BLASTX g2493694 NCBI GI 316 BLAST score 4.0e-29E value Match length 126 56 % identity

NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII

6.1 KD PROTEIN) $>gi_1076268_pir_S53025_photosystem II protein - spinach <math>>gi_728716_emb_CAA59409_ (X85038)_protein$

of photosystem II [Spinacia oleracea]

Seq. No. 220901

LIB3165-002-Q1-K1-E3 Seq. ID

Method BLASTX



```
g3426043
NCBI GI
                  436
BLAST score
                  3.0e-43
E value
Match length
                  135
                   66
% identity
                   (AC005168) putative choline kinase [Arabidopsis thaliana]
NCBI Description
                  220902
Seq. No.
                  LIB3165-002-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g2511691
NCBI GI
BLAST score
                   274
                   3.0e-24
E value
                   80
Match length
% identity
                   69
                  (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   220903
                  LIB3165-002-Q1-K1-E5
Seq. ID
Method
                   BLASTX
                   g2764574
NCBI GI
                   302
BLAST score
                   2.0e-27
E value
                   128
Match length
                   52
% identity
                  (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
NCBI Description
Seq. No.
                   220904
                   LIB3165-002-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g2765081
NCBI GI
                   455
BLAST score
                   2.0e-45
E value
                   128
Match length
                   71
% identity
                  (Y10557) g5bf [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   220905
                   LIB3165-002-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g4406530
NCBI GI
                   349
BLAST score
                   5.0e - 33
E value
                   93
Match length
                   76
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   220906
Seq. No.
                   LIB3165-002-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3355486
BLAST score
                   494
```

E value 5.0e-50 131 Match length % identity 72

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

BLAST score

Match length

E value

434

109

4.0e-43



```
220907
Seq. No.
                   LIB3165-002-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   q3687652
NCBI GI
                   537
BLAST score
                   1.0e-62
E value
                   129
Match length
                   95
% identity
                   (AF047352) rubisco activase precursor [Datisca glomerata]
NCBI Description
                   220908
Seq. No.
                   LIB3165-002-Q1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   9.0e-11
E value
                   37
Match length
 % identity
                   61
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   220909
Seq. No.
                   LIB3165-002-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   g1495251
NCBI GI
BLAST score
                   244
                   9.0e-21
E value
                   126
Match length
 % identity
                   44
                   (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   220910
 Seq. No.
                   LIB3165-002-Q1-K1-F3
 Seq. ID
Method
                   BLASTX
                   g2505872
NCBI GI
                   144
 BLAST score
                   5.0e-09
 E value
                   63
Match length
% identity
                   52
 NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]
                   220911
 Seq. No.
                   LIB3165-002-Q1-K1-F4
 Seq. ID
 Method
                   BLASTX
                   g3201969
 NCBI GI
 BLAST score
                   450
                   7.0e-45
 E value
 Match length
                   110
 % identity
                   70
 NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]
                   220912
 Seq. No.
                   LIB3165-002-Q1-K1-F5
 Seq. ID
 Method
                   BLASTX
                   g3694811
 NCBI GI
```

BLAST score

E value Match length 41 8.0e-14



```
% identity
                   (AF060481) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis
NCBI Description
                  thaliana]
                  220913
Seq. No.
                  LIB3165-002-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  q289920
NCBI GI
                  601
BLAST score
                  1.0e-62
E value
Match length
                  115
                  98
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  220914
Seq. No.
                  LIB3165-002-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  g4096662
NCBI GI
                  569
BLAST score
                  8.0e-59
E value
Match length
                  111
                  98
% identity
                  (U35026) Rab1-like small GTP-binding protein [Petunia x
NCBI Description
                  hybrida]
Seq. No.
                  220915
                  LIB3165-002-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  398
E value
                   8.0e-39
                  75
Match length
                   95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   220916
Seq. No.
Seq. ID
                   LIB3165-002-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   q1657948
BLAST score
                   468
                   5.0e-47
E value
Match length
                   103
% identity
NCBI Description
                 (U73466) MipC [Mesembryanthemum crystallinum]
                   220917
Seq. No.
Seq. ID
                   LIB3165-002-Q1-K1-G12
Method
                   BLASTN
NCBI GI
                   g1399549
```



% identity

NCBI Description Anemone trifolia nuclear 26S ribosomal RNA gene, partial

sequence

Seq. No.

220918

Seq. ID Method

LIB3165-002-Q1-K1-G2

NCBI GI

BLASTX g2160185

BLAST score

298

E value Match length 5.0e-27

% identity

90 61

NCBI Description

(AC000132) Similar to S. pombe ISP4 (gb D83992).

[Arabidopsis thaliana]

Seq. No.

220919

Seq. ID

LIB3165-002-Q1-K1-G4

Method NCBI GI BLASTX g2995384

BLAST score

167

E value Match length 8.0e-12

59 57

% identity

NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.

220920

Seq. ID

LIB3165-002-Q1-K1-G6

Method

BLASTX

NCBI GI

q3065814

BLAST score

250

E value

2.0e-21

Match length

124

% identity

46

NCBI Description

(AF058714) sodium-dicarboxylate cotransporter SDCT1 [Rattus

norvegicus] >gi_3168585_dbj_BAA28609 (AB001321)

sodium-dependent dicarboxylate transporter [Rattus norvegicus]

Seq. No.

220921

Seq. ID

LIB3165-002-Q1-K1-G7

Method

BLASTX

NCBI GI

g1170897

BLAST score

483

E value

1.0e-48

Match length

113

% identity

MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

NCBI Description

>gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase

[Cucumis sativus]

Seq. No.

220922

Seq. ID

LIB3165-002-Q1-K1-G8

Method

BLASTX

NCBI GI

g1168408

BLAST score

638

E value

6.0e-67



Match length 135 % identity 92

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 NCBI Description

>gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 220923

Seq. ID LIB3165-002-Q1-K1-G9

BLASTX Method NCBI GI g1181599 BLAST score 518 7.0e-53 E value Match length 133 77 % identity

(D83007) subunit of photosystem I [Cucumis sativus] NCBI Description

Seq. No. 220924

Seq. ID LIB3165-002-Q1-K1-H10

BLASTX Method NCBI GI q1168411 BLAST score 507 1.0e-51 E value Match length 126 82 % identity

FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description

220925 Seq. No.

Seq. ID LIB3165-002-Q1-K1-H11

Method BLASTX q2661021 NCBI GI BLAST score 593 1.0e-61 E value Match length 113

96 % identity

(AF035255) catalase [Glycine max] NCBI Description

220926 Seq. No.

Seq. ID LIB3165-002-Q1-K1-H12

BLASTX Method q3738316 NCBI GI 235 BLAST score 1.0e-19 E value Match length 65 69 % identity

(AC005170) unknown protein [Arabidopsis thaliana] NCBI Description

220927 Seq. No.

LIB3165-002-Q1-K1-H3 Seq. ID

Method BLASTX NCBI GI q3123745 285 BLAST score E value 1.0e-25 Match length 125 46 % identity

NCBI Description (AB013447) aluminum-induced [Brassica napus]



```
Seq. No.
                  220928
                  LIB3165-002-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  q4455356
NCBI GI
BLAST score
                  207
                  2.0e-16
E value
Match length
                  98
% identity
                  41
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  220929
Seq. No.
                  LIB3165-002-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g166834
                  281
BLAST score
                   3.0e-25
E value
Match length
                   65
% identity
                   78
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
                   220930
Seq. No.
Seq. ID
                   LIB3165-002-Q1-K1-H6
                   BLASTX
Method
NCBI GI
                   g120658
BLAST score
                   424
                   8.0e-42
E value
Match length
                   114
% identity
                   75
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                   CHLOROPLAST >gi 66025 pir DEPMNA
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   garden pea >gi 12159 emb_CAA36396_ (X52148) GAPA [Pisum
                   sativum]
Seq. No.
                   220931
                   LIB3165-002-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   q4490321
NCBI GI
                   428
BLAST score
E value
                   3.0e-42
                   95
Match length
                   87
% identity
NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]
                   220932
Seq. No.
                   LIB3165-002-Q1-K1-H8
Seq. ID
Method
                   BLASTX
                   g1345698
NCBI GI
BLAST score
                   637
```

E value 8.0e-67 Match length 126 % identity 94

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

a/b-binding protein - upland cotton
>gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding
protein [Gossypium hirsutum]

 Seq. No.
 220933

 Seq. ID
 LIB3165-003-P1-K1-A1

 Method
 BLASTX

 NCBI GI
 g1703129

 BLAST score
 471

 E value
 2.0e-47

 Match length
 91

 % identity
 96

% identity 96
NCBI Description ACTIN 11 >gi_2129522_pir_S68109 actin 11 - Arabidopsis

thaliana $>gi_1002533(U27981)$ actin-11 [Arabidopsis

thaliana]

Seq. No. 220934

Seq. ID LIB3165-003-P1-K1-A12

Method BLASTX
NCBI GI g1352821
BLAST score 305
E value 3.0e-28
Match length 61
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 220935

Seq. ID LIB3165-003-P1-K1-A3

Method BLASTX
NCBI GI g3603401
BLAST score 321
E value 7.0e-30
Match length 82
% identity 70

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 220936

Seq. ID LIB3165-003-P1-K1-A4

Method BLASTX
NCBI GI g3510256
BLAST score 150
E value 9.0e-10
Match length 89
% identity 40

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 220937

Seq. ID LIB3165-003-P1-K1-A5

Method BLASTX
NCBI GI g3687237
BLAST score 246
E value 4.0e-24
Match length 113

% identity (AC005169) putative Cys3His zinc-finger protein NCBI Description [Arabidopsis thaliana] Seq. No. 220938 Seq. ID LIB3165-003-P1-K1-A6 BLASTX Method NCBI GI q68200 BLAST score 282 3.0e-25 E value 62 Match length 92 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi 22633 emb CAA47293 (X66814) fructose-bisphosphate aldolase [Spinacia oleracea] Seq. No. 220939 LIB3165-003-P1-K1-A7 BLASTN

 Seq. ID
 LIB3165-003-P1-K1-A7

 Method
 BLASTN

 NCBI GI
 g18058

 BLAST score
 188

 E value
 1.0e-102

Match length 212 % identity 98

NCBI Description Citrus limon cistron for 26S ribosomal RNA

Seq. No. 220940

Seq. ID LIB3165-003-P1-K1-A9

Method BLASTX
NCBI GI g228403
BLAST score 527
E value 6.0e-54
Match length 120
% identity 85

NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 220941

Seq. ID LIB3165-003-P1-K1-B1

Method BLASTX
NCBI GI g441457
BLAST score 624
E value 3.0e-65
Match length 118
% identity 97

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No. 220942

Seq. ID LIB3165-003-P1-K1-B12

Method BLASTX
NCBI GI g1352821
BLAST score 311
E value 7.0e-29
Match length 61
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

Seq. No.

Seq. ID

220947

LIB3165-003-P1-K1-C10



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

220943 Seq. No. Seq. ID LIB3165-003-P1-K1-B3 Method BLASTX NCBI GI q462187 BLAST score 634 2.0e-66 E value Match length 125 % identity 96 NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_282928_pir__A42906 serine hydroxymethyltransferase - garden pea >gi 169158 (M87649) serine hydroxymethyltransferase [Pisum sativum] Seq. No. 220944 Seq. ID LIB3165-003-P1-K1-B6 Method BLASTX NCBI GI g70644 BLAST score 547 E value 3.0e-56Match length 113 % identity 19 NCBI Description ubiquitin precursor - common sunflower (fragment) 220945 Seq. No. Seq. ID LIB3165-003-P1-K1-B7 Method BLASTX NCBI GI g115813 BLAST score 377 E value 2.0e-36 Match length 109 % identity 69 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] Seq. No. 220946 Seq. ID LIB3165-003-P1-K1-C1 Method BLASTX NCBI GI g131393 BLAST score 292 E value 2.0e-26 Match length 61 % identity 92 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360_pir__S15005 photosystem II oxygen-evolving
complex protein 2 - common tobacco >gi 19911 emb CAA39039.1 (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum]

```
Method
                  BLASTX
                  g3063392
NCBI GI
BLAST score
                  338
                  8.0e-32
E value
Match length
                  98
                  72
% identity
                  (AB012932) Ca2+/H+ exchanger [Vigna radiata]
NCBI Description
Seq. No.
                  220948
                  LIB3165-003-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g136707
BLAST score
                  222
                  2.0e-18
E value
Match length
                  65
                  68
% identity
                  CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                   (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  iron-sulfur protein precursor - garden pea
                  >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS
                  protein [Pisum sativum]
Seq. No.
                  220949
Seq. ID
                  LIB3165-003-P1-K1-C3
                  BLASTX
Method
                  q3288821
NCBI GI
BLAST score
                   416
                   6.0e-41
E value
                  101
Match length
                   79
% identity
NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   220950
Seq. No.
                   LIB3165-003-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3033513
NCBI GI
                   220
BLAST score
                   2.0e-21
E value
                   92
Match length
                   66
% identity
NCBI Description (AF041068) rubisco activase [Phaseolus vulgaris]
                   220951
Seq. No.
                   LIB3165-003-P1-K1-C6
Seq. ID
                   BLASTX
Method
                   g461501
NCBI GI
                   377
BLAST score
E value
                   1.0e-36
Match length
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE 2, CHLOROPLAST
                   >gi_418803_pir__S29048 fructose-bisphosphate aldolase (EC
```

Seq. No. 220952

4.1.2.13) - garden pea (fragment)



```
LIB3165-003-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g2864617
NCBI GI
BLAST score
                  360
                  2.0e-34
E value
                  102
Match length
% identity
                  75
                  (AL021811) H+-transporting ATP synthase chain9 - like
NCBI Description
                  protein [Arabidopsis thaliana]
                  220953
Seq. No.
                  LIB3165-003-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  q166708
NCBI GI
                  186
BLAST score
                   3.0e-14
E value
Match length
                   68
                   54
% identity
                  (M64118) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   220954
Seq. No.
                   LIB3165-003-P1-K1-E1
Seq. ID
Method
                   BLASTX
                   q1168411
NCBI GI
BLAST score
                   396
                   1.0e-38
E value
Match length
                   101
% identity
                   81
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   220955
Seq. No.
                   LIB3165-003-P1-K1-E2
Seq. ID
                   BLASTN
Method
                   g18058
NCBI GI
                   212
BLAST score
                   1.0e-116
E value
Match length
                   264
                   96
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                   220956
Seq. No.
                   LIB3165-003-P1-K1-E3
Seq. ID
                   BLASTX
Method
                   q119932
NCBI GI
                   361
BLAST score
                   1.0e-34
E value
Match length
                   96
                   69
 % identity
NCBI Description FERREDOXIN I >gi_65749_pir__FEFW1 ferredoxin [2Fe-2S] I -
                   Virginian pokeweed
                   220957
 Seq. No.
                   LIB3165-003-P1-K1-E4
 Seq. ID
                   BLASTX
 Method
```

31179

g1352821

472

NCBI GI

BLAST score



```
2.0e-47
E value
                  96
Match length
                  94
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  220958
Seq. No.
                  LIB3165-003-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g3913651
NCBI GI
                  324
BLAST score
                  3.0e-30
E value
Match length
                  97
                  65
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                  (FNR) >qi 2225993 emb CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                  220959
Seq. No.
                  LIB3165-003-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g1881585
NCBI GI
BLAST score
                  146
                  3.0e-09
E value
Match length
                  71
% identity
                  59
NCBI Description (U72489) remorin [Solanum tuberosum]
                  220960
Seq. No.
                  LIB3165-003-P1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1531758
                   223
BLAST score
                   3.0e-18
E value
Match length
                   45
                   89
% identity
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
Seq. No.
                   220961
                   LIB3165-003-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3288821
BLAST score
                   445
E value
                   3.0e-44
Match length
                   107
% identity
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
```

transaminase [Arabidopsis thaliana]

Seq. No. 220962

Seq. ID LIB3165-003-P1-K1-F3

Method BLASTX NCBI GI g1362086



BLAST score 515 E value 1.0e-52 Match length 106 % identity 92

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_2129919_pir__S65957

 $5-\overline{methyltetrahydropteroyltriglutamate--homocysteine}$

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 220963

Seq. ID LIB3165-003-P1-K1-F4

Method BLASTX
NCBI GI g120663
BLAST score 472
E value 2.0e-47
Match length 121
% identity 74

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi_66027_pir__DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]

Seq. No. 220964

Seq. ID LIB3165-003-P1-K1-F5

Method BLASTX
NCBI GI g282995
BLAST score 180
E value 3.0e-13
Match length 85
% identity 52

NCBI Description seed protein B32E - barley (fragment)

>gi_1345530_emb_CAA45538_ (X64254) B32E [Hordeum vulgare]

Seq. No. 220965

Seq. ID LIB3165-003-P1-K1-F8

Method BLASTN
NCBI GI g3298532
BLAST score 44
E value 1.0e-15
Match length 80
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC T26B15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 220966

Seq. ID LIB3165-003-P1-K1-F9

Method BLASTN
NCBI GI g3108248
BLAST score 287
E value 1.0e-160

Match length 338 % identity 96



```
NCBI Description Gossypium barbadense clone pXP027 repetitive DNA sequence
                  220967
Seq. No.
                  LIB3165-003-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  q1709651
NCBI GI
BLAST score
                  215
                  1.0e-23
E value
Match length
                  114
% identity
                  53
                  PLASTOCYANIN A PRECURSOR >gi_2117431_pir___S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus
                  nigra]
                  220968
Seq. No.
                  LIB3165-003-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q20729
NCBI GI
BLAST score
                  452
E value
                  4.0e-45
Match length
                  124
% identity
                  75
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                220969
Seq. No.
                  LIB3165-003-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q68200
BLAST score
                  499
                  1.0e-50
E value
Match length
                  123
                  83
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                  220970
                  LIB3165-003-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  244
E value
                  1.0e-20
                  54
Match length
                  85
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
Seq. No.
                  220971
Seq. ID
                  LIB3165-003-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   q4006884
BLAST score
                   139
E value
                   1.0e-08
Match length
                   44
% identity
                  (Z99707) BEL1-like homeodomain protein [Arabidopsis
NCBI Description
```

31182

thaliana]

```
220972
```

Seq. No. LIB3165-004-P1-K1-A11 Seq. ID BLASTX Method NCBI GI g1709825 267 BLAST score 2.0e-23 E value Match length 126 49 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR NCBI Description (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana] 220973 Seq. No. Seq. ID LIB3165-004-P1-K1-A12 BLASTX Method g1588365 NCBI GI BLAST score 171 E value 3.0e-12Match length 82 40 % identity NCBI Description signal peptidase:SUBUNIT=12kD [Homo sapiens] 220974 Seq. No. Seq. ID LIB3165-004-P1-K1-A6 Method BLASTX q1781348 NCBI GI BLAST score 151 4.0e-10 E value Match length 42 74 % identity (Y10380) homologous to plastidic aldolases [Solanum NCBI Description tuberosum] 220975 Seq. No. LIB3165-004-P1-K1-A7 Seq. ID BLASTX Method NCBI GI g343369 BLAST score 561 E value 6.0e-58 Match length 108 95 % identity NCBI Description (M27308) 44 kd photosystem II protein [Spinacia oleracea] Seq. No. 220976 Seq. ID LIB3165-004-P1-K1-A8 Method BLASTX q400890 NCBI GI BLAST score 235 1.0e-19 E value Match length 110 % identity 45 PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR NCBI Description

>gi 282837 pir S26953 photosystem II 22K protein precursor - spinach >gi 21307 emb CAA48557 (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

```
220977
Seq. No.
                  LIB3165-004-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  q1617274
NCBI GI
                  514
BLAST score
                  2.0e-52
E value
                  123
Match length
                  75
% identity
                  (Z72152) AMP-binding protein [Brassica napus]
NCBI Description
                  220978
Seq. No.
                  LIB3165-004-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g1345698
NCBI GI
                  640
BLAST score
                  3.0e-67
E value
                  121
Match length
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
NCBI Description
                  (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
                  220979
Seq. No.
                  LIB3165-004-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100196
                  178
BLAST score
                  1.0e-13
E value
Match length
                  46
                  74
% identity
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
                  220980
Seq. No.
Seq. ID
                  LIB3165-004-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  a1170897
                   558
BLAST score
                  1.0e-57
E value
Match length
                  123
% identity
                  89
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber
                   >gi_695311 (L31900) glyoxysomal malate dehydrogenase
                   [Cucumis sativus]
Seq. No.
                   220981
                   LIB3165-004-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2677828
BLAST score
                   286
E value
                   2.0e-30
Match length
                   114
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
```



```
220982
Seq. No.
Seq. ID
                  LIB3165-004-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g507275
BLAST score
                  165
                  2.0e-11
E value
Match length
                  108
                  35
% identity
                  (L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama
NCBI Description
                  guanicoe]
Seq. No.
                  220983
                  LIB3165-004-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g2501568
NCBI GI
BLAST score
                  157
                  1.0e-10
E value
Match length
                  97
                  38
% identity
                  HYPOTHETICAL 28.8 KD PROTEIN SLL0506
NCBI Description
                  >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein
                   [Synechocystis sp.]
                  220984
Seq. No.
                  LIB3165-004-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g231688
NCBI GI
BLAST score
                  555
E value
                   5.0e-61
Match length
                  127
                   96
% identity
                 CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC
NCBI Description
                   1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)
                   subunit 2 of cotton catalase [Gossypium hirsutum]
                   220985
Seq. No.
                   LIB3165-004-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2970051
BLAST score
                   380
                   1.0e-36
E value
                   95
Match length
                   74
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
                   220986
Seq. No.
                   LIB3165-004-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1354515
NCBI GI
BLAST score
                   234
                   1.0e-19
E value
                   125
Match length
                   46
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
```

tremuloides]



Seq. No. 220987

Seq. ID LIB3165-004-P1-K1-C12

Method BLASTX
NCBI GI g1458245
BLAST score 252
E value 1.0e-21
Match length 123
% identity 46

NCBI Description (U64834) coded for by C. elegans cDNA cm17a1; coded for by

C. elegans cDNA cm7g1; coded for by C. elegans cDNA

CEMSE26F; similar to methyltransferases [Caenorhabditis

elegans]

Seq. No. 220988

Seq. ID LIB3165-004-P1-K1-C3

Method BLASTX
NCBI GI 9400890
BLAST score 224
E value 2.0e-18
Match length 94
% identity 44

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 220989

Seq. ID LIB3165-004-P1-K1-C4

Method BLASTX
NCBI GI g3128176
BLAST score 316
E value 3.0e-29
Match length 86
% identity 65

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 220990

Seq. ID LIB3165-004-P1-K1-C5

Method BLASTX
NCBI GI g231610
BLAST score 274
E value 3.0e-24
Match length 101
% identity 60

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 220991

Seq. ID LIB3165-004-P1-K1-C7

Method BLASTX NCBI GI g2864617 BLAST score 227



E value 9.0e-19
Match length 94

Match length 94 % identity 54

NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like

protein [Arabidopsis thaliana]

Seq. No. 220992

Seq. ID LIB3165-004-P1-K1-C8

Method BLASTX
NCBI GI g2984709
BLAST score 426
E value 4.0e-42
Match length 83
% identity 98

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 220993

Seq. ID LIB3165-004-P1-K1-C9

Method BLASTN
NCBI GI g2687434
BLAST score 320
E value 1.0e-180
Match length 375
% identity 97

NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 220994

Seq. ID LIB3165~004-P1-K1-D1

Method BLASTX
NCBI GI g974782
BLAST score 374
E value 5.0e-36
Match length 78
% identity 95

NCBI Description (Z49150) cobalamine-independent methionine synthase

[Solenostemon scutellarioides]

Seq. No. 220995

Seq. ID LIB3165-004-P1-K1-D10

Method BLASTX
NCBI GI g136636
BLAST score 286
E value 1.0e-25
Match length 56
% identity 95

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi_442594 pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894 pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 220996



50

[Glycine max]

% identity

NCBI Description

```
LIB3165-004-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242704
BLAST score
                  302
                  1.0e-27
E value
                  113
Match length
% identity
                  53
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  220997
Seq. No.
                  LIB3165-004-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168411
BLAST score
                  462
                  2.0e-46
E value
Match length
                  116
% identity
                  81
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  220998
Seq. No.
                  LIB3165-004-P1-K1-D5
Seq. ID
                  BLASTX
Method
                  g1781348
NCBI GI
BLAST score
                  512
                   6.0e-55
E value
Match length
                  124
                   90
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
                   220999
Seq. No.
                  LIB3165-004-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g118564
                   622
BLAST score
                   4.0e-65
E value
                   125
Match length
                   94
% identity
                  GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE
NCBI Description
                   REDUCTASE) (HPR) (GDH) >gi_65955 pir__DEKVG glycerate
                   dehydrogenase (EC 1.1.1.29) - cucumber
                   >gi 18264 emb CAA41434_ (X58542) NADH-dependent
                   hydroxypyruvate reductase [Cucumis sativus]
                   >gi 18275 emb_CAA32764_ (X14609) NAPH-dependent
                   hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
                   221000
Seq. No.
                   LIB3165-004-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g541951
BLAST score
                   313
                   7.0e-29
E value
                   63
Match length
```

31188

SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26



```
221001
Seq. No.
Seq. ID
                  LIB3165-004-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q131397
BLAST score
                  320
                  1.0e-29
E value
                  120
Match length
                  58
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi_81480_pir__S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                  [Spinacia oleracea]
                  221002
Seq. No.
                  LIB3165-004-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  616
E value
                  2.0e-64
                  116
Match length
% identity
                  98
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  221003
Seq. No.
                  LIB3165-004-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2493146
BLAST score
                  396
                   1.0e-38
E value
Match length
                  94
% identity
                   56
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                   [Gossypium hirsutum] >qi 4519415 dbj BAA75542.1 (AB024275)
                   vácuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                   221004
                  LIB3165-004-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g18058
BLAST score
                  211
E value
                   1.0e-115
                  274
Match length
                   94
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
Seq. No.
                   221005
```

Seq. ID LIB3165-004-P1-K1-E4

Method BLASTN NCBI GI g2687437 BLAST score 33

E value 2.0e-09



```
Match length
                   90
                   82
% identity
NCBI Description
                  Jepsonia parryi large subunit 26S ribosomal RNA gene,
                  partial sequence
                  221006
Seq. No.
                  LIB3165-004-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2623881
BLAST score
                  223
E value
                  3.0e-18
Match length
                  48
                  94
% identity
                 (AF031318) catalase [Raphanus sativus]
NCBI Description
                  221007
Seq. No.
                  LIB3165-004-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  g487046
NCBI GI
BLAST score
                   304
E value
                  8.0e-28
Match length
                  118
                   55
% identity
                  photosystem I chain II precursor - wood tobacco
NCBI Description
                  >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
                   221008
Seq. No.
                  LIB3165-004-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g166834
BLAST score
                   557
E value
                   5.0e-60
Match length
                  127
% identity
                   89
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
                   221009
Seq. No.
Seq. ID
                   LIB3165-004-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q68200
BLAST score
                   351
E value
                   3.0e-33
Match length
                   93
% identity
                   80
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi 22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
```

Seq. No. 221010

Seq. ID LIB3165-004-P1-K1-F4

Method BLASTX NCBI GI q2864617 BLAST score 283 E value 2.0e-25



```
Match length 127
% identity 48
NCBI Description (AL
```

(AL021811) H+-transporting ATP synthase chain9 - like

protein [Arabidopsis thaliana]

Seq. No. 221011

Seq. ID LIB3165-004-P1-K1-F6

Method BLASTX
NCBI GI g4106696
BLAST score 264
E value 4.0e-23
Match length 64
% identity 81

NCBI Description (AB021872) ribosome-sedimenting protein [Pisum sativum]

Seq. No. 221012

Seq. ID LIB3165-004-P1-K1-F7

Method BLASTX
NCBI GI g2894306
BLAST score 466
E value 8.0e-47
Match length 121
% identity 80

NCBI Description (AJ223329) ubiquitin extension protein [Nicotiana tabacum]

Seq. No. 221013

Seq. ID LIB3165-004-P1-K1-F8

Method BLASTX
NCBI GI g1053047
BLAST score 506
E value 2.0e-51
Match length 102
% identity 100

NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)

histone H3 [Glycine max] >gi_1053051 (U38427) histone H3

[Glycine max]

Seq. No. 221014

Seq. ID LIB3165-004-P1-K1-G10

Method BLASTX
NCBI GI g1170897
BLAST score 343
E value 1.0e-32
Match length 82
% identity 83

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi_1076276_pir__S52039 NAD-malate_dehydrogenase - cucumber

>gi_695311 (L31900) glyoxysomal malate dehydrogenase

[Cucumis sativus]

Seq. No. 221015

Seq. ID LIB3165-004-P1-K1-G4

Method BLASTX
NCBI GI g4376650
BLAST score 268
E value 1.0e-23
Match length 81

NCBI Description

Seq. No.



```
% identity
                  (AE001621) GcpE Protein [Chlamydia pneumoniae]
NCBI Description
                   221016
Seq. No.
                  LIB3165-004-P1-K1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1129145
BLAST score
                   225
                   1.0e-18
E value
Match length
                   73
% identity
                   62
                  (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
NCBI Description
Seq. No.
                   221017
                  LIB3165-004-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   g131385
NCBI GI
                   525
BLAST score
                   1.0e-53
E value
                   125
Match length
                   86
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
                   221018
Seq. No.
Seq. ID
                   LIB3165-004-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g228403
BLAST score
                   456
E value
                   1.0e-45
                   108
Match length
                   81
% identity
NCBI Description glycolate oxidase [Lens culinaris]
                   221019
Seq. No.
Seq. ID
                   LIB3165-004-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q486827
BLAST score
                   236
E value
                   8.0e-20
Match length
                   104
                   60
% identity
NCBI Description translation elongation factor Tu.B precursor, chloroplast -
                   wood tobacco
Seq. No.
                   221020
Seq. ID
                   LIB3165-004-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g1632831
BLAST score
                   426
E value
                   4.0e-42
                   95
Match length
% identity
                   87
```

31192

(Z49698) orf [Ricinus communis]



```
LIB3165-004-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g1256595
NCBI GI
                  283
BLAST score
                  2.0e-25
E value
                  87
Match length
                  60
% identity
                  (U38915) LytB [Synechocystis PCC6803]
NCBI Description
                  221022
Seq. No.
                  LIB3165-004-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1172664
                  180
BLAST score
                  2.0e-13
E value
Match length
                  39
                  90
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_419791_pir__S31165 photosystem I chain III precursor -
                  Flaveria trinervia >gi_298482_bbs_127083 photosystem I
                  reaction center subunit III, PSI-RC PsaF [Flaveria
                  trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                  I subunit III [Flaveria trinervīa]
                  221023
Seq. No.
                  LIB3165-004-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  g3024127
NCBI GI
                   311
BLAST score
                   3.0e-50
E value
                   119
Match length
                   92
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                  >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
Seq. No.
                   221024
                   LIB3165-004-P1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g289920
BLAST score
                   566
                   2.0e-58
E value
Match length
                   103
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   221025
Seq. No.
                   LIB3165-005-P1-K1-A12
Seq. ID
Method
                   BLASTX
                   g1354515
NCBI GI
                   235
BLAST score
                   9.0e-20
E value
```

121

47

Match length % identity



```
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
                  221026
Seq. No.
Seq. ID
                  LIB3165-005-P1-K1-A2
Method
                  BLASTN
NCBI GI
                   q2062691
BLAST score
                   35
                   3.0e-10
E value
Match length
                   35
                  100
% identity
NCBI Description
                  Human sodium phosphate transporter (NPT4) mRNA, complete
Seq. No.
                   221027
Seq. ID
                   LIB3165-005-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q4106657
BLAST score
                   315
                   4.0e-31
E value
Match length
                   122
                   60
% identity
                  (AL035064) activator 1 subunit (replication factor subunit)
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   221028
                   LIB3165-005-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2505876
BLAST score
                   349
                   5.0e-33
E value
                   103
Match length
                   66
% identity
                  (Y12776) MYB-related protein [Arabidopsis thaliana]
NCBI Description
                   221029
Seq. No.
                   LIB3165-005-P1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3193285
BLAST score
                   236
                   5.0e-27
E value
                   115
Match length
% identity
                   54
NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
                   221030
Seq. No.
                   LIB3165-005-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   g100200
NCBI GI
BLAST score
                   243
                   9.0e-21
E value
                   82
Match length
                   61
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
```

31194

221031

LIB3165-005-P1-K1-A9

Seq. No.

Seq. ID

% identity

59



```
Method
                  BLASTX
NCBI GI
                  g2501353
BLAST score
                  243
                  1.0e-20
E value
                  52
Match length
                  90
% identity
NCBI Description
                 TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300
                  transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
                  (fragment) >gi 664901 emb CAA86607 (Z46646) transketolase
                  [Craterostigma plantagineum]
                  221032
Seq. No.
Seq. ID
                  LIB3165-005-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2764396
BLAST score
                  476
                  4.0e-51
E value
Match length
                  109
% identity
                  90
                 (AJ000004) starch branching enzyme II, SBE-II [Solanum
NCBI Description
                  tuberosum]
                  221033
Seq. No.
Seq. ID
                  LIB3165-005-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3036945
BLAST score
                  449
E value
                  6.0e-45
Match length
                  104
% identity
                  90
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
Seq. No.
                  221034
                  LIB3165-005-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821...
BLAST score
                  488
E value
                  2.0e-49
Match length
                  94
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221035
Seq. No.
Seq. ID
                  LIB3165-005-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3023752
BLAST score
                  298
E value
                  4.0e-27
Match length
                  108
```

31195

NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

495

128

q125578

4.0e-50



```
Seq. No.
                   221036
Seq. ID
                   LIB3165-005-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   535
E value
                    7.0e-55
Match length
                   102
% identity
                    98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >qi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                    221037
                   LIB3165-005-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   563
E value
                    4.0e-58
Match length
                   108
% identity
                    99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor - upland cotton >gi 450505 emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                    221038
Seq. ID
                   LIB3165-005-P1-K1-B6
Method
                   BLASTX
NCBI GI
                    q289920
BLAST score
                    563
E value
                    3.0e-58
Match length
                   104
                    100
% identity
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
                    221039
Seq. No.
Seq. ID
                   LIB3165-005-P1-K1-C10
                   BLASTX
Method
NCBI GI
                    g3785986
BLAST score
                    162
E value
                    4.0e-11
                    78
Match length
% identity
NCBI Description (AC005560) RGA1 protein [Arabidopsis thaliana]
Seq. No.
                    221040
                   LIB3165-005-P1-K1-C12
Seq. ID
```



% identity 74 PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) NCBI Description (PRK) >gi 167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum] 221041 Seq. No. LIB3165-005-P1-K1-C2 Seq. ID Method BLASTX g3202030 NCBI GI BLAST score 395 2.0e-38 E value Match length 126 % identity 67 (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum NCBI Description crystallinum] Seq. No. 221042 Seq. ID LIB3165-005-P1-K1-C3 Method BLASTX NCBI GI g1352821 BLAST score 506 2.0e-51 E value Match length 96 % identity 100 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 221043 Seq. No. LIB3165-005-P1-K1-C4 Seq. ID Method BLASTX NCBI GI g289920 BLAST score 653 1.0e-68 E value 122 Match length 99 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum]

221044 Seq. No.

LIB3165-005-P1-K1-C7 Seq. ID

Method BLASTX NCBI GI g505482 BLAST score 472 2.0e-47 E value Match length 117 83 % identity

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

221045 Seq. No.

LIB3165-005-P1-K1-C8 Seq. ID

Method BLASTX NCBI GI g289920 BLAST score 577



E value 7.0e-60 Match length 109 % identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221046

LIB3165-005-P1-K1-C9 Seq. ID

Method BLASTX NCBI GI g289920 BLAST score 674 E value 4.0e-71Match length 128 98 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

Seq. No. 221047

LIB3165-005-P1-K1-D1 Seq. ID

Method BLASTN NCBI GI q18058 BLAST score 305 E value 1.0e-171 Match length 344

% identity NCBI Description Citrus limon cistron for 26S ribosomal RNA

Seq. No. 221048

Seq. ID LIB3165-005-P1-K1-D10

97

Method BLASTX NCBI GI q289920 593 BLAST score 1.0e-61 E value Match length 112 97 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

221049 Seq. No.

LIB3165-005-P1-K1-D11 Seq. ID

Method BLASTX NCBI GI g4406530 BLAST score 337 1.0e-31 E value Match length 88 % identity 78

NCBI Description (AF126870) rubisco activase [Vigna radiata]

221050 Seq. No.

LIB3165-005-P1-K1-D4 Seq. ID

Method BLASTX g100616 NCBI GI BLAST score 437 E value 2.0e-43 Match length 117 68 % identity

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -



barley >gi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi 167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

221051 Seq. No.

LIB3165-005-P1-K1-D7 Seq. ID

Method BLASTX g4454459 NCBI GI 552 BLAST score 7.0e-57 E value Match length 126 % identity 82

(AC006234) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 221052

LIB3165-005-P1-K1-D9 Seq. ID

Method BLASTX q4210948 NCBI GI 597 BLAST score 4.0e-62 E value Match length 115 % identity 97

(AF085275) DnaJ protein [Hevea brasiliensis] NCBI Description

Seq. No. 221053

LIB3165-005-P1-K1-E1 Seq. ID

Method BLASTN g2687435 NCBI GI 74 BLAST score 6.0e-34 E value Match length 82 98 % identity

NCBI Description Hamamelis virginiana large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 221054

LIB3165-005-P1-K1-E10 Seq. ID

Method BLASTX g1352821 NCBI GI 365 BLAST score E value 5.0e - 3575 Match length 96 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

221055 Seq. No.

Seq. ID LIB3165-005-P1-K1-E11

Method BLASTX NCBI GI g4406530 BLAST score 330 E value 8.0e-31 Match length 90



98

% identity

```
% identity
                  76
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  221056
Seq. No.
                  LIB3165-005-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539351
BLAST score
                  166
                  1.0e-11
E value
Match length
                  59
% identity
                  63
                 (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  221057
                  LIB3165-005-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  419
                  3.0e-41
E value
Match length
                  112
                  73
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  221058
Seq. No.
                  LIB3165-005-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267120
BLAST score
                  189
                  2.0e-14
E value
Match length
                  83
                  54
% identity
NCBI Description
                  THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi 100070 pir S20929
                  thioredoxin f precursor - garden pea
                  >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum
                  satīvum] >gi 1388086 (U35830) thioredoxin f [Pisum satīvum]
Seq. No.
                  221059
                  LIB3165-005-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  520
E value
                  2.0e-53
Match length
                  95
                  99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  221060
Seq. ID
                  LIB3165-005-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3869088
BLAST score
                  639
E value
                  5.0e-67
Match length
                  126
```

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]



221061 Seg. No.

LIB3165-005-P1-K1-F12 Seq. ID

Method BLASTX NCBI GI q1352821 516 BLAST score E value 1.0e-52 Match length 100 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

221062 Seq. No.

Seq. ID LIB3165-005-P1-K1-F2

Method BLASTX NCBI GI q289920 BLAST score 447 E value 1.0e-44 Match length 121 98 % identity

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

221063 Seq. No.

Seq. ID LIB3165-005-P1-K1-F3

Method BLASTX g417103 NCBI GI BLAST score 355 E value 2.0e-56 Match length 119

% identity 99

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 ($\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa] >gi_488569 (\overline{U} 09461) histone

H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana

tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 221064

LIB3165-005-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI g2760834



BLAST score 502 E value 5.0e-51 Match length 127 % identity 76

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

Seq. No. 221065

Seq. ID LIB3165-005-P1-K1-F5

Method BLASTX
NCBI GI g2827715
BLAST score 335
E value 2.0e-31
Match length 79
% identity 84

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 221066

Seq. ID LIB3165-005-P1-K1-F6

Method BLASTX
NCBI GI g1168411
BLAST score 358
E value 4.0e-34
Match length 94

% identity 80

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 221067

Seq. ID LIB3165-005-P1-K1-F8

Method BLASTX
NCBI GI g2677828
BLAST score 370
E value 2.0e-35
Match length 101
% identity 67

NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 221068

Seq. ID LIB3165-005-P1-K1-G10

Method BLASTX
NCBI GI g1352821
BLAST score 538
E value 3.0e-55
Match length 106
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221069

Seq. ID LIB3165-005-P1-K1-G2

Method BLASTX NCBI GI g1353352 BLAST score 322



E value 7.0e-30 Match length 87

75 % identity

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

221070 Seq. No.

Seq. ID LIB3165-005-P1-K1-G4

BLASTX Method q3075488 NCBI GI 325 BLAST score 3.0e-30 E value Match length 110

58 % identity

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 221071

LIB3165-005-P1-K1-G6 Seq. ID

Method BLASTX q167367 NCBI GI 607 BLAST score 3.0e-63 E value 131 Match length % identity 91

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

221072 Seq. No.

LIB3165-005-P1-K1-G7 Seq. ID

Method BLASTX NCBI GI q1168411 BLAST score 345 8.0e-33 E value Match length 89 81 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 221073

LIB3165-005-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 324 2.0e-30 E value Match length 63 98 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC $\overline{4.1.1.39}$) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221074

LIB3165-005-P1-K1-H1 Seq. ID

BLASTX Method q2829916 NCBI GI BLAST score 267 2.0e-23 E value 55 Match length

% identity NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana] 221075 Seq. No. LIB3165-005-P1-K1-H10 Seq. ID Method BLASTX NCBI GI q2811025 BLAST score 318 2.0e-29 E value Match length 98 % identity 67 NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607 (AB002695) aspartic endopeptidase [Cucurbita pepo] Seq. No. 221076 Seq. ID LIB3165-005-P1-K1-H2 Method BLASTX NCBI GI g4406530 BLAST score 306 E value 5.0e-28 Match length 85 74 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] Seq. No. 221077 Seq. ID LIB3165-005-P1-K1-H4 Method BLASTX NCBI GI q3738295 BLAST score 282 E value 3.0e-25 Match length 119 % identity 54 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] Seq. No. 221078 LIB3165-005-P1-K1-H5 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g4210948
BLAST score 416
E value 6.0e-41
Match length 83
% identity 96

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 221079

Seq. ID LIB3165-005-P1-K1-H6

Method BLASTX
NCBI GI g551047
BLAST score 364
E value 4.0e-35
Match length 93
% identity 76

NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 221080

Seq. ID LIB3165-005-P1-K1-H7

Method BLASTX



```
NCBI GI
                   g3158476
BLAST score
                   547
E value
                   3.0e-56
Match length
                   120
                   87
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                   221081
Seq. No.
                   LIB3165-006-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1084372
BLAST score
                   637
E value
                   7.0e-67
Match length
                   126
% identity
                   96
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC
                   1.2.1.9) - garden pea
Seq. No.
                   221082
                   LIB3165-006-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2239089
BLAST score
                   223
E value
                   3.0e-18
Match length
                   108
% identity
                   40
NCBI Description
                  (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus] >gi 3288180 emb CAB11466 (Z98758)
                   anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
Seq. No.
                   221083
Seq. ID
                   LIB3165-006-P1-K1-A12
Method
                   BLASTX
                   g3882081
NCBI GI
BLAST score
                   579
E value
                   5.0e-60
Match length
                   120
% identity
                   37
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
Seq. No.
                   221084
                   LIB3165-006-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1353352
BLAST score
                   196
E value
                   3.0e-15
Match length
                   53
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                   221085
Seq. ID
                  LIB3165-006-P1-K1-A6
```

Method BLASTX NCBI GI g136707 BLAST score 415



E value 8.0e-41 Match length 116 % identity 70

NCBI Description CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR

(RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__\$26199

plastoquinol--plastocyanin reductase (\overline{EC} 1.10. $\overline{9}$ 9.1)

iron-sulfur protein precursor - garden pea

>gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS

protein [Pisum sativum]

Seq. No. 221086

Seq. ID LIB3165-006-P1-K1-B11

Method BLASTX
NCBI GI g115765
BLAST score 394
E value 2.0e-38
Match length 92
% identity 77

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546 prf 1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 221087

Seq. ID LIB3165-006-P1-K1-B12

Method BLASTX
NCBI GI g4406530
BLAST score 280
E value 5.0e-25
Match length 101
% identity 61

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221088

Seq. ID LIB3165-006-P1-K1-B2

Method BLASTX
NCBI GI g1657617
BLAST score 334
E value 3.0e-31
Match length 82
% identity 77

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)

putative nuclear DNA-binding protein G2p [Arabidopsis

thaliana]

Seq. No. 221089

Seq. ID LIB3165-006-P1-K1-B3

Method BLASTX
NCBI GI 93822036
BLAST score 215
E value 2.0e-17
Match length 110
% identity 46

V25.

BLAST score

Match length

E value

35

75

3.0e-10



```
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                   221090
Seq. No.
Seq. ID
                   LIB3165-006-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g1928981
BLAST score
                   485
E value
                   5.0e-49
Match length
                   107
% identity
                   89
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
Seq. No.
                   221091
Seq. ID
                   LIB3165-006-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q2529342
BLAST score
                   237
E value
                   1.0e-22
Match length
                   100
% identity
                   58
NCBI Description (L76554) transketolase [Spinacia oleracea]
                   221092
Seq. No.
Seq. ID
                   LIB3165-006-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g4406814
BLAST score
                   303
E value
                   1.0e-27
Match length
                   75
% identity
NCBI Description
                  (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                   thaliana]
Seq. No.
                   221093
Seq. ID
                   LIB3165-006-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g121080
BLAST score
                   496
E value
                   3.0e-50
Match length
                   115
% identity
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                   >gi_1070638_pir_ GCPMH glycine cleavage system protein H
                   precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H
                   protein [Pisum sativum] >g\overline{1}_1690\overline{9}3 (\overline{J}05164) H-protein of
                   glycine decarboxylase precursor (EC 2.1.2.10) [Pisum
                   sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum
                   sativum]
Seq. No.
                   221094
Seq. ID
                   LIB3165-006-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g602358
```

% identity 87

NCBI Description P.sativum mRNA for type II chlorophyll a/b binding protein

Seq. No.

221095

Seq. ID LIB3165-006-P1-K1-C2

Method BLASTX
NCBI GI g2911085
BLAST score 328
E value 1.0e-30
Match length 118
% identity 62

NCBI Description (AL021960) photosystem II oxygen-evolving complex protein 3

- like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3

- like [Arabidopsis thaliana]

Seq. No. 221096

Seq. ID LIB3165-006-P1-K1-C6

Method BLASTX
NCBI GI g115765
BLAST score 248
E value 3.0e-21
Match length 74
% identity 66

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546 prf 1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 221097

Seq. ID LIB3165-006-P1-K1-C9

Method BLASTX
NCBI GI g2369714
BLAST score 565
E value 2.0e-58
Match length 118
% identity 88

NCBI Description (297178) elongation factor 2 [Beta vulgaris]

Seq. No. 221098

Seq. ID LIB3165-006-P1-K1-D2

Method BLASTX
NCBI GI g115765
BLAST score 528
E value 5.0e-54
Match length 123
% identity 49

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A



chlorophyll a/b binding protein II [Lycopersicon esculentum]

221099 Seq. No. LIB3165-006-P1-K1-D3 Seq. ID BLASTX Method NCBI GI g1172664 BLAST score 190 2.0e-14 E value 41 Match length 90 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi 419791 pir S31165 photosystem I chain III precursor -Flaveria trinervia >gi 298482 bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem I subunit III [Flaveria trinervia] 221100 Seq. No. LIB3165-006-P1-K1-D4 Seq. ID BLASTN Method g4545261 NCBI GI BLAST score 331 0.0e + 00E value 375 Match length 97 % identity Gossypium hirsutum metallothionein-like protein mRNA, NCBI Description complete cds Seq. No. 221101 LIB3165-006-P1-K1-D6 Seq. ID BLASTX Method NCBI GI g3894183 BLAST score 168 7.0e-12 E value Match length 107 39 % identity (AC005662) calmodulin-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 221102

LIB3165-006-P1-K1-D7 Seq. ID

BLASTX Method q1709651 NCBI GI BLAST score 364 6.0e-35 E value 97 Match length 71 % identity

PLASTOCYANIN A PRECURSOR >gi 2117431 pir_ S58209 NCBI Description

plastocyanin a precursor - black poplar

>gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 221103

LIB3165-006-P1-K1-E10 Seq. ID

BLASTX Method NCBI GI g1362086



```
BLAST score
                  632
                  3.0e-66
E value
                  122
Match length
                  97
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 886471 emb CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
                  221104
Seq. No.
                  LIB3165-006-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549063
                  321
BLAST score
                  8.0e-30
E value
```

E value 8.0e-30

Match length 102

% identity 63

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

...

21kd polypeptide [Oryza sativa]

Seq. No. 221105

Seq. ID LIB3165-006-P1-K1-E2

Method BLASTX
NCBI GI g2511691
BLAST score 385
E value 2.0e-37
Match length 119
% identity 64

NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 221106

Seq. ID LIB3165-006-P1-K1-E3

Method BLASTX
NCBI GI g167097
BLAST score 610
E value 1.0e-63
Match length 126
% identity 92

NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase

[Hordeum vulgare]

Seq. No. 221107

Seq. ID LIB3165-006-P1-K1-E4

Method BLASTX
NCBI GI g1168411
BLAST score 292
E value 2.0e-26
Match length 92
% identity 72

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 221108

```
LIB3165-006-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914136
BLAST score
                  240
E value
                  3.0e-20
Match length
                  107
                  45
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein
                   [Cicer arietinum]
Seq. No.
                  221109
Seq. ID
                  LIB3165-006-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  314
E value
                  5.0e-29
Match length
                  90
                  61
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  221110
                  LIB3165-006-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928543
BLAST score
                  387
E value
                  2.0e-37
Match length
                  103
% identity
                  66
NCBI Description
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  221111
Seq. ID
                  LIB3165-006-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  468
E value
                   5.0e-47
Match length
                  91
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221112
Seq. ID
                  LIB3165-006-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3928089
```

Method BLASTX
NCBI GI g3928089
BLAST score 358
E value 4.0e-34
Match length 116
% identity 65

NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No. 221113



Seq. ID LIB3165-006-P1-K1-F4 Method BLASTX g1352821 NCBI GI BLAST score 510 6.0e - 52E value Match length 98 98 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 221114 LIB3165-006-P1-K1-F5 Seq. ID Method BLASTX q1771778 NCBI GI BLAST score 551 9.0e-57E value Match length 127 % identity 79 (X99320) 23 kDa oxygen evolving protein of photosystem II NCBI Description [Solanum tuberosum] Seq. No. 221115 LIB3165-006-P1-K1-F9 Seq. ID Method BLASTX NCBI GI q4406530 BLAST score 311 1.0e-28 E value 85 Match length 75 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] 221116 Seq. No. LIB3165-006-P1-K1-G1 Seq. ID Method BLASTX NCBI GI g231610 BLAST score 167 1.0e-11 E value Match length 67 54 % identity NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi 67880 pir PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum] Seq. No. 221117 LIB3165-006-P1-K1-G11 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g2935298
BLAST score 328
E value 1.0e-30
Match length 98
% identity 66

NCBI Description (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase



1 [Gossypium hirsutum]

 Seq. No.
 221118

 Seq. ID
 LIB3165-006-P1-K1-G12

 Method
 BLASTX

 NCBI GI
 q231610

NCBI GI g231610
BLAST score 274
E value 3.0e-24
Match length 101
% identity 60

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 221119

Seq. ID LIB3165-006-P1-K1-G4

Method BLASTX
NCBI GI g100203
BLAST score 361
E value 2.0e-34
Match length 91
% identity 77

NCBI Description cysteine proteinase (EC 3.4.22.-) precursor - tomato

>gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine

proteinase [Lycopersicon esculentum]

Seq. No. 221120

Seq. ID LIB3165-006-P1-K1-G5

Method BLASTX
NCBI GI g445116
BLAST score 571
E value 4.0e-59
Match length 122
% identity 89

NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No. 221121

Seq. ID LIB3165-006-P1-K1-G6

Method BLASTX
NCBI GI g430947
BLAST score 589
E value 3.0e-61
Match length 123
% identity 88

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 221122

Seq. ID LIB3165-006-P1-K1-G7

Method BLASTX
NCBI GI g3033513
BLAST score 380
E value 1.0e-36
Match length 109
% identity 70

% identity

99

```
NCBI Description (AF041068) rubisco activase [Phaseolus vulgaris]
Seq. No.
                  221123
                  LIB3165-006-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  q585322
NCBI GI
BLAST score
                  151
                  7.0e-10
E value
                  58
Match length
                  45
% identity
                 INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE)
NCBI Description
                  (PPASE) >gi 539751 pir A45153 inorganic pyrophosphatase
                  (EC 3.6.1.1) - bovine
Seq. No.
                  221124
Seq. ID
                  LIB3165-006-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q4512667
                  550
BLAST score
                  1.0e-56
E value
                  127
Match length
                  79
% identity
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  221125
                  LIB3165-006-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  317
E value
                  3.0e-29
                  109
Match length
                  62
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  221126
Seq. No.
Seq. ID
                  LIB3165-006-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3582333
BLAST score
                  466
                  9.0e-47
E value
Match length
                  119
% identity
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  221127
                  LIB3165-006-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  468
E value
                  6.0e-47
Match length
                  91
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) $>gi_279581_pir_RKCNSU$ ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Match length

% identity

```
221128
Seq. No.
Seq. ID
                  LIB3165-006-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g131385
BLAST score
                  512
                  3.0e-52
E value
Match length
                  128
% identity
                  81
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
                   221129
Seq. No.
                  LIB3165-006-P1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2244811
BLAST score
                   226
E value
                   1.0e-18
Match length
                   107
% identity
                   56
                  (Z97336) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   221130
                  LÌB3165-006-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g100200
BLAST score
                   345
E value
                   1.0e-32
Match length
                   98
                   68
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                   221131
                   LIB3165-006-P1-K2-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1084372
BLAST score
                   741
                   7.0e-79
E value
                   145
Match length
                   97
% identity
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC
                   1.2.1.9) - garden pea
                   221132
Seq. No.
                   LIB3165-006-P1-K2-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2239089
BLAST score
                   293
E value
                   3.0e-26
```

NCBI Description (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180 emb_CAB11466_ (Z98758)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

137

```
Seq. No.
                  221133
Seq. ID
                  LIB3165-006-P1-K2-A12
Method
                  BLASTX
NCBI GI
                  q1076708
BLAST score
                  669
                  2.0e-70
E value
Match length
                  138
% identity
                  27
NCBI Description
                  seed tetraubiquitin - common sunflower
                  >gi 303901 dbj BAA03764 (D16248) ubiquitin [Glycine max]
                  >gi 456714 dbj BAA05670 (D28123) Ubiquitin [Glycine max]
                  >gi 556688 emb CAA84440 (Z34988) seed tetraubiquitin
                  [Helianthus annuus] >gi 994785 dbj BAA05085 (D26092)
                  Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                  putative polyubiquitin [Arabidopsis thaliana]
                  >gi 1096513 prf 2111434A tetraubiquitin [Helianthus
                  annuus]
Seq. No.
                  221134
Seq. ID
                  LIB3165-006-P1-K2-A3
Method
                  BLASTN
NCBI GI
                  g1498381
BLAST score
                  37
E value
                  7.0e-12
Match length
                  68
                  90
% identity
NCBI Description Zea mays actin (Maz95) gene, partial cds
Seq. No.
                  221135
                  LIB3165-006-P1-K2-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136707
BLAST score
                  651
E value
                  3.0e-68
Match length
                  162
                  75
% identity
                 CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                  (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397 pir S26199
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  iron-sulfur protein precursor - garden pea
                  >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS
                  protein [Pisum sativum]
Seq. No.
                  221136
                  LIB3165-006-P1-K2-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121344
BLAST score
                  259
E value
                  2.0e-22
Match length
                  87
                  57
% identity
```

31216

(GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)

>gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC
6.3.1.2) delta precursor, chloroplast - garden pea

>gi 169059 (M20664) glutamine synthetase (chloroplast GS2)

NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR

(EC 6.3.1.2) [Pisum sativum]

Seq. No. 221137 LIB3165-006-P1-K2-B1 Seq. ID Method BLASTX NCBI GI g1351208 BLAST score 175 E value 6.0e-13Match length 61 % identity 67 NCBI Description T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_1046266 (U25632) CCT-2 [Caenorhabditis elegans] Seq. No. 221138 Seq. ID LIB3165-006-P1-K2-B11 Method BLASTX NCBI GI g115765 BLAST score 809 1.0e-86 E value Match length 174 83 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201 pir S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi 19180 emb CAA32197 (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 226546 prf 1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum] 221139 Seq. No. Seq. ID LIB3165-006-P1-K2-B12 Method BLASTX g3914605 NCBI GI BLAST score 354 E value 4.0e-43Match length 156 % identity 64 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__\$39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica] Seq. No. 221140 Seq. ID LIB3165-006-P1-K2-B4 Method BLASTX NCBI GI q1928981 BLAST score 858 E value 2.0e-92 Match length 189 % identity

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 221141

Seq. ID LIB3165-006-P1-K2-B7



```
Method BLASTX
NCBI GI g1657617
BLAST score 600
E value 3.0e-62
Match length 138
% identity 82
```

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis

thaliana]

Seq. No. 221142

Seq. ID LIB3165-006-P1-K2-B8

Method BLASTX
NCBI GI g3822036
BLAST score 286
E value 2.0e-25
Match length 157
% identity 42

NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 221143

Seq. ID LIB3165-006-P1-K2-B9

Method BLASTX
NCBI GI 94406814
BLAST score 303
E value 8.0e-43
Match length 115
% identity 79

NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis

thaliana]

Seq. No. 221144

Seq. ID LIB3165-006-P1-K2-C10

Method BLASTX
NCBI GI g542100
BLAST score 723
E value 1.0e-76
Match length 165
% identity 84

NCBI Description H-protein - Flaveria pringlei >gi_2147453_pir__\$60195

H-protein precursor (clone HFC1) - Flaveria cronquistii >gi_437993_emb_CAA81073_ (Z25854) H-protein [Flaveria cronquistii] >gi_437999_emb_CAA81074_ (Z25855) H-protein [Flaveria pringlei] >gi_3688299_emb_CAB16912_ (Z99763)

H-protein [Flaveria pringlei]

Seq. No. 221145

Seq. ID LIB3165-006-P1-K2-C11

Method BLASTX
NCBI GI g115765
BLAST score 681
E value 9.0e-72
Match length 153
% identity 53

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_

(X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 226546 prf 1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

221146 Seq. No. LIB3165-006-P1-K2-C7 Seq. ID

Method BLASTX NCBI GI g131397 BLAST score 441 E value 1.0e-43Match length 172 % identity 57

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi 755802 emb CAA29056 (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597 prf 1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 221147

LIB3165-006-P1-K2-C8 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 304 E value 5.0e-28 Match length 61 97

% identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221148

LIB3165-006-P1-K2-D2 Seq. ID

Method BLASTX g115765 NCBI GI BLAST score 712 E value 2.0e-75 Match length 162 55 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 221149

LIB3165-006-P1-K2-D4 Seq. ID

Method BLASTN



NCBI GI g4545261 BLAST score 150 E value 8.0e-79 200 Match length 95 % identity Gossypium hirsutum metallothionein-like protein mRNA, NCBI Description complete cds Seq. No. 221150 Seq. ID

LIB3165-006-P1-K2-D6

Method BLASTX NCBI GI g3894183 BLAST score 309 4.0e-28 E value Match length 170 % identity 30

(AC005662) calmodulin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 221151

LIB3165-006-P1-K2-D7 Seq. ID

Method BLASTX NCBI GI g1709651 BLAST score 515 3.0e-52 E value Match length 132 % identity 73

PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209 NCBI Description

plastocyanin a precursor - black poplar

>gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus

nigra]

221152 Seq. No.

LIB3165-006-P1-K2-E10 Seq. ID

Method BLASTX NCBI GI g974782 960 BLAST score 1.0e-104 E value Match length 188 % identity 96

(Z49150) cobalamine-independent methionine synthase NCBI Description

[Solenostemon scutellarioides]

Seq. No. 221153

LIB3165-006-P1-K2-E11 Seq. ID

Method BLASTX NCBI GI g4193388 BLAST score 529 E value 5.0e-54 Match length 147 % identity 73

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 221154

Seq. ID LIB3165-006-P1-K2-E2

Method BLASTX NCBI GI g2511691



```
BLAST score
                  737
                  3.0e-78
E value
Match length
                  193
% identity
                  73
NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.
                  221155
                  LIB3165-006-P1-K2-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266893
BLAST score
                  523
E value
                  1.0e-53
Match length
                  103
                  94
% identity
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                  sativus]
Seq. No.
                  221156
                  LIB3165-006-P1-K2-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168411
BLAST score
                  635
E value
                  2.0e-66
Match length
                  157
                  82
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  221157
                  LIB3165-006-P1-K2-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3747111
BLAST score
                  197
                  2.0e-15
E value
Match length
                  67
% identity
                  54
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
Seq. No.
                  221158
                  LIB3165-006-P1-K2-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3928543
BLAST score
                  534
E value
                  2.0e-54
Match length
                  166
                  57
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
```

thaliana]

221159 Seq. No.

LIB3165-006-P1-K2-F10 Seq. ID

Method BLASTX g3894183 NCBI GI BLAST score 314 E value 1.0e-28



Match length 191 % identity 29

NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No. 221160

Seq. ID LIB3165-006-P1-K2-F12

Method BLASTX
NCBI GI g1352821
BLAST score 858
E value 2.0e-92
Match length 163
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221161

Seq. ID LIB3165-006-P1-K2-F2

Method BLASTX
NCBI GI g3928089
BLAST score 358
E value 5.0e-34
Match length 116
% identity 65

NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No. 221162

Seq. ID LIB3165-006-P1-K2-F4

Method BLASTX
NCBI GI g1352821
BLAST score 848
E value 3.0e-91
Match length 162
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221163

Seq. ID LIB3165-006-P1-K2-F5

Method BLASTX
NCBI GI g1771778
BLAST score 824
E value 2.0e-88
Match length 183
% identity 83

NCBI Description (X99320) 23 kDa oxygen evolving protein of photosystem II

[Solanum tuberosum]

Seq. No. 221164

Seq. ID LIB3165-006-P1-K2-F9

Method BLASTX NCBI GI g4406530

```
BLAST score
                    484
  E value
                    1.0e-48
                    132
  Match length
                    75
  % identity
  NCBI Description (AF126870) rubisco activase [Vigna radiata]
                    221165
  Seq. No.
                    LIB3165-006-P1-K2-G11
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2935298
  BLAST score
                    415
                    1.0e-40
  E value
                    132
  Match length
                    64
  % identity
  NCBI Description
                    (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
                    1 [Gossypium hirsutum]
                    221166
  Seq. No.
                    LIB3165-006-P1-K2-G12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g231610
  BLAST score
                    489
  E value
                    3.0e-49
                    152
  Match length
  % identity
                    68
  NCBI Description
                    ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                    >gi_67880_pir PWNTG H+-transporting ATP synthase (EC
                    3.6.1.34) gamma chain precursor, chloroplast - common
                    tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
                    (gamma subunit) [Nicotiana tabacum]
  Seq. No.
                    221167
                    LIB3165-006-P1-K2-G3
  Seq. ID
  Method
                    BLASTX
                    g2511693
  NCBI GI
  BLAST score
                    481
  E valuè
                    3.0e-48
  Match length
                    156
  % identity
                    63
  NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
  Seq. No.
                    221168
                    LIB3165-006-P1-K2-G4
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    g2511691
  BLAST score
                    521
  E value
                    4.0e-63
 Match length
                    154
  % identity
 NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
```

Seq. No. 221169

Seq. ID LIB3165-006-P1-K2-G5

Method BLASTX
NCBI GI g445116
BLAST score 947
E value 1.0e-103



```
Match length
                  195
% identity
                  92
NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]
Seq. No.
                  221170
                  LIB3165-006-P1-K2-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  661
E value
                  2.0e-69
Match length
                  162
% identity
                  82
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  221171
Seq. ID
                  LIB3165-006-P1-K2-G8
Method
                  BLASTX
NCBI GI
                  q585322
BLAST score
                  283
                  4.0e-25
E value
Match length
                  111
% identity
                  51
NCBI Description
                  INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE)
                  (PPASE) >gi 539751 pir A45153 inorganic pyrophosphatase
                  (EC 3.6.1.1) - bovine
Seq. No.
                  221172
Seq. ID
                  LIB3165-006-P1-K2-H1
Method
                  BLASTX
NCBI GI
                  g4512667
BLAST score
                  750
                  7.0e-80
E value
Match length
                  176
% identity
                  78
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  221173
Seq. ID
                  LIB3165-006-P1-K2-H10
Method
                  BLASTX
NCBI GI
                  g286001
BLAST score
                  194
                  1.0e-14
E value
Match length
                  149
% identity
                  32
NCBI Description (D13630) KIAA0005 [Homo sapiens]
                  221174
Seq. No.
Seq. ID
                  LIB3165-006-P1-K2-H11
Method
                  BLASTX
NCBI GI
                  g3914605
BLAST score
                  507
```

E value 3.0e-51 Match length 155 % identity 65

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

Authorities and

apple tree >gi_415852_emb_CAA79857_ (Z21794)
ribulose-1,5-bisphosphate carboxylase/oxygenase activase
[Malus domestica]

Seq. No. 221175

Seq. ID LIB3165-006-P1-K2-H2

Method BLASTX
NCBI GI g3482918
BLAST score 146
E value 3.0e-18
Match length 108
% identity 59

NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 221176

Seq. ID LIB3165-006-P1-K2-H3

Method BLASTX
NCBI GI g3582333
BLAST score 820
E value 5.0e-88

E value 5.0e-88
Match length 175
% identity 86

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 221177

Seq. ID LIB3165-006-P1-K2-H5

Method BLASTX
NCBI GI g1352821
BLAST score 837
E value 5.0e-90
Match length 159
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221178

Seq. ID LIB3165-006-P1-K2-H6

Method BLASTX
NCBI GI g100454
BLAST score 603
E value 9.0e-63
Match length 144
% identity 84

 ${\tt NCBI\ Description\ photosystem\ II\ oxygen-evolving\ complex\ protein\ 1\ -\ potato}$

>gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein

of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 221179

Seq. ID LIB3165-006-P1-K2-H7

Method BLASTX
NCBI GI g4103635
BLAST score 321
E value 2.0e-29



Match length 142 % identity 50

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No. 221180

Seq. ID LIB3165-006-P1-K2-H8

Method BLASTX
NCBI GI g2244811
BLAST score 238
E value 6.0e-20
Match length 129
% identity 51

NCBI Description (Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No. 221181

Seq. ID LIB3165-006-P1-K2-H9

Method BLASTX
NCBI GI g100200
BLAST score 634
E value 3.0e-66
Match length 152
% identity 64

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 221182

Seq. ID LIB3165-006-P1-K3-A10

Method BLASTX
NCBI GI g3914605
BLAST score 745
E value 4.0e-79
Match length 204
% identity 72

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 221183

Seq. ID LIB3165-006-P1-K3-A11

Method BLASTX
NCBI GI g121344
BLAST score 248
E value 3.0e-21
Match length 87
% identity 59

NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR

(GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)

>gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC
6.3.1.2) delta precursor, chloroplast - garden pea

>gi_169059 (M20664) glutamine synthetase (chloroplast GS2)

(EC 6.3.1.2) [Pisum sativum]

Seq. No. 221184

Seq. ID LIB3165-006-P1-K3-A12

Method BLASTX



```
NCBI GI
                    g1084372
  BLAST score
                    952
  E value
                    1.0e-103
 Match length
                    208
  % identity
                    88
                    glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC
 NCBI Description
                    1.2.1.9) - garden pea
  Seq. No.
                    221185
                    LIB3165-006-P1-K3-A2
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    g1353352
  BLAST score
                     424
                    1.0e-41
 E value
 Match length
                     121
  % identity
                    71
 NCBI Description
                    (U31975) alanine aminotransferase [Chlamydomonas
                    reinhardtii]
                    221186
  Seq. No.
                    LIB3165-006-P1-K3-A3
  Seq. ID
 Method
                    BLASTX
⇒ NCBI GI
                    q1531672
 BLAST score
                     642
                     3.0e-67
 E value
                    130
 Match length
                     94
  % identity
 NCBI Description (U68461) actin [Striga asiatica]
  Seq. No.
                    221187
  Seq. ID
                    LIB3165-006-P1-K3-A6
 Method
                    BLASTX
  NCBI GI
                     g136707
  BLAST score
                     702
                     3.0e-74
  E value
                     177
  Match length
                     75
  % identity
  NCBI Description
                   CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
                     (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397 pir S26199
                    plastoquinol--plastocyanin reductase (E\overline{C} \ 1.10.\overline{9}9.1)
                     iron-sulfur protein precursor - garden pea
                     >gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS
                     protein [Pisum sativum]
                     221188
  Seq. No.
                    LIB3165-006-P1-K3-A8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     g4206122
  BLAST score
                     321
  E value
                     1.0e-29
                    174
  Match length
  % identity
                     45
                    (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
  NCBI Description
                     crystallinum]
```

Seq. No. 221189

Seq. ID LIB3165-006-P1-K3-B1



```
Method
                  BLASTX
NCBI GI
                  g3024702
BLAST score
                  600
                  3.0e-62
E value
Match length
                  192
                  64
% identity
NCBI Description
                  T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) >qi 1871210
                   (U91327) T-complex protein 1, Beta subunit (TCP-1-BETA)
                  [Homo sapiens]
Seq. No.
                  221190
Seq. ID
                  LIB3165-006-P1-K3-B10
Method
                  BLASTX
NCBI GI
                  q3603456
BLAST score
                  711
                  3.0e-75
E value
Match length
                  144
% identity
                  30
NCBI Description (AF088848) polyubiquitin [Capsicum chinense]
                  221191
Seq. No.
                  LIB3165-006-P1-K3-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406814
BLAST score
                  303
                  1.0e-42
E value
Match length
                  115
                  79
% identity
NCBI Description
                  (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                  thaliana]
Seq. No.
                  221192
                  LIB3165-006-P1-K3-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1928981
BLAST score
                  834
                  1.0e-89
E value
Match length
                  178
% identity
                  69
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
                  221193
Seq. No.
Seq. ID
                  LIB3165-006-P1-K3-B6
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  682
                  7.0e-72
E value
Match length
                  173
                  76
% identity
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
```

Seq. No. 221194

Seq. ID LIB3165-006-P1-K3-B7

Method BLASTX NCBI GI G1657617



```
BLAST score
                  600
E value
                  3.0e-62
Match length
                  138
% identity
                  82
                  (U72503) G2p [Arabidopsis thaliana] >qi 3068707 (AF049236)
NCBI Description
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
                  221195
Seq. No.
                  LIB3165-006-P1-K3-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3822036
BLAST score
                  349
E value
                  9.0e-33
Match length
                  185
% identity
                  42
NCBI Description
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
Seq. No.
                  221196
                  LIB3165-006-P1-K3-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2239089
BLAST score
                  249
E value
                  3.0e-21
Match length
                  117
% identity
                  41
NCBI Description
                  (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus] >gi 3288180 emb CAB11466 (Z98758)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
Seq. No.
                  221197
Seq. ID
                  LIB3165-006-P1-K3-C10
Method
                  BLASTX
NCBI GI
                  g3914605
BLAST score
                  681
                  1.0e-71
E value
Match length
                  192
                  70
% identity
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857 (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Malus domestica]
Seq. No.
                  221198
Seq. ID
                  LIB3165-006-P1-K3-C11
Method
                  BLASTX
NCBI GI
                  g2369714
                  1035
```

Method BLASTX
NCBI GI g2369714
BLAST score 1035
E value 1.0e-113
Match length 219
% identity 90

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 221199



LIB3165-006-P1-K3-C12

Method BLASTX
NCBI GI g121080
BLAST score 444
E value 3.0e-44
Match length 108
% identity 81

Seq. ID

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

>gi_1070638_pir__GCPMH glycine cleavage system protein H
precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H
protein [Pisum sativum] >gi_169093 (J05164) H-protein of
glycine decarboxylase precursor (EC 2.1.2.10) [Pisum

sativum] >gi 287815 emb CAA37704 (X53656) H-protein [Pisum

sativum]

Seq. No. 221200

Seq. ID LIB3165-006-P1-K3-C7

Method BLASTX
NCBI GI g131397
BLAST score 443
E value 7.0e-44
Match length 172
% identity 56

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 221201

Seq. ID LIB3165-006-P1-K3-C8

Method BLASTX
NCBI GI g1352821
BLAST score 848
E value 3.0e-91
Match length 162
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221202

Seq. ID LIB3165-006-P1-K3-C9

Method BLASTX
NCBI GI g115765
BLAST score 849
E value 2.0e-91
Match length 182
% identity 83

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_

(X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon

esculentum]

221203 Seq. No.

Seq. ID LIB3165-006-P1-K3-D2

BLASTX Method NCBI GI g115765 BLAST score 872 4.0e-94 E value 188 Match length 59 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR NCBI Description

> (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197 (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] > gi 226546 prf 1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

221204 Seq. No.

LIB3165-006-P1-K3-D3 Seq. ID

Method BLASTX g3885892 NCBI GI BLAST score 202 4.0e-30 E value 97 Match length

75 % identity

NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 221205

LIB3165-006-P1-K3-D4 Seq. ID

Method BLASTX NCBI GI q4545262 BLAST score 239 4.0e-20 E value 44 Match length 100 % identity

NCBI Description (AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No. 221206

LIB3165-006-P1-K3-D6 Seq. ID

Method BLASTX NCBI GI g3894183 BLAST score 358 E value 8.0e-34191 Match length % identity 32

NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

221207 Seq. No.

Seq. ID LIB3165-006-P1-K3-D7

Method BLASTX



```
NCBI GI g1709651
BLAST score 500
E value 2.0e-50
Match length 129
% identity 74
```

NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209

plastocyanin a precursor - black poplar

>gi 929813 emb_CAA90564_ (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 221208

Seq. ID LIB3165-006-P1-K3-D8

Method BLASTN
NCBI GI g3869069
BLAST score 36
E value 1.0e-10
Match length 87

Match length 87 % identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 221209

Seq. ID LIB3165-006-P1-K3-D9

Method BLASTX
NCBI GI g115765
BLAST score 795
E value 4.0e-85
Match length 172
% identity 83

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546 prf 1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 221210

Seq. ID LIB3165-006-P1-K3-E11

Method BLASTX
NCBI GI g3747111
BLAST score 364
E value 8.0e-42
Match length 167
% identity 56

NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 221211

Seq. ID LIB3165-006-P1-K3-E12

Method BLASTX
NCBI GI g974782
BLAST score 995
E value 1.0e-108
Match length 195

% identity 96

NCBI Description (Z49150) cobalamine-independent methionine synthase



[Solenostemon scutellarioides]

```
Seq. No.
                   221212
Seq. ID
                   LIB3165-006-P1-K3-E2
Method
                   BLASTX
NCBI GI
                   q2511691
BLAST score
                   839
E value
                   3.0e-90
                   224
Match length
 % identity
                  (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   221213
                   LIB3165-006-P1-K3-E3
Seq. ID
                   BLASTX
Method
                   q3687652
NCBI GI
BLAST score
                   992
                   1.0e-108
E value
Match length
                   192
 % identity
                   97
NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]
                   221214
Seq. No.
Seq. ID
                   LIB3165-006-P1-K3-E4
Method
                   BLASTX
NCBI GI
                   g68200
BLAST score
                   747
                   2.0e-79
E value
Match length
                   179
 % identity
                   83
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >qi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
 Seq. No.
                   221215
                   LIB3165-006-P1-K3-E8
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914136
 BLAST score
                   268
 E value
                   3.0e-23
Match length
                   116
 % identity
                   46
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   >gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
                   [Cicer arietinum]
                   221216
 Seq. No.
                   LIB3165-006-P1-K3-F1
 Seq. ID
Method
                   BLASTX
                   q3928543
NCBI GI
 BLAST score
                   659
E value
                   4.0e-69
                   201
Match length
                   59
 % identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
```

thaliana]



```
221217
Seq. No.
Seq. ID
                  LIB3165-006-P1-K3-F11
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  701
                  5.0e-74
E value
                  173
Match length
% identity
                  81
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  221218
Seq. No.
Seq. ID
                  LIB3165-006-P1-K3-F12
                  BLASTX
Method
NCBI GI
                  g3894183
BLAST score
                  267
                  3.0e-23
E value
                  164
Match length
                  27
% identity
NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]
                  221219
Seq. No.
Seq. ID
                  LIB3165-006-P1-K3-F2
                  BLASTX
Method
NCBI GI
                  q3928089
BLAST score
                  358
                  8.0e-34
E value
                  116
Match length
                  65
% identity
NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]
                   221220
Seq. No.
                  LIB3165-006-P1-K3-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  848
                   3.0e-91
E value
Match length
                   162
                   96
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU-
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   221221
                  LIB3165-006-P1-K3-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1771778
BLAST score
                  832
E value
                   2.0e-89
Match length
                  183
                  83
```

% identity

NCBI Description (X99320) 23 kDa oxygen evolving protein of photosystem II

[Solanum tuberosum]

Seq. No. 221222

Seq. ID LIB3165-006-P1-K3-F9



```
Method BLASTX
NCBI GI g4193388
BLAST score 633
E value 5.0e-66
Match length 168
% identity 75
```

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 221223

Seq. ID LIB3165-006-P1-K3-G1

Method BLASTX
NCBI GI g231610
BLAST score 160
E value 1.0e-19
Match length 129
% identity 52

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 221224

Seq. ID LIB3165-006-P1-K3-G10

Method BLASTX
NCBI GI g1352821
BLAST score 724
E value 8.0e-77
Match length 149
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221225

Seq. ID LIB3165-006-P1-K3-G3

Method BLASTX
NCBI GI g2828252
BLAST score 381
E value 8.0e-41
Match length 141
% identity 63

NCBI Description (AJ003137) CYP1 [Lycopersicon esculentum]

Seq. No. 221226

Seq. ID LIB3165-006-P1-K3-G4

Method BLASTX
NCBI GI g2511691
BLAST score 521
E value 3.0e-72
Match length 170
% identity 79

NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]



221227 Seq. No. Seq. ID LIB3165-006-P1-K3-G5 Method BLASTX g421826 NCBI GI BLAST score 973 1.0e-106 E value 202 Match length % identity chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >gi 298036 emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana] 221228 Seq. No. Seq. ID LIB3165-006-P1-K3-G6 BLASTX Method q82080 NCBI GI BLAST score 916 3.0e-99 E value Match length 224 78 % identity chlorophyll a/b-binding protein type III precursor - tomato NCBI Description >gi 226872 prf 1609235A chlorophyll a/b binding protein [Lycopersicon esculentum] 221229 Seq. No. Seq. ID LIB3165-006-P1-K3-G7 BLASTX Method g4406530 NCBI GI BLAST score 705 1.0e-74 E value 171 Match length % identity 83 NCBI Description (AF126870) rubisco activase [Vigna radiata] 221230 Seq. No. LIB3165-006-P1-K3-G8 Seq. ID BLASTX Method q585322 NCBI GI BLAST score 398 E value 2.0e-38 147 Match length % identity 53 INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) NCBI Description (PPASE) >gi 539751 pir A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine 221231 Seq. No. LIB3165-006-P1-K3-H1 Seq. ID BLASTX Method NCBI GI g4512667 BLAST score 782 1.0e-83 E value

Match length 183 % identity

(AC006931) putative MAP kinase [Arabidopsis thaliana] NCBI Description

221232 Seq. No.

```
LIB3165-006-P1-K3-H10
Seq. ID
Method
                  BLASTX
                  q231610
NCBI GI
BLAST score
                  452
                  6.0e-45
E value
                  155
Match length
% identity
                  62
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
Seq. No.
                  221233
Seq. ID
                  LIB3165-006-P1-K3-H11
                  BLASTX
Method
NCBI GI
                  q100200
BLAST score
                  715
E value
                  5.0e-79
Match length
                  185
                  82
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  221234
Seq. No.
                  LIB3165-006-P1-K3-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  313
E value
                  7.0e-29
Match length
                  106
                  59
% identity
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
Seq. No.
                  221235
                  LIB3165-006-P1-K3-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3582333
BLAST score
                  730
E value
                  2.0e-77
Match length
                  175
% identity
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  221236
                  LIB3165-006-P1-K3-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  870
                  7.0e-94
E value
Match length
                  168
% identity
                  96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
```

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
221237
Seq. No.
Seq. ID
                  LIB3165-006-P1-K3-H6
                  {\tt BLASTX}
Method
                  g505482
NCBI GI
BLAST score
                  745
                  3.0e-79
E value
                  177
Match length
                  84
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                  photosystem II [Nicotiana tabacum]
                   221238
Seq. No.
                  LIB3165-006-P1-K3-H7
Seq. ID
                  {\tt BLASTX}
Method
                   g4103635
NCBI GI
                   432
BLAST score
                   2.0e-42
E value
                   162
Match length
                   56
% identity
                 (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                   221239
Seq. No.
                   LIB3165-006-P1-K3-H8
Seq. ID
                  BLASTX
Method
                   g2244811
NCBI GI
BLAST score
                   511
                   8.0e-52
E value
                   184
Match length
                   63
% identity
NCBI Description (297336) unnamed protein product [Arabidopsis thaliana]
                   221240
Seq. No.
                   LIB3165-006-P1-K3-H9
Seq. ID
Method
                   BLASTX
                   g2935300
NCBI GI
BLAST score
                   348
                   2.0e-41
E value
                   145
Match length
% identity
                  (AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                   2 [Gossypium hirsutum]
                   221241
Seq. No.
Sea. ID
                   LIB3165-006-P1-K4-A10
Method
                   BLASTX
                   g1084372
NCBI GI
BLAST score
                   931
                   1.0e-101
E value
Match length
                   208
% identity
                   87
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC
                   1.2.1.9) - garden pea
                   221242
Seq. No.
                   LIB3165-006-P1-K4-A11
Seq. ID
```

31238

BLASTX

Method



```
q2239089
NCBI GI
                  290
BLAST score
                  5.0e-26
E value
                  137
Match length
% identity
                  41
                  (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                  [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
Seq. No.
                  221243
                  LIB3165-006-P1-K4-A12
Seq. ID
                  BLASTX
Method
                  g100490
NCBI GI
                  748
BLAST score
                  1.0e-79
E value
                  153
Match length
% identity
                  33
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  221244
Seq. No.
                  LIB3165-006-P1-K4-A2
Seq. ID
Method
                  BLASTX
                  q1353352
NCBI GI
BLAST score
                  440
                  2.0e-43
E value
                  125
Match length
                  71
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  221245
Seq. No.
                  LIB3165-006-P1-K4-A3
Seq. ID
                  BLASTX
Method
                  g1531672
NCBI GI
BLAST score
                  644
E value
                  2.0e-67
                  131
Match length
                  93
% identity
NCBI Description (U68461) actin [Striga asiatica]
                  221246
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-A6
                  BLASTX
Method
NCBI GI
                  q136707
BLAST score
                   720
                  2.0e-76
E value
```

181 Match length 75 % identity

NCBI Description CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397 pir S26199

plastoquinol--plastocyanin reductase $(E\overline{C}\ 1.10.\overline{9}9.1)$

iron-sulfur protein precursor - garden pea

>gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS

protein [Pisum sativum]



```
221247
Seq. No.
                  LIB3165-006-P1-K4-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206122
                  378
BLAST score
                  4.0e-36
E value
Match length
                  175
                  46
% identity
                  (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                  crystallinum]
                  221248
Seq. No.
                  LIB3165-006-P1-K4-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121353
BLAST score
                  827
                  1.0e-88
E value
Match length
                  201
                  76
% identity
                  GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)
NCBI Description
                   (GLUTAMATE-AMMONIA LIGASE) >gi 68596_pir__AJFBQD
                  glutamate--ammonia ligase (EC 6.3.1.2) delta precursor,
                   chloroplast - kidney bean >gi_21005_emb_CAA31234_ (X12738)
                  GS precursor protein [Phaseolus vulgaris]
Seq. No.
                   221249
                  LIB3165-006-P1-K4-B1
Seq. ID
                  BLASTX
Method
                  g2559012
NCBI GI
BLAST score
                   497
E value
                   3.0e-50
                   155
Match length
% identity
                   65
                   (AF026293) chaperonin containing t-complex polypeptide 1,
NCBI Description
                   beta subunit; CCT-beta [Homo sapiens] >gi_4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
                   221250
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-B10
                   BLASTX
Method
NCBI GI
                   q4406814
BLAST score
                   243
                   4.0e-34
E value
                   115
Match length
                   68
% identity
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   221251
```

Seq. ID LIB3165-006-P1-K4-B11

Method BLASTX NCBI GI q115765 BLAST score 803 5.0e-86 E value Match length 174



% identity

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding

protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_

(X14036) chlorophyll a/b-binding protein [Lycopersicon

esculentum] >gi_170431 (M20241) chlorophyll a/b-binding

protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 221252

Seq. ID LIB3165-006-P1-K4-B12

Method BLASTX
NCBI GI g3914605
BLAST score 593
E value 2.0e-61
Match length 175
% identity 67

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 221253

Seq. ID LIB3165-006-P1-K4-B4

Method BLASTX
NCBI GI g1928981
BLAST score 880
E value 5.0e-95
Match length 198
% identity 89

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 221254

Seq. ID LIB3165-006-P1-K4-B6

Method BLASTX
NCBI GI g2529342
BLAST score 577
E value 1.0e-59
Match length 151
% identity 75

NCBI Description (L76554) transketolase [Spinacia oleracea]

Seq. No. 221255

Seq. ID LIB3165-006-P1-K4-B7

Method BLASTX
NCBI GI g1657617
BLAST score 593
E value 2.0e-61
Match length 152
% identity 74

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)

putative nuclear DNA-binding protein G2p [Arabidopsis

thaliana]



```
221256
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-B8
Method
                   BLASTX
                   g3822036
NCBI GI
BLAST score
                   357
                   1.0e-33
E value
                   185
Match length
                   43
% identity
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
NCBI Description
                   221257
Seq. No.
Seq. ID
                   LIB3165-006-P1-K4-B9
                   BLASTX
Method
                   g4406814
NCBI GI
BLAST score
                   303
                   1.0e-42
E value
                   115
Match length
                   79
% identity
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   221258
Seq. No.
                   LIB3165-006-P1-K4-C10
```

Seq. ID BLASTX Method NCBI GI g542100 723 BLAST score 1.0e-76 E value 165 Match length 84 % identity

NCBI Description H-protein - Flaveria pringlei >gi_2147453_pir___S60195 H-protein precursor (clone HFC1) - Flaveria cronquistii >gi 437993 emb CAA81073 (Z25854) H-protein [Flaveria cronquistii] >gi 437999 emb CAA81074 (Z25855) H-protein [Flaveria pringlei] >gi 3688299 emb CAB16912 (Z99763)

H-protein [Flaveria pringlei]

221259 Seq. No. LIB3165-006-P1-K4-C11 Seq. ID Method BLASTX q115765 NCBI GI BLAST score 759 E value 7.0e-81 167 Match length 56 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >qi 100201 pir S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi 19180 emb CAA32197 (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546 prf 1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

221260 Seq. No.

LIB3165-006-P1-K4-C7 Seq. ID

BLASTX Method



NCBI GI g131397 BLAST score 498 E value 3.0e-50 Match length 186 % identity 58

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 221261

Seq. ID LIB3165-006-P1-K4-C8

Method BLASTX
NCBI GI g1352821
BLAST score 679
E value 1.0e-71
Match length 134
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221262

Seq. ID LIB3165-006-P1-K4-C9

Method BLASTX
NCBI GI g2369714
BLAST score 859
E value 1.0e-92
Match length 181
% identity 89

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 221263

Seq. ID LIB3165-006-P1-K4-D2

Method BLASTX
NCBI GI g115765
BLAST score 708
E value 5.0e-75
Match length 161
% identity 54

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 221264

Seq. ID LIB3165-006-P1-K4-D3



Method BLASTX
NCBI GI g1172664
BLAST score 521
E value 5.0e-53
Match length 102
% identity 94

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_419791_pir__S31165 photosystem I chain III precursor Flaveria trinervia >gi_298482_bbs_127083 photosystem I
reaction center subunit III, PSI-RC PsaF [Flaveria

trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem

I subunit III [Flaveria trinervia]

Seq. No. 221265

Seq. ID LIB3165-006-P1-K4-D6

Method BLASTX
NCBI GI g3894183
BLAST score 342
E value 6.0e-32
Match length 184
% identity 31

NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No. 221266

Seq. ID LIB3165-006-P1-K4-D7

Method BLASTX
NCBI GI g1709651
BLAST score 515
E value 3.0e-52
Match length 132
% identity 73

NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209

plastocyanin a precursor - black poplar

>gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 221267

Seq. ID LIB3165-006-P1-K4-D8

Method BLASTN
NCBI GI g3869069
BLAST score 39
E value 2.0e-12
Match length 133
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 221268

Seq. ID LIB3165-006-P1-K4-E10

Method BLASTX
NCBI GI g974782
BLAST score 1097
E value 1.0e-120
Match length 216
% identity 96

NCBI Description (Z49150) cobalamine-independent methionine synthase

BLAST score

E value

268 3.0e-23



[Solenostemon scutellarioides]

```
221269
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-E11
                  BLASTX
Method
                  g549063
NCBI GI
                  598
BLAST score
                  5.0e-62
E value
                  161
Match length
                  72
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
                  221270
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-E2
                  BLASTX
Method
                  g2511691
NCBI GI
BLAST score
                  756
E value
                  2.0e-80
                  194
Match length
                  73
% identity
                  (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                  221271
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-E3
                  BLASTX
Method
                  g266893
NCBI GI
BLAST score
                  836
E value
                  5.0e-90
Match length
                  163
                  96
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                  satīvus]
Seq. No.
                  221272
                  LIB3165-006-P1-K4-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q68200
BLAST score
                   580
                   6.0e-60
E value
Match length
                   142
% identity
                  83
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   221273
Seq. No.
                  LIB3165-006-P1-K4-E8
Seq. ID
Method
                  BLASTX
                  q3914136
NCBI GI
```



Match length 116 % identity 46

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)

>gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein

[Cicer arietinum]

Seq. No. 221274

Seq. ID LIB3165-006-P1-K4-E9

Method BLASTX
NCBI GI g3747111
BLAST score 380
E value 2.0e-36
Match length 121
% identity 60

NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 221275

Seq. ID LIB3165-006-P1-K4-F1

Method BLASTX
NCBI GI g3928543
BLAST score 563
E value 7.0e-58
Match length 179
% identity 56

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 221276

Seq. ID LIB3165-006-P1-K4-F10

Method BLASTX
NCBI GI g3894183
BLAST score 347
E value 2.0e-32
Match length 196
% identity 32

NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No. 221277

Seq. ID LTB3165-006-P1-K4-F12

Method BLASTX
NCBI GI g1352821
BLAST score 819
E value 7.0e-88
Match length 166
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221278

Seq. ID LIB3165-006-P1-K4-F2

Method BLASTX
NCBI GI g3928089
BLAST score 358
E value 8.0e-34



```
Match length
                  116
                  65
% identity
                  (AC005770) putative osr40 [Arabidopsis thaliana]
NCBI Description
                  221279
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-F4
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                  848
                  3.0e-91
E value
                  162
Match length
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221280
Seq. No.
                  LIB3165-006-P1-K4-F5
Seq. ID
                  BLASTX
Method
                  q1771778
NCBI GI
BLAST score
                  824
                  2.0e-88
E value
                  183
Match length
                  83
% identity
                  (X99320) 23 kDa oxygen evolving protein of photosystem II
NCBI Description
                  [Solanum tuberosum]
                  221281
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-F9
                  BLASTX
Method
                  q4406530
NCBI GI
BLAST score
                   605
E value
                  8.0e-63
                  154
Match length
                  79
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  221282
                  LIB3165-006-P1-K4-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q461550
BLAST score
                   142
E value
                   1.0e-08
Match length
                   48
                   67
% identity
NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
                   >gi 81635 pir B39732 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma-1 chain precursor, chloroplast -
                   Arabidopsis thaliana >gi_166632 (M61741) ATP synthase
                   gamma-subunit [Arabidopsis thaliana]
```

Seq. No. 221283

Seq. ID LIB3165-006-P1-K4-G11

Method BLASTX NCBI GI g2935298



```
646
BLAST score
                  1.0e-67
E value
Match length
                  189
                  69
% identity
                  (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                  1 [Gossypium hirsutum]
                  221284
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-G12
                  BLASTX
Method
                  g231610
NCBI GI
BLAST score
                  447
                  2.0e-44
E value
                  153
Match length
                  62
% identity
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, chloroplast - common
                   tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
                   (gamma subunit) [Nicotiana tabacum]
                  221285
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-G3
                  BLASTX
Method
                  g2511693
NCBI GI
                   475
BLAST score
                  1.0e-47
E value
                  138
Match length
                   68
% identity
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
                   221286
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-G4
                  BLASTX
Method
NCBI GI
                   g2511691
BLAST score
                   521
                   5.0e-73
E value
                   174
Match length
% identity
                   79
NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
                   221287
Seq. No.
                   LIB3165-006-P1-K4-G5
Seq. ID
                   BLASTX
Method
                   q445116
NCBI GI
BLAST score
                   771
                   2.0e-82
E value
Match length
                   159
                   91
% identity
NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]
Seq. No.
                   221288
```

Seq. ID LIB3165-006-P1-K4-G6

Method BLASTX
NCBI GI g82080
BLAST score 822
E value 2.0e-88

```
170
Match length
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  221289
Seq. No.
Seq. ID
                  LIB3165-006-P1-K4-G7
                  BLASTX
Method
                  q4406530
NCBI GI
                  695
BLAST score
                  2.0e-73
E value
Match length
                  171
                  82
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
Seq. No.
                  221290
                  LIB3165-006-P1-K4-G8
Seq. ID
Method
                  BLASTX
                  a585322
NCBI GI
                  354
BLAST score
                  2.0e-33
E value
                  137
Match length
                  53
% identity
                  INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE)
NCBI Description
                  (PPASE) >gi 539751_pir__A45153 inorganic pyrophosphatase
                  (EC 3.6.1.1) - bovine
Seq. No.
                  221291
                  LIB3165-006-P1-K4-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4512667
BLAST score
                  763
E value
                  2.0e-81
Match length
                  178
                  79
% identity
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 221292

LIB3165-006-P1-K4-H10 Seq. ID

Method BLASTX NCBI GI g4426565 BLAST score 246 1.0e-20 E value 203 Match length 32 % identity

NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 221293

LIB3165-006-P1-K4-H11 Seq. ID

Method BLASTX NCBI GI q3914605 BLAST score 702 E value 4.0e-74Match length 193 71 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE



PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase -apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

 Seq. No.
 221294

 Seq. ID
 LIB3165-006-P1-K4-H2

 Method
 BLASTX

NCBI GI g2462746 BLAST score 269 E value 4.0e-28 Match length 117 % identity 61

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 221295

Seq. ID LIB3165-006-P1-K4-H3

Method BLASTX
NCBI GI g3582333
BLAST score 820
E value 5.0e-88
Match length 175
% identity 86

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 221296

Seq. ID LIB3165-006-P1-K4-H5

Method BLASTX
NCBI GI g1352821
BLAST score 795
E value 4.0e-85
Match length 152
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221297

Seq. ID LIB3165-006-P1-K4-H6

Method BLASTX
NCBI GI g505482
BLAST score 795
E value 4.0e-85
Match length 192
% identity 83

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 221298

Seq. ID LIB3165-006-P1-K4-H7

Method BLASTX NCBI GI g4103635 BLAST score 324

NCBI Description



```
6.0e-30
E value
                  138
Match length
                  51
% identity
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                  221299
Seq. No.
                  LIB3165-006-P1-K4-H8
Seq. ID
                  BLASTX
Method
                  g2244811
NCBI GI
BLAST score
                  534
                  2.0e-54
E value
                  184
Match length
                  65
% identity
                  (Z97336) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  221300
Seq. No.
                  LIB3165-006-P1-K4-H9
Seq. ID
                  BLASTX
Method
                  g100200
NCBI GI
BLAST score
                  712
                  2.0e-75
E value
                  165
Match length
                  67
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  221301
Seq. No.
                  LIB3165-007-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  g1928981
NCBI GI
BLAST score
                   257
E value
                  1.0e-22
Match length
                  57
                  88
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                   221302
Seq. No.
Seq. ID
                   LIB3165-007-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q4406530
BLAST score
                   252
E value
                   9.0e-22
                   71
Match length
                   75
% identity
                 (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                   221303
Seq. No.
                   LIB3165-007-P1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1172664
BLAST score
                   218
                   1.0e-17
E value
Match length
                   48
                   90
% identity
```

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi 419791_pir__S31165 photosystem I chain III precursor -



Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

 Seq. No.
 221304

 Seq. ID
 LIB3165-007-P1-K1-A6

 Method
 BLASTX

 NCBI GI
 g266893

 BLAST score
 648

E value 4.0e-68
Match length 127
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >qi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis

sativus]

Seq. No. 221305

Seq. ID LIB3165-007-P1-K1-A8

Method BLASTX
NCBI GI g1352821
BLAST score 390
E value 7.0e-38
Match length 95
% identity 80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221306

Seq. ID LIB3165-007-P1-K1-B1

Method BLASTX
NCBI GI g1352821
BLAST score 494
E value 5.0e-50
Match length 96
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221307

Seq. ID LIB3165-007-P1-K1-B11

Method BLASTX
NCBI GI g1168411
BLAST score 446
E value 2.0e-44
Match length 119
% identity 79

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Match length

58

tetragonoloba]



```
221308
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-B2
                  BLASTX
Method
                  g1931640
NCBI GI
                  488
BLAST score
                  2.0e-49
E value
                  124
Match length
                  71
% identity
                  (U95973) Serine carboxypeptidase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  221309
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-B4
                  BLASTN
Method
NCBI GI
                  g450504
                  132
BLAST score
                  4.0e-68
E value
                  247
Match length
                  97
% identity
NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate
                  carboxylase, small subunit
                  221310
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-B5
                  BLASTX
Method
                  g1352821
NCBI GI
                  460
BLAST score
                  4.0e-46
E value
                  87
Match length
                  100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221311
                  LIB3165-007-P1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4406530
BLAST score
                  349
E value
                   4.0e-33
Match length
                  93
                  76
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  221312
                  LIB3165-007-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021357
BLAST score
                  271
                   5.0e-24
E value
```

% identity 84
NCBI Description (AJ005082) UDP-galactose 4-epimerase [Cyamopsis



```
221313
Seq. No.
                  LIB3165-007-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  q3036944
NCBI GI
                  213
BLAST score
                  3.0e-23
E value
                  114
Match length
                  57
% identity
                  (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  221314
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-C1
                  BLASTX
Method
                  g3510256
NCBI GI
                  179
BLAST score
                  4.0e-13
E value
Match length
                  98
                  43
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221315
Seq. No.
                  LIB3165-007-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g68200
NCBI GI
BLAST score
                  350
                  3.0e-33
E value
                   92
Match length
                   79
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >qi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   221316
Seq. No.
Seq. ID
                   LIB3165-007-P1-K1-C12
                   BLASTX
Method
                   g115813
NCBI GI
BLAST score
                   395
                   2.0e-38
E value
                   96
Match length
                   77
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                   (CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   221317
Seq. No.
                   LIB3165-007-P1-K1-C2
Seq. ID
                   BLASTN
Method
                   g169818
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   79
Match length
                   87
% identity
NCBI Description Rice 25S ribosomal RNA gene
```

Seq. No. 221318

Seq. ID LIB3165-007-P1-K1-C8



```
BLASTX
Method
                  g2244797
NCBI GI
BLAST score
                  144
                   5.0e-09
E value
                   52
Match length
                   58
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  221319
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-C9
                  BLASTX
Method
                  g231688
NCBI GI
                   683
BLAST score
                   3.0e-72
E value
                   130
Match length
                   99
% identity
                  CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC
NCBI Description
                   1.11.1.6) - upland cot\overline{t}on >g\overline{i}_18\overline{48}8_emb_CAA39998_ (X56675)
                   subunit 2 of cotton catalase [Gossypium hirsutum]
                   221320
Seq. No.
                   LIB3165-007-P1-K1-D10
Seq. ID
                   BLASTX
Method
                   q1545805
NCBI GI
                   172
BLAST score
                   7.0e-13
E value
                   65
Match length
                   62
% identity
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
Seq. No.
                   221321
Seq. ID
                   LIB3165-007-P1-K1-D11
                   BLASTX
Method
                   q115471
NCBI GI
BLAST score
                   557
                   2.0e-57
E value
                   127
Match length
                   82
% identity
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                   DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase
                   (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792
                   (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
                   221322
Seq. No.
                   LIB3165-007-P1-K1-D12
Seq. ID
Method
                   BLASTX
                   g1354515
NCBI GI
BLAST score
                   205
                   3.0e-16
E value
Match length
                   94
% identity
                   51
NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus
                   tremuloides]
                   221323
Seq. No.
                   LIB3165-007-P1-K1-D2
Seq. ID
```

31255

BLASTX

Method



NCBI GI g1346155 BLAST score 315 E value 5.0e-50 Match length 124 % identity 78

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi_481942_pir__S40212 glycine

hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei

>gi_437995_emb_CAA81078_ (Z25859) glycine
hydroxymethyltransferase [Flaveria pringlei]

Seq. No. 221324

Seq. ID LIB3165-007-P1-K1-D3

Method BLASTX
NCBI GI g1352821
BLAST score 238
E value 2.0e-20
Match length 56
% identity 82

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221325

Seq. ID LIB3165-007-P1-K1-D4

Method BLASTX
NCBI GI g1362086
BLAST score 558
E value 1.0e-57
Match length 117
% identity 89

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919_pir__S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 221326

Seq. ID LIB3165-007-P1-K1-D5

Method BLASTX
NCBI GI g2583125
BLAST score 642
E value 2.0e-67
Match length 124
% identity 94

NCBI Description (AC002387) putative transketolase precursor [Arabidopsis

thaliana]

Seq. No. 221327

Seq. ID LIB3165-007-P1-K1-D6

Method BLASTX NCBI GI g3334405



```
BLAST score
                   484
E value
                  7.0e-49
Match length
                  103
% identity
                  98
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >qi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                  221328
Seq. No.
                  LIB3165-007-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  q100203
NCBI GI
BLAST score
                  370
                  2.0e-35
E value
Match length
                  94
                  77
% identity
                  cysteine proteinase (EC 3.4.22.-) precursor - tomato
NCBI Description
                  >gi 19195 emb CAA78403 (Z14028) pre-pro-cysteine
                  proteinase [Lycopersicon esculentum]
                  221329
Seq. No.
                  LIB3165-007-P1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q430947
                   448
BLAST score
                   1.0e-44
E value
                  109
Match length
                   82
% identity
NCBI Description
                  (U01103) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
                   221330
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-E11
Method
                  BLASTX
NCBI GI
                   g4406530
BLAST score
                   339
                  7.0e-32
E value
Match length
                  89
% identity
                   78
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                   221331
                  LIB3165-007-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2191136
                   310
BLAST score
                   2.0e-28
E value
                   110
Match length
                   60
% identity
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
```

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 221332

LIB3165-007-P1-K1-E3 Seq. ID

Method BLASTX

```
g2739375
NCBI GI
BLAST score
                  219
                  7.0e-18
E value
                  83
Match length
                  55
% identity
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221333
Seq. No.
                  LIB3165-007-P1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q902584
BLAST score
                  425
                  4.0e-42
E value
                  94
Match length
                  15
% identity
                  (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
NCBI Description
                  mays]
                  221334
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  q4220633
                  39
BLAST score
                  1.0e-12
E value
                  203
Match length
                  80
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K7J8, complete sequence [Arabidopsis thaliana]
                  221335
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  q421826
BLAST score
                  309
                  2.0e-28
E value
Match length
                  61
                  87
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  221336
Seq. ID
                  LIB3165-007-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  q547683
BLAST score
                   538
                   3.0e-55
E value
Match length
                  113
                   92
% identity
NCBI Description
                  HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
```

shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80

[Lycopersicon esculentum]

221337 Seq. No.

LIB3165-007-P1-K1-F5 Seq. ID

BLASTX Method



g115765 NCBI GI BLAST score 661 1.0e-69 E value 127 Match length 92 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR NCBI Description (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum] 221338 Seq. No. LIB3165-007-P1-K1-F7 Seq. ID BLASTX Method NCBI GI q1709651 BLAST score 347 8.0e-33 E value 114 Match length % identity PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 NCBI Description plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra] 221339 Seq. No. Seq. ID LIB3165-007-P1-K1-F8 Method BLASTX q100616 NCBI GI BLAST score 189 2.0e-14 E value Match length 47 % identity 81 ribulose-bisphosphate carboxylase activase B precursor -NCBI Description barley >gi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] 221340 Seq. No. LIB3165-007-P1-K1-G10 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g1419090
BLAST score 317
E value 3.0e-29
Match length 92
% identity 68

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 221341

Seq. ID LIB3165-007-P1-K1-G2

Method BLASTN NCBI GI g4545261 BLAST score 355



E value 0.0e+00 Match length 391 98

NCBI Description Gossypium hirsutum metallothionein-like protein mRNA,

complete cds

Seq. No. 221342

Seq. ID LIB3165-007-P1-K1-G3

Method BLASTX
NCBI GI g2662310
BLAST score 449
E value 7.0e-45
Match length 118
% identity 70

NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 221343

Seq. ID LIB3165-007-P1-K1-G4

Method BLASTX
NCBI GI 9441457
BLAST score 249
E value 2.0e-21
Match length 53
% identity 91

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No. 221344

Seq. ID LIB3165-007-P1-K1-G8

Method BLASTX
NCBI GI g2493144
BLAST score 345
E value 1.0e-32
Match length 87
% identity 82

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 221345

Seq. ID LIB3165-007-P1-K1-H1

Method BLASTX
NCBI GI g170354
BLAST score 545
E value 5.0e-56
Match length 113
% identity 21

NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No. 221346

Seq. ID LIB3165-007-P1-K1-H12

Method BLASTX NCBI GI g231688 BLAST score 574



2.0e-59 E value Match length 111 98 % identity CATALASE ISOZYME 2 >gi 99599 pir_S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton >gi 18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum] 221347 Seq. No. LIB3165-007-P1-K1-H2 Seq. ID BLASTX Method q3687652 NCBI GI 515 BLAST score 1.0e-52 E value 106 Match length 94 % identity (AF047352) rubisco activase precursor [Datisca glomerata] NCBI Description 221348 Seq. No. Seq. ID LIB3165-007-P1-K1-H3 Method BLASTX NCBI GI g2245096 BLAST score 450 6.0e-45E value 103 Match length 80 % identity (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis NCBI Description thaliana] 221349 Seq. No. Seq. ID LIB3165-007-P1-K1-H4 Method BLASTN q2687435 NCBI GI 128 BLAST score 6.0e-66 E value Match length 192 92 % identity Hamamelis virginiana large subunit 26S ribosomal RNA gene, NCBI Description partial sequence Seq. No. 221350 LIB3165-007-P1-K1-H6 Seq. ID Method BLASTX q3738285 NCBI GI BLAST score 382 5.0e-37 E value Match length 111 % identity NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] 221351 Seq. No. LIB3165-007-P1-K1-H7 Seq. ID

Method BLASTX
NCBI GI g1246823
BLAST score 321
E value 1.0e-34
Match length 118

% identity

31261



```
NCBI Description (X89865) unknown [Phoenix dactylifera]
                  221352
Seq. No.
                  LIB3165-007-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  q1572819
NCBI GI
                  191
BLAST score
E value
                  8.0e-15
                  79
Match length
% identity
                  51
                  (U70855) similar to the RAS gene family [Caenorhabditis
NCBI Description
                  elegans]
                  221353
Seq. No.
Seq. ID
                  LIB3165-007-P1-K1-H9
                  BLASTX
Method
NCBI GI
                  q115813
BLAST score
                  306
E value
                  3.0e-28
                  96
Match length
                  65
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                  (CAB-8) >qi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  221354
Seq. No.
Seq. ID
                  LIB3165-008-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  q1352821
BLAST score
                  510
                   6.0e - 52
E value
Match length
                  98
                  98
% identity
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221355
                  LIB3165-008-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
BLAST score
                  315
                  5.0e-29
E value
                  87
Match length
                  75
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  221356
Seq. No.
                  LIB3165-008-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  g3914472
NCBI GI
BLAST score
                   376
                   3.0e - 36
E value
                   90
Match length
```

31262

81

% identity



NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No. 221357

Seq. ID LIB3165-008-P1-K1-A9

Method BLASTX
NCBI GI g4406530
BLAST score 262
E value 6.0e-23
Match length 96
% identity 60

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221358

Seq. ID LIB3165-008-P1-K1-B10

Method BLASTX
NCBI GI g1171577
BLAST score 549
E value 2.0e-56
Match length 129
% identity 80

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 221359

Seq. ID LIB3165-008-P1-K1-B12

Method BLASTX
NCBI GI g1352821
BLAST score 524
E value 1.0e-53
Match length 99
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221360

Seq. ID LIB3165-008-P1-K1-B2

Method BLASTX
NCBI GI g2738949
BLAST score 325
E value 2.0e-38
Match length 95
% identity 88

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 221361

Seq. ID LIB3165-008-P1-K1-B3

Method BLASTX
NCBI GI g4008159
BLAST score 635
E value 1.0e-66
Match length 131



93

% identity

```
% identity
                 (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
                  221362
Seq. No.
Seq. ID
                  LIB3165-008-P1-K1-B4
                  BLASTX
Method
                  q430947
NCBI GI
                  433
BLAST score
                  6.0e-43
E value
                  109
Match length
                  80
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  221363
Seq. No.
                  LIB3165-008-P1-K1-B6
Seq. ID
                  BLASTX
Method
                  g68200
NCBI GI
                  417
BLAST score
                  5.0e-41
E value
                  105
Match length
                  81
% identity
                 fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
                  221364
Seq. No.
                  LIB3165-008-P1-K1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q586797
BLAST score
                  227
                  9.0e-19
E value
Match length
                  85
                  48
% identity
NCBI Description HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III
                  221365
Seq. No.
                  LIB3165-008-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3869088
BLAST score
                  535
                  7.0e-55
E value
Match length
                  102
                   100
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                   221366
Seq. No.
                  LIB3165-008-P1-K1-C1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g450504
                   83
BLAST score
                   5.0e-39
E value
Match length
                   118
```

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit



Seq. No. Seq. ID

221367

LIB3165-008-P1-K1-C10

```
BLASTX
Method
                  g3881507
NCBI GI
                  367
BLAST score
                   4.0e-35
E value
                  129
Match length
                   52
% identity
                  (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
NCBI Description
                  yk375c3.3 comes from this gene [Caenorhabditis elegans]
                   221368
Seq. No.
Seq. ID
                  LIB3165-008-P1-K1-C12
                   BLASTX
Method
                   q2832682
NCBI GI
                   209
BLAST score
                   1.0e-16
E value
                   97
Match length
                   54
% identity
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   221369
Seq. No.
                   LIB3165-008-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g119640
NCBI GI
                   327
BLAST score
                   2.0e-30
E value
                   106
Match length
                   59
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
NCBI Description
                   E8) >gi 82109 pir__S01642 ripening protein E8 - tomato
                   >gi 19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon
                   esculentum]
Seq. No.
                   221370
                   LIB3165-008-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g2213610
NCBI GI
BLAST score
                   178
E value
                   5.0e-13
Match length
                   112
% identity
                   19
NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]
Seq. No.
                   221371
                   LIB3165-008-P1-K1-C5
Seq. ID
                   BLASTX
Method
                   g1354515
NCBI GI
                   223
BLAST score
                   2.0e-18
E value
                   94
Match length
                   54
 % identity
                   (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   221372
 Seq. No.
                   LIB3165-008-P1-K1-D1
 Seq. ID
```



Method BLASTX
NCBI GI g289920
BLAST score 584
E value 1.0e-60
Match length 119
% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221373

Seq. ID LIB3165-008-P1-K1-D10

Method BLASTX
NCBI GI 9400890
BLAST score 261
E value 1.0e-22
Match length 116
% identity 45

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 221374

Seq. ID LIB3165-008-P1-K1-D11

Method BLASTX
NCBI GI g1168251
BLAST score 570
E value 6.0e-59
Match length 130
% identity 78

NCBI Description PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR

>gi_1076384_pir__S46535 probable cysteine proteinase (EC
3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment)
>gi_516865_emb_CAA52403_ (X74359) putative thiol protease

[Arabidopsis thaliana]

Seq. No. 221375

Seg. ID LIB3165-008-P1-K1-D12

Method BLASTX
NCBI GI g1352821
BLAST score 562
E value 5.0e-58
Match length 106
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221376

Seq. ID LIB3165-008-P1-K1-D3

Method BLASTX NCBI GI g100616 BLAST score 614



4.0e-64 E value 130 Match length 85 % identity ribulose-bisphosphate carboxylase activase B precursor -NCBI Description barley >gi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi 167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] 221377 Seq. No. Seq. ID LIB3165-008-P1-K1-D4 BLASTX Method g4406530 NCBI GI BLAST score 330 8.0e-31 E value 87 Match length 78 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] 221378 Seq. No. LIB3165-008-P1-K1-D5 Seq. ID BLASTX Method g602292 NCBI GI 453 BLAST score 3.0e-45E value 108 Match length % identity 81 NCBI Description (U17987) RCH2 protein [Brassica napus] 221379 Seq. No. Seq. ID LIB3165-008-P1-K1-D6 BLASTX Method NCBI GI q1346156 621 BLAST score 5.0e-65 E value 131 Match length % identity NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >qi 481943 pir S40213 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >qi 437997 emb CAA81079 (Z25860) glycine hydroxymethyltransferase [Flaveria pringlei] 221380 Seq. No. LIB3165-008-P1-K1-D7 Seq. ID BLASTX Method g131385 NCBI GI

Method BLASTX
NCBI GI g131385
BLAST score 497
E value 2.0e-50
Match length 122
% identity 84

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 221381



LIB3165-008-P1-K1-D9 Seq. ID BLASTX Method NCBI GI g1354517 BLAST score 294 1.0e-26 E value 129 Match length 54 % identity NCBI Description (U55838) carbonic anhydrase [Populus tremula x Populus tremuloides] 221382 Seq. No. LIB3165-008-P1-K1-E12 Seq. ID Method BLASTX NCBI GI g2129538 BLAST score 319 2.0e-29 E value 67 Match length 88 % identity AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) NCBI Description AT103 [Arabidopsis thaliana] 221383 Seq. No. LIB3165-008-P1-K1-E3 Seq. ID BLASTN Method g2687430 NCBI GI BLAST score 63 E value 1.0e-27 67 Match length 99 % identity NCBI Description Acorus gramineus large subunit 26S ribosomal RNA gene, partial sequence 221384 Seq. No. Seq. ID LIB3165-008-P1-K1-E4 Method BLASTX NCBI GI g166834 BLAST score 602 1.0e-62 E value Match length 124 % identity 92 (M86720) ribulose bisphosphate carboxylase/oxygenase NCBI Description activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana] 221385 Seq. No. LIB3165-008-P1-K1-E5 Seq. ID BLASTX Method NCBI GI g3738261 BLAST score 179 4.0e-13 E value 45 Match length 87 % identity NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]
Seq. No. 221386

Seq. ID LIB3165-008-P1-K1-E6



Method BLASTX
NCBI GI g3334245
BLAST score 325
E-value 3.0e-30
Match length 74
% identity 84

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer

arietinum]

Seq. No. 221387

Seq. ID LIB3165-008-P1-K1-E8

Method BLASTX
NCBI GI g417154
BLAST score 628
E value 9.0e-66
Match length 123
% identity 98

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 221388

Seq. ID LIB3165-008-P1-K1-F1

Method BLASTX
NCBI GI g3659907
BLAST score 388
E value 1.0e-37
Match length 105
% identity 74

NCBI Description (AF091857) protein translation factor SUI1 homolog

[Pimpinella brachycarpa]

Seq. No. 221389

Seq. ID LIB3165-008-P1-K1-F10

Method BLASTX
NCBI GI g1352821
BLAST score 584
E value 1.0e-60
Match length 119
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221390

Seq. ID LIB3165-008-P1-K1-F11

Method BLASTX
NCBI GI g3335350
BLAST score 393
E value 3.0e-38
Match length 126

% identity 55

NCBI Description (AC004512) Similar to gb Z84386 anthranilate

N-hydroxycinnamoyl/benzoyltransferase from Dianthus

caryophyllus. [Arabidopsis thaliana]

Seq. No. 221391

Seq. ID LIB3165-008-P1-K1-F12

Method BLASTN
NCBI GI g18511
BLAST score 96
E value 1.0e-46
Match length 160
% identity 90

NCBI Description G.hirsutum light regulated unknown reading frame DNA

Seq. No. 221392

Seq. ID LIB3165-008-P1-K1-F2

Method BLASTX
NCBI GI g2494076
BLAST score 492
E value 9.0e-50
Match length 104
% identity 88

NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase

[Nicotiana plumbaginifolia]

Seq. No. 221393

Seq. ID LIB3165-008-P1-K1-F5

Method BLASTX
NCBI GI g393707
BLAST score 561
E value 6.0e-58
Match length 129
% identity 86

NCBI Description (X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No. 221394

Seq. ID LIB3165-008-P1-K1-F6

Method BLASTX
NCBI GI g2443886
BLAST score 262
E value 7.0e-23
Match length 68
% identity 79

NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 221395

Seq. ID LIB3165-008-P1-K1-F7

Method BLASTX
NCBI GI g1694976
BLAST score 275
E value 2.0e-24
Match length 106



% identity 52

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 221396

Seq. ID LIB3165-008-P1-K1-G10

Method BLASTX
NCBI GI g2501356
BLAST score 437
E value 2.0e-43
Match length 85

% identity 93

NCBI Description TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)

>gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor

[Solanum tuberosum]

Seq. No. 221397

Seq. ID LIB3165-008-P1-K1-G11

Method BLASTX
NCBI GI g131397
BLAST score 291
E value 3.0e-26
Match length 128
% identity 54

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597 prf 1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 221398

Seq. ID LIB3165-008-P1-K1-G3

Method BLASTX
NCBI GI g2864617
BLAST score 221
E value 5.0e-18
Match length 111
% identity 43

NCBI Description (ALO21811) H+-transporting ATP synthase chain9 - like

protein [Arabidopsis thaliana]

Seq. No. 221399

Seq. ID LIB3165-008-P1-K1-G4

Method BLASTX
NCBI GI g1352683
BLAST score 219
E value 8.0e-18
Match length 60
% identity 73

NCBI Description PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803)

protein phosphatase homolog [Arabidopsis thaliana]

Seq. No. 221400



Seq. ID LIB3165-008-P1-K1-G5 Method BLASTX NCBI GI g4538913 BLAST score 415

E value 8.0e-41 Match length 100 79 % identity

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

221401 Seq. No.

Seq. ID LIB3165-008-P1-K1-G7

Method BLASTX NCBI GI g3914603 BLAST score 489 E value 2.0e-49 Match length 115 % identity 78

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >qi 1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

Seq. No. 221402

Seq. ID LIB3165-008-P1-K1-G8

Method BLASTX NCBI GI g2970051 BLAST score 373 7.0e-36 E value Match length 100 % identity 70

NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 221403

Seq. ID LIB3165-008-P1-K1-G9

Method BLASTX NCBI GI g122106 BLAST score 375 E value 4.0e-36 Match length 76 % identity 100

HISTONE H4 >gi 70771 pir HSZM4 histone H4 - maize NCBI Description

>gi 81642 pir S06904 histone H4 - Arabidopsis thaliana

>gi 2119028 pir S60475 histone H4 - garden pea

>gi 21795 emb CAA24924 (X00043) histone H4 [Triticum aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi 168501 (M13370) histone H4 [Zea mays] >gi 168503

(M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone

H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata]

>gi 3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi 4580385 gb AAD24364.1 AC007184 4 (AC007184) histone H4 [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4

[Arabidopsis thaliana]

Seq. No. 221404



```
LIB3165-008-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  g2894599
NCBI GI
BLAST score
                  414
                  1.0e-40
E value
Match length
                  108
                  67
% identity
                 (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                  221405
Seq. No.
Seq. ID
                  LIB3165-008-P1-K1-H5
                  BLASTX
Method
NCBI GI
                  g119194
BLAST score
                  182
                  8.0e-14
E value
                  69
Match length
                  64
% identity
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                  >gi_81607_pir__S09152 translation elongation factor Tu
                  precursor, chloroplast - Arabidopsis thaliana
                  >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu
                  precursor [Arabidopsis thaliana] >gi 226817_prf__1607332A
                  elongation factor Tu [Arabidopsis thaliana]
                ~ 221406
Seq. No.
                  LIB3165-008-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4056506
BLAST score
                  369
                  2.0e-35
E value
Match length
                  111
% identity
                  61
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  221407
                  LIB3165-008-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  q1565225
NCBI GI
BLAST score
                  227
E value
                  9.0e-19
Match length
                  49
% identity
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                  221408
                  LIB3165-008-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2465773
```

Method BLASTX
NCBI GI g2465773
BLAST score 147
E value 6.0e-12
Match length 92
% identity 33

NCBI Description (AF022186) homologous to orf238 in Porphyra purpurea

[Cyanidium caldarium]

Seq. No. 221409

Seq. ID LIB3165-009-P1-K1-A1



```
BLASTX
Method
NCBI GI
                  q3880432
                  165
BLAST score
                  2.0e-11
E value
                  114
Match length
                  37
% identity
                  (Z66521) similar to kinensin-like protein; cDNA EST
NCBI Description
                  yk198e10.3 comes from this gene; cDNA EST yk198e10.5 comes
                  from this gene [Caenorhabditis elegans]
                  221410
Seq. No.
Seq. ID
                  LIB3165-009-P1-K1-A10
                  BLASTX
Method
                  g4337025
NCBI GI
BLAST score
                  443
                  4.0e-44
E value
                  114
Match length
                  75
% identity
                  (AF123253) AIM1 protein [Arabidopsis thaliana]
NCBI Description
                  221411
Seq. No.
Seq. ID
                  LIB3165-009-P1-K1-A11
                  BLASTX
Method
NCBI GI
                  g1168408
BLAST score
                  533
E value
                  1.0e-54
                  121
Match length
                  88
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                  >gi 2118268_pir__S58168 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea > gi 927507 emb CAA61946 (X89828)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
                   221412
Seq. No.
                  LIB3165-009-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g3158474
NCBI GI
BLAST score
                   327
                   2.0e-30
E value
Match length
                  90
                  73
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                   221413
Seq. No.
                  LIB3165-009-P1-K1-A3
Seq. ID
                  BLASTX
Method
                   q128194
NCBI GI
BLAST score
                   464
E value
                   1.0e-46
                   110
Match length
                   77
% identity
NCBI Description NITRATE REDUCTASE (NR) >gi 81572 pir A41667 nitrate
                   reductase (NADH) (EC 1.6.6.1) - winter squash >gi 167499
```

Seq. ID LIB3165-009-P1-K1-A7

(M33154) nitrate reductase [Cucurbita maxima]



```
Method
                  BLASTX
NCBI GI
                  g3880432
BLAST score
                  171
                  3.0e-12
E value
Match length
                  60
                  50
% identity
                  (Z66521) similar to kinensin-like protein; cDNA EST
NCBI Description
                  yk198e10.3 comes from this gene; cDNA EST yk198e10.5 comes
                  from this gene [Caenorhabditis elegans]
                  221415
Seq. No.
                  LIB3165-009-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  g3914605
NCBI GI
                  530
BLAST score
                  3.0e-54
E value
Match length
                  124
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                   apple tree >gi 415852 emb CAA79857 (Z21794)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Malus domestica]
                  221416
Seq. No.
                  LIB3165-009-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q289920
BLAST score
                  587
                   5.0e-61
E value
Match length
                   108
                   99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   221417
Seq. No.
                   LIB3165-009-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g551428
BLAST score
                   92
                   1.0e-08
E value
                   89
Match length
                   43
% identity
                  (X78996) tetrafunctional protein [Cucumis sativus]
NCBI Description
                   221418
Seq. No.
                   LIB3165-009-P1-K1-B4
Seq. ID
Method
                   BLASTX
                   g4091806
NCBI GI
BLAST score
                   364
```

8.0e-35 E value 115 Match length % identity

(AF052585) CONSTANS-like protein 2 [Malus domestica] NCBI Description

221419 Seq. No.



```
Seq. ID
                  LIB3165-009-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4337025
BLAST score
                  186
                  5.0e-14
E value
Match length
                  92
                  48
% identity
                  (AF123253) AIM1 protein [Arabidopsis thaliana]
NCBI Description
                  221420
Seq. No.
Seq. ID
                  LIB3165-009-P1-K1-B6
                  BLASTX
Method
NCBI GI
                  g2661021
BLAST score
                  559
                  1.0e-57
E value
                  107
Match length
% identity
                  96
NCBI Description (AF035255) catalase [Glycine max]
Seq. No.
                  221421
                  LIB3165-009-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204267
BLAST score
                   461
                   3.0e-46
E value
Match length
                  114
                  77
% identity
NCBI Description (AC005223) 55585 [Arabidopsis thaliana]
Seq. No.
                  221422
                  LIB3165-009-P1-K1-C1
Seq. ID
Method
                  BLASTX
                   g551428
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   108
Match length
                   40
% identity
NCBI Description (X78996) tetrafunctional protein [Cucumis sativus]
                   221423
Seq. No.
                   LIB3165-009-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g115705
NCBI GI
                   479
BLAST score
                   2.0e-48
E value
                   105
Match length
                   87
% identity
                  CATALASE >gi_279448_pir__CSPM catalase (EC 1.11.1.6) -
NCBI Description
                   garden pea >gi_20677_emb_CAA42736_ (X60169) catalase [Pisum
                   sativum]
                   221424
Seq. No.
Seq. ID
                   LIB3165-009-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q4406530
                   293
BLAST score
```

2.0e-26

E value



```
Match length
                  104
                  62
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  221425
Seq. No.
                  LIB3165-009-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g2306917
NCBI GI
                  301
BLAST score
                  1.0e-27
E value
Match length
                  71
                  86
% identity
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   221426
Seq. ID
                  LIB3165-009-P1-K1-D10
                   BLASTX
Method
                   g4406530
NCBI GI
BLAST score
                   302
                   1.0e-27
E value
Match length
                   107
                   62
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   221427
Seq. No.
                   LIB3165-009-P1-K1-D11
Seq. ID
Method
                   BLASTX
                   q4115357
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
                   90
Match length
                   44
% identity
NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]
                   221428
Seq. No.
                   LIB3165-009-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g3928760
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   108
Match length
                   48
% identity
NCBI Description (AB011797) homolog to plastid-lipid-associated protein
                   [Citrus unshiu]
                   221429
Seq. No.
                   LIB3165-009-P1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2661021
                   566
BLAST score
                   2.0e-58
E value
                   110
Match length
% identity
                   96
                  (AF035255) catalase [Glycine max]
NCBI Description
```

31277

221430

Seq. No.



LIB3165-009-P1-K1-D5 Seq. ID BLASTX Method NCBI GI q1352821 486 BLAST score 4.0e-49 E value 94 Match length 97 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 221431 Seq. No. LIB3165-009-P1-K1-D6 Seq. ID BLASTX Method g4455208 NCBI GI BLAST score 309 2.0e-28 E value Match length 117 59 % identity NCBI Description (AL035440) putative protein [Arabidopsis thaliana] 221432 Seq. No. LIB3165-009-P1-K1-D7 Seq. ID BLASTX Method g1709690 NCBI GI 318 BLAST score 2.0e-29 E value Match length 87 70 % identity NCBI Description PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE) >gi 1076454 pir S55365 probable peptide methionine sulfoxide reductase - rape >gi_853739_emb_CAA88538_ (Z48619) peptide methionine sulfoxide reductase [Brassica napus] >qi 1143406 emb CAA63919 (X94225) methionine sulfoxide reductase [Brassica napus] Seq. No. 221433 LIB3165-009-P1-K1-D8 Seq. ID Method BLASTX q3298548 NCBI GI 434 BLAST score 5.0e-43E value Match length 115 71 % identity (AC004681) putative spliceosomal protein [Arabidopsis NCBI Description thaliana] 221434 Seq. No. LIB3165-009-P1-K1-D9 Seq. ID Method BLASTN q18058 NCBI GI

293

357

1.0e-164

BLAST score

Match length

E value



% identity Citrus limon cistron for 26S ribosomal RNA NCBI Description 221435 Seq. No. Seq. ID LIB3165-009-P1-K1-E3 BLASTX Method q132794 NCBI GI BLAST score 437 2.0e-43 E value 112 Match length 75 % identity CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi_71288_pir__R5NT22 NCBI Description ribosomal protein L22 - common tobacco chloroplast >gi 11866 emb CAA77382_ (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi 225236 prf 1211235BU ribosomal protein L22 [Nicotiana Tabacum] 221436 Seq. No.

Seq. ID LIB3165-009-P1-K1-E6 Method BLASTX a81548 NCBI GI 433 BLAST score 6.0e-43E value Match length 110 77 % identity

NCBI Description catalase (EC 1.11.1.6) chain 1 - upland cotton

221437 Seq. No. Seq. ID LIB3165-009-P1-K1-E7 Method BLASTX q166834 NCBI GI BLAST score 631 4.0e-66 E value Match length 128 % identity 95

(M86720) ribulose bisphosphate carboxylase/oxygenase NCBI Description activase [Arabidopsis thaliana] >gi 2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 221438

Seq. ID LIB3165-009-P1-K1-E8

Method BLASTX q1352821 NCBI GI 546 BLAST score E value 3.0e-56 Match length 114 % identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

221439 Seq. No.

LIB3165-009-P1-K1-E9 Seq. ID

Method BLASTX g3550519 NCBI GI



```
BLAST score
                  367
                  3.0e - 35
E value
                  106
Match length
                  63
% identity
                  (AJ007630) oxygenase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  221440
                  LIB3165-009-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  574
BLAST score
                  2.0e-59
E value
                  112
Match length
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   221441
Seq. No.
                  LIB3165-009-P1-K1-F11
Seq. ID
Method
                  BLASTX
                   g2661021
NCBI GI
BLAST score
                  525
                  1.0e-53
E value
Match length
                  109
                   92
% identity
NCBI Description (AF035255) catalase [Glycine max]
                   221442
Seq. No.
                  LIB3165-009-P1-K1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4415992
                   607
BLAST score
                   2.0e-63
E value
                   121
Match length
                   96
% identity
NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]
                   221443
Seq. No.
                   LIB3165-009-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4454458
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
                   104
Match length
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                   221444
Seq. No.
```

LIB3165-009-P1-K1-G10 Seq. ID

BLASTX Method NCBI GI q1354515 BLAST score 220 6.0e-18 E value Match length 101



```
% identity
                  50
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
Seq. No.
                  221445
                  LIB3165-009-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q131384
BLAST score
                  311
                  1.0e-28
E value
Match length
                  75
                  80
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir S04132
                  photosystem II oxygen-evolving complex protein 1 precursor
                  - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA
                  -81 to 248) [Pisum satīvum] >gi_344004_dbj_BAA02554_
                   (D13297) precursor for 33-kDa protein of photosystem II
                   [Pisum sativum] >gi_226937_prf _1611461A O2 evolving
                  complex 33kD protein [Arachis hypogaea]
Seq. No.
                  221446
                  LIB3165-009-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  479
E value
                  4.0e-50
Match length
                  108
                  95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   221447
Seq. No.
                  LIB3165-009-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g1256595
NCBI GI
                   369
BLAST score
                   2.0e-35
E value
                   106
Match length
                   65
% identity
NCBI Description (U38915) LytB [Synechocystis PCC6803]
Seq. No.
                   221448 -
                   LIB3165-009-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g20729
BLAST score
                   462
                   2.0e-46
E value
                   125
Match length
% identity
```

31281

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

221449

Seq. No.

```
Seq. ID
                  LIB3165-009-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  377
                  2.0e-36
E value
                  78
Match length
                  88
% identity
                  (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
                  221450
Seq. No.
                  LIB3165-009-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q131167
BLAST score
                  311
                   1.0e-28
E value
                  120
Match length
                   62
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi 100292 pir S18348 photosystem I chain II precursor -
                   wood tobacco >qi 19748 emb CAA42623 (X60008) PSI-D2
                   [Nicotiana sylvestris]
Seq. No.
                   221451
                   LIB3165-009-P1-K1-H3
Seq. ID
                   BLASTN
Method
                   q18058
NCBI GI
                   76
BLAST score
E value
                   1.0e-34
Match length
                   260
                   83
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
Seq. No.
                   221452
                   LIB3165-009-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   q3096949
NCBI GI
                   397
BLAST score
E value
                   1.0e-38
Match length
                   121
% identity
                   60
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   221453
Seq. No.
                   LIB3165-009-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   g3914940
NCBI GI
BLAST score
                   389
                   9.0e-38
E value
                   128
Match length
                   65
% identity
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
```

[Spinacia oleracea]

>gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

```
Seq. No.
                   221454
Seq. ID
                  LIB3165-009-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g2245066
BLAST score
                   348
                   6.0e-33
E value
Match length
                   117
                   53
% identity
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   221455
Seq. ID
                   LIB3165-011-P1-K1-A11
                   BLASTX
Method
                   q169199
NCBI GI
                   143
BLAST score
                   3.0e-09
E value
                   48
Match length
% identity
                   33
NCBI Description (K00973) Major Cab protein [Petunia sp.]
                   221456
Seq. No.
                   LIB3165-011-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   q3023752
NCBI GI
BLAST score
                   280
                   6.0e-25
E value
                   103
Match length
                   58
% identity
                 FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                   221457
                   LIB3165-011-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   g4406530
NCBI GI
                   349
BLAST score
                   5.0e-33
E value
Match length
                   118
% identity
                   63
                   (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                   221458
Seq. No.
                   LIB3165-011-P1-K1-A4
Seq. ID
                   BLASTN
Method
                   g2687430
NCBI GI
                   42
BLAST score
                   6.0e-15
E value
```

86 Match length 87 % identity

NCBI Description Acorus gramineus large subunit 26S ribosomal RNA gene,

partial sequence

221459 Seq. No.

LIB3165-011-P1-K1-A7 Seq. ID

Method BLASTX NCBI GI g1352821



BLAST score 554 E value 5.0e-57 Match length 108 % identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221460

Seq. ID LIB3165-011-P1-K1-A8

Method BLASTX
NCBI GI g541979
BLAST score 313
E value 9.0e-29
Match length 79
% identity 80

NCBI Description guanine nucleotide regulatory protein - fava bean

>gi_303744_dbj_BAA02113 (D12545) GTP-binding protein
[Pisum sativum] >gi 452361 emb CAA82709 (Z29592) guanine

nucleotide regulatory protein [Vicia faba]

>gi_738937_prf__2001457E GTP-binding protein [Pisum sativum] >gi_1098295_prf__2115367C small GTP-binding

protein [Vicia faba]

Seq. No. 221461

Seq. ID LIB3165-011-P1-K1-A9

Method BLASTX
NCBI GI g289920
BLAST score 678
E value 1.0e-71
Match length 128
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221462

Seq. ID LIB3165-011-P1-K1-B1

Method BLASTX
NCBI GI g1346155
BLAST score 639
E value 5.0e-67
Match length 138
% identity 89

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi_481942_pir__S40212 glycine

hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei

>gi_437995_emb_CAA81078_ (Z25859) glycine
hydroxymethyltransferase [Flaveria pringlei]

Seq. No. 221463

Seq. ID LIB3165-011-P1-K1-B11

Method BLASTX NCBI GI g2677828 BLAST score 460



```
5.0e-46
E value
                   131
Match length
% identity
                   66
                   (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                   221464
Seq. No.
                   LIB3165-011-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   q2911085
NCBI GI
                   341
BLAST score
                   5.0e-32
E value
                   134
Match length
                   57
% identity
                   (AL021960) photosystem II oxygen-evolving complex protein 3
NCBI Description
                   - like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_
                   (ALO31187) photosystem II oxygen-evolving complex protein 3
                   - like [Arabidopsis thaliana]
                   221465
Seq. No.
                   LIB3165-011-P1-K1-B4
Seq. ID
                   BLASTX
Method
                   g231688
NCBI GI
                   237
BLAST score
                   4.0e-21
E value
                   99
Match length
                   63
% identity
                   CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC
NCBI Description
                   1.11.1.6) - upland cot\overline{t}on >g\overline{t}_18\overline{48}8_emb_CAA39998_ (X56675)
                   subunit 2 of cotton catalase [Gossypium hirsutum]
                   221466
Seq. No.
                   LIB3165-011-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   q100615
NCBI GI
BLAST score
                   261
                   8.0e-23
E value
                   115
Match length
% identity
                   ribulose-bisphosphate carboxylase activase A short form
NCBI Description
                   precursor - barley >gi 167091 (M55447) ribulose
                   1,5-bisphosphate carboxylase activase [Hordeum vulgare]
                    221467
Seq. No.
Seq. ID
                    LIB3165-011-P1-K1-B7
                    BLASTX
Method
NCBI GI
                    q4115726
                    152
BLAST score
                    6.0e-10
E value
Match length
                    115
 % identity
 NCBI Description (AB015947) aquaporin-4 [Bos taurus]
                    221468
 Seq. No.
                    LIB3165-011-P1-K1-B8
 Seq. ID
 Method
                    BLASTX
```

31285

q1053216

486

NCBI GI BLAST score

```
4.0e-49
E value
                  92
Match length
                  98
% identity
                  (U39475) chlorophyll a/b-binding protein [Glycine max]
NCBI Description
                  221469
Seq. No.
                  LIB3165-011-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q289920
                   450
BLAST score
                   6.0e-45
E value
                   112
Match length
                   79
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   221470
Seq. No.
                   LIB3165-011-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
                   604
BLAST score
                   7.0e-63
E value
                   112
Match length
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(EC\ 4.1.1.39)} small chain
                   precursor - upland cotton >gi 450505_emb CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   221471
                   LIB3165-011-P1-K1-C3
 Seq. ID
                   BLASTX
Method
                   g505482
NCBI GI
                   524
BLAST score
                   2.0e-53
E value
                   139
Match length
                   78
 % identity
                   (X64349) 33 kDa polypeptide of water-oxidizing complex of
 NCBI Description
                   photosystem II [Nicotiana tabacum]
                   221472
 Seq. No.
                   LIB3165-011-P1-K1-C6
 Seq. ID
                   BLASTX
 Method
                   g4539335
 NCBI GI
                    262
```

NCBI GI g4539335
BLAST score 262
E value 8.0e-23
Match length 132
% identity 44
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No. 221473
Seq. ID LIB3165-011-P1-K1-C8
Method BLASTX

Method BLASTX
NCBI GI g166835
BLAST score 729
E value 1.0e-77



141 Match length % identity

(M86720) ribulose bisphosphate carboxylase/oxygenase NCBI Description

activase [Arabidopsis thaliana] >gi_2642170 (AC003000)

Rubisco activase [Arabidopsis thaliana]

221474 Seq. No.

LIB3165-011-P1-K1-D1 Seq. ID

BLASTX Method q3128177 NCBI GI 529 BLAST score 4.0e-54 E value Match length 125 % identity 82

(AC004521) unknown protein [Arabidopsis thaliana] NCBI Description

221475 Seq. No.

LIB3165-011-P1-K1-D10 Seq. ID

BLASTX Method g417103 NCBI GI 654 BLAST score 9.0e-69 E value Match length 131 % identity 100

NCBI Description HISTONE H3.2, MINOR >gi 282871_pir _S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >qi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AFO93633) histone H3 [Oryza sativa] >qi 4038469 qb AAC97380 (AF109910) histone H3 [Porteresia

coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

221476 Seq. No.

Seq. ID LIB3165-011-P1-K1-D11

Method BLASTX q2462931 NCBI GI BLAST score 512 3.0e-52E value 102 Match length 90 % identity

(Z83833) UDP-glucose:sterol glucosyltransferase NCBI Description

[Arabidopsis thaliana]

221477 Seq. No.

LIB3165-011-P1-K1-D2 Seq. ID



BLASTX Method g3122232 NCBI GI 278 BLAST score 1.0e-24 E value 105 Match length 58 % identity MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR NCBI Description >gi 1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana] 221478 Seq. No. LIB3165-011-P1-K1-D6 Seq. ID BLASTX Method g1935914 NCBI GI 184 BLAST score 1.0e-13 E value 63 Match length 56 % identity (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana] NCBI Description 221479 Seq. No. LIB3165-011-P1-K1-D8 Seq. ID BLASTX Method NCBI GI g289920 699 BLAST score 4.0e-74E value 130 Match length 99 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 221480 Seq. No. LIB3165-011-P1-K1-D9 Seq. ID BLASTX Method g2970051 NCBI GI 421 BLAST score E value 2.0e-41 113 Match length 71 % identity NCBI Description (AB012110) ARG10 [Vigna radiata] Seq. No. 221481 Seq. ID LIB3165-011-P1-K1-E10 BLASTX Method q2501578 NCBI GI 619 BLAST score 1.0e-64 E value 132 Match length % identity NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree

>gi_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 221482

BLAST score

E value

578

7.0e-60

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1/ 1/2 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4 × 1/4
```

```
LIB3165-011-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  g1168411
NCBI GI
                  529
BLAST score
E value
                  4.0e-54
Match length
                  128
                  84
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  221483
Seq. No.
                  LIB3165-011-P1-K1-E3
Seq. ID
                  BLASTX
Method
                  q3023281
NCBI GI
                  429
BLAST score
                  2.0e-42
E value
Match length
                  131
% identity
                  63
                  HIGH AFFINITY AMMONIUM TRANSPORTER
NCBI Description
                  >gi 2065194 emb CAA64475 (X95098) ammonium transporter
                   [Lycopersicon esculentum]
Seq. No.
                  221484
                  LIB3165-011-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  q3702332
NCBI GI
                  235
BLAST score .
                  1.0e-19
E value
                  80
Match length
                  54
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   221485
Seq. ID
                  LIB3165-011-P1-K1-E6
                  BLASTX
Method
                  g4467158
NCBI GI
BLAST score
                   281
                   5.0e-25
E value
                  125
Match length
                   57
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   221486
Seq. No.
Seq. ID
                   LIB3165-011-P1-K1-E8
                   BLASTX
Method
NCBI GI
                   g20729
BLAST score
                   508
E value
                   1.0e-51
                  134
Match length
                   78
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                   221487
                   LIB3165-011-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1332579
```



```
Match length 116 % identity 10
```

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 221488

Seq. ID LIB3165-011-P1-K1-F1

Method BLASTX
NCBI GI g1708313
BLAST score 475
E value 8.0e-48
Match length 100
% identity 95

NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637

(S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

thaliana]

Seq. No. 221489

Seq. ID LIB3165-011-P1-K1-F12

Method BLASTX
NCBI GI g2501568
BLAST score 177
E value 8.0e-13
Match length 55
% identity 55

NCBI Description HYPOTHETICAL 28.8 KD PROTEIN SLL0506

>qi 1001342 dbj BAA10829_ (D64006) hypothetical protein

[Synechocystis sp.]

Seq. No. 221490

Seq. ID LIB3165-011-P1-K1-F2

Method BLASTX
NCBI GI g1352821
BLAST score 742
E value 4.0e-79
Match length 141
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221491

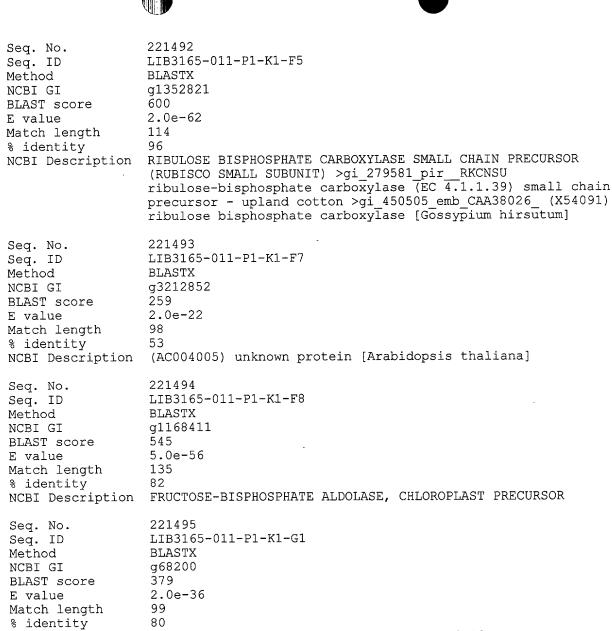
Seq. ID LIB3165-011-P1-K1-F4

Method BLASTX
NCBI GI g266893
BLAST score 564
E value 3.0e-58
Match length 122
% identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi 322416_pir__S28172

ribulose-bisphosphate carboxylase activase - cucumber >gi 18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis

satīvus]



NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 221496

Seq. ID LIB3165-011-P1-K1-G10

Method BLASTX
NCBI GI g1483218
BLAST score 182
E value 2.0e-13
Match length 102
% identity 41

NCBI Description (X99793) induced upon wounding stress [Arabidopsis

thaliana]



```
Seq. No.
                  221497
                  LIB3165-011-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  594
                  1.0e-61
E value
Match length
                  111
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221498
Seq. No.
                  LIB3165-011-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g20729
                  405
BLAST score
                  1.0e-39
E value
                  108
Match length
% identity
                  75
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  221499
Seq. No.
                  LIB3165-011-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  g1703129
NCBI GI
                  553
BLAST score
                  6.0e-57
E value
                  103
Match length
                  98
% identity
NCBI Description ACTIN 11 >gi 2129522_pir__S68109 actin 11 - Arabidopsis
                  thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                  thaliana]
                  221500
Seq. No.
                  LIB3165-011-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g231610
                  395
BLAST score
                  2.0e-38
E value
Match length
                  128
                   66
% identity
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                   >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, chloroplast - common
                   tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase
                   (gamma subunit) [Nicotiana tabacum]
```

Seq. ID LIB3165-011-P1-K1-G5

Method BLASTX
NCBI GI g131384
BLAST score 534
E value 8.0e-55
Match length 115



```
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132
                  photosystem II oxygen-evolving complex protein 1 precursor
                  - garden pea >gi_20621 emb_CAA33408 (X15350) precursor (AA
                  -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_
                  (D13297) precursor for 33-kDa protein of photosystem II
                  [Pisum sativum] >gi 226937 prf__1611461A 02 evolving
                  complex 33kD protein [Arachis hypogaea]
Seq. No.
                  221502
                  LIB3165-011-P1-K1-G6
Seq. ID
                  BLASTX
Method
                  q1781348
NCBI GI
                  645
BLAST score
E value
                  1.0e-67
                  140
Match length
                  89
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
                  221503
Seq. No.
                  LIB3165-011-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  q4105798
NCBI GI
                  229
BLAST score
                  6.0e-19
E value
Match length
                  61
                  61
% identity
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                  221504
Seq. No.
                  LIB3165-011-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g1351630
NCBI GI
                  254
BLAST score
                  7.0e-22
E value
                  104
Match length
                   48
% identity
                  PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE
NCBI Description
                   (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)
                   >gi_2130253_pir__S62537 hypothetical protein SPAC12G12.06c
                   - fission yeast (Schizosaccharomyces pombe)
                   >gi_1052524_emb_CAA91501_ (Z66568) SPAC12G12.06c, unknown,
                   len: 363 [Schizosaccharomyces pombe]
                   221505
Seq. No.
                   LIB3165-011-P1-K1-H11
Seq. ID
                   BLASTX
Method
                   q3738261
NCBI GI
                   212
BLAST score
                   5.0e-17
E value
                   54
Match length
% identity
```

31293

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

```
221506
Seq. No.
                  LIB3165-011-P1-K1-H4
Seq. ID
                  BLASTX
Method
                  g4490728
NCBI GI
                  324
BLAST score
                  4.0e-30
E value
                  99
Match length
                  64
% identity
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
                  221507
Seq. No.
                  LIB3165-011-P1-K1-H9
Seq. ID
                  BLASTN
Method
                  a16472
NCBI GI
BLAST score
                  41
                  9.0e-14
E value
                  228
Match length
                  79
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                   221508
Seq. No.
                  LIB3165-012-P1-K1-A10
Seq. ID
                   BLASTX
Method
                   q2864617
NCBI GI
BLAST score
                   266
                   3.0e-23
E value
                   124
Match length
% identity
                  (AL021811) H+-transporting ATP synthase chain9 - like
NCBI Description
                   protein [Arabidopsis thaliana]
                   221509
Seq. No.
                   LIB3165-012-P1-K1-A2
Seq. ID
Method
                   BLASTX
                   q4406530
NCBI GI
                   355
BLAST score
E value
                   1.0e-33
                   98
Match length
                   74
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   221510
Seq. No.
                   LIB3165-012-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   g115470
NCBI GI
                   259
BLAST score
                   9.0e-23
E value
                   91
Match length
                   60
% identity
NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                   DEHYDRATASE) >gi 320554_pir__$28412 carbonate dehydratase
```

[Arabidopsis thaliana]

(EC 4.2.1.1) precursor - Arabidopsis thaliana

>gi 14343_emb_CAA46508_ (X65541) carbonic anhydrase



```
LIB3165-012-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  g1168411
NCBI GI
                  537
BLAST score
                  4.0e-55
E value
Match length
                  127
                  87
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  221512
Seq. ID
                  LIB3165-012-P1-K1-A9
Method
                  BLASTX
                  q1352821
NCBI GI
                  539
BLAST score
                  3.0e-55
E value
                  102
Match length
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221513
Seq. No.
                  LIB3165-012-P1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1709651
BLAST score
                  391
                  6.0e-38
E value
                  119
Match length
                  65
% identity
NCBI Description PLASTOCYANIN A PRECURSOR >gi 2117431 pir __S58209
                  plastocyanin a precursor - black poplar
                  >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
                  221514
Seq. No.
                  LIB3165-012-P1-K1-B2
Seq. ID
                  BLASTX
Method
                  g20729
NCBI GI
                  383
BLAST score
                   4.0e-37
E value
Match length
                  106
                  74
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  221515
Seq. No.
                  LIB3165-012-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4406530
BLAST score
                   247
                  2.0e-28
E value
                   92
Match length
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
```



```
LIB3165-012-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  q1199772
NCBI GI
                  284
BLAST score
E value
                  2.0e-25
Match length
                  120
                  56
% identity
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                  >qi 1199774 dbj BAA11855 (D83227) extensin like protein
                   [Populus nigra]
Seq. No.
                  221517
Seq. ID
                  LIB3165-012-P1-K1-B8
                  BLASTX
Method
                  q3335341
NCBI GI
                   149
BLAST score
E value
                   1.0e-09
                   109
Match length
                   42
% identity
                  (AC004512) T8F5.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   221518
                   LIB3165-012-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   q4454466
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
Match length
                   52
                   69
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                   221519
Seq. No.
                   LIB3165-012-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q68200
BLAST score
                   381
                   6.0e-37
E value
                   102
Match length
                   79
% identity
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi_22633_emb CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   221520
Seq. No.
                   LIB3165-012-P1-K1-C5
Seq. ID
                   BLASTX
Method
                   q131385
NCBI GI
                   525
BLAST score
                   1.0e-53
E value
                   127
Match length
                   84
% identity
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
```

Seq. ID LIB3165-012-P1-K1-C6

```
BLASTX
Method
                  g1172664
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
                  37
Match length
                  92
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_419791_pir__S31165 photosystem I chain III precursor -
                  Flaveria trinervia >gi_298482_bbs 127083 photosystem I
                  reaction center subunit III, PSI-RC PsaF [Flaveria
                  trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                  I subunit III [Flaveria trinervia]
                  221522
Seq. No.
                  LIB3165-012-P1-K1-C7
Seq. ID
                  BLASTX
Method
                  g1168728
NCBI GI
                  339
BLAST score
                  8.0e-32
E value
Match length
                  116
% identity
                   53
                  CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi 598071 (L37883)
NCBI Description
                  cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                   221523
Seq. No.
                  LIB3165-012-P1-K1-C8
Seq. ID
                  BLASTX
Method
                   g487046
NCBI GI
BLAST score
                   264
                   4.0e-23
E value
                   109
Match length
                   49
% identity
                  photosystem I chain II precursor - wood tobacco
NCBI Description
                   >gi 407769 dbj BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
                   221524
Seq. No.
                   LIB3165-012-P1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4481934
                   143
BLAST score
                   7.0e-09
E value
Match length
                   101
                   15
% identity
NCBI Description (AL035640) CDA peptide synthetase I [Streptomyces
                   coelicolor]
                   221525
Seq. No.
Seq. ID
                   LIB3165-012-P1-K1-D10
                   BLASTX
Method
                   g4545262
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
Match length
                   44
% identity
```

NCBI Description (AF118230) metallothionein-like protein [Gossypium



hirsutum]

```
221526
Seq. No.
                  LIB3165-012-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123271
                  497
BLAST score
                  2.0e-50
E value
                  114
Match length
% identity
                  40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
                  221527
Seq. No.
                  LIB3165-012-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1617206
                  344
BLAST score
                  2.0e-32
E value
                  78
Match length
                  78
% identity
NCBI Description (Z72489) CP12 [Pisum sativum]
                  221528
Seq. No.
                  LIB3165-012-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q542020
BLAST score
                   348
                   4.0e-45
E value
                   121
Match length
                   77
% identity
NCBI Description
                  sucrose transport protein - castor bean
                   >gi 468562 emb_CAA83436_ (Z31561) sucrose carrier [Ricinus
                   communis]
                   221529
Seq. No.
                   LIB3165-012-P1-K1-D5
Seq. ID
Method
                   BLASTX
                   g282833
NCBI GI
                   296
BLAST score
                   8.0e-27
E value
                   73
Match length
                   84
% identity
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
                   221530
Seq. No.
Seq. ID
                   LIB3165-012-P1-K1-D6
                   BLASTX
Method
                   g693916
NCBI GI
BLAST score
                   171
E value
                   3.0e-12
Match length
                   66
                   59
% identity
NCBI Description (U21111) chlorophyll a/b binding protein [Solanum
                   tuberosum]
```

221531

Seq. No.



```
LIB3165-012-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  g3831458
NCBI GI
                  133
BLAST score
                  3.0e-16
E value
                  114
Match length
% identity
                  36
                  (AC005700) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  221532
Seq. No.
                  LIB3165-012-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  q3193326
NCBI GI
                  171
BLAST score
                  3.0e-12
E value
                  83
Match length
                  52
% identity
                  (AF069299) contains similarity to transcriptional
NCBI Description
                  activators such as Ra-like and myc-like regulatory R
                  proteins [Arabidopsis thaliana]
Seq. No.
                   221533
                  LIB3165-012-P1-K1-E11
Seq. ID
                  BLASTX
Method
                   q1352683
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
                   46
Match length
                   72
% identity
                  PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi 995839 (U34803)
NCBI Description
                   protein phosphatase homolog [Arabidopsis thaliana]
                   221534
Seq. No.
                   LIB3165-012-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   g3377812
NCBI GI
                   194
BLAST score
                   7.0e-15
E value
                   62
Match length
                   68
% identity
                  (AF076275) contains similarity to heavy-metal-associated
NCBI Description
                   domain containing proteins (Pfam: HMA.hm, score: 12.02)
                   [Arabidopsis thaliana]
                   221535
Seq. No.
Seq. ID
                   LIB3165-012-P1-K1-E2
                   BLASTX
Method
                   q1408471
NCBI GI
                   535
BLAST score
                   7.0e-55
E value
Match length
                   120
 % identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
```

factor 1 [Arabidopsis thaliana]



LIB3165-012-P1-K1-E3 Seq. ID BLASTX Method g131187 NCBI GI 301 BLAST score 2.0e-27 E value 132 Match length 55 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_72681_pir__F1SP3 photosystem I chain III precursor spinach >gi 21303 emb CAA31523 (X13133) PSI subunit IV preprotein (AA -77 to 154) [Spinacia oleracea] >gi 226166 prf__1413236A photosystem I reaction center IV [Spinacia oleracea] 221537 Seq. No. LIB3165-012-P1-K1-E5 Seq. ID Method BLASTX g4510373 NCBI GI BLAST score 266 3.0e-23 E value Match length 72 71 % identity (AC007017) putative harpin-induced protein [Arabidopsis NCBI Description thaliana] 221538 Seq. No. LIB3165-012-P1-K1-E6 Seq. ID BLASTX Method g1130682 NCBI GI BLAST score 323 5.0e-30 E value 62 Match length 100 % identity NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum] 221539 Seq. No. LIB3165-012-P1-K1-E7 Seq. ID BLASTX Method g2209332 NCBI GI BLAST score 610 1.0e-63 E value 133 Match length 86 % identity (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis NCBI Description thaliana] >gi 3927828 (AC005727) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] 221540 Seq. No. LIB3165-012-P1-K1-E8 Seq. ID BLASTN Method q2687434 NCBI GI 307 BLAST score E value 1.0e-172 Match length 367

NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,

96

% identity



partial sequence

 Seq. No.
 221541

 Seq. ID
 LIB3165-012-P1-K1-E9

 Method
 BLASTX

 NCBI GI
 q4406530

NCBI GI g4406530
BLAST score 329
E value 1.0e-30
Match length 92
% identity 74

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221542

Seq. ID LIB3165-012-P1-K1-F10

Method BLASTX
NCBI GI g1706107
BLAST score 632
E value 3.0e-66
Match length 130
% identity 95

NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)

>gi 1143709 (U13630) chloroplast phosphate/triose-phosphate

translocator precursor [Brassica oleracea]

Seq. No. 221543

Seq. ID LIB3165-012-P1-K1-F11

Method BLASTX
NCBI GI 9421826
BLAST score 291
E value 2.0e-26
Match length 57
% identity 88

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 221544

Seq. ID LIB3165-012-P1-K1-F3

Method BLASTX
NCBI GI g1168408
BLAST score 574
E value 2.0e-59
Match length 128
% identity 89

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 221545

Seq. ID LIB3165-012-P1-K1-F6

Method BLASTX
NCBI GI g1352821
BLAST score 671
E value 8.0e-71
Match length 126
% identity 95

BLAST score

E value Match length 394 2.0e-38

92



```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221546
Seq. No.
                  LIB3165-012-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  q4105794
NCBI GI
                  200
BLAST score
                  2.0e-15
E value
                  45
Match length
                  62
% identity
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
                  221547
Seq. No.
                  LIB3165-012-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g4008159
NCBI GI
BLAST score
                  269
                  8.0e-24
E value
                  84
Match length
% identity
                  64
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
                  221548
Seq. No.
                  LIB3165-012-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g462195
NCBI GI
BLAST score
                  432
                  9.0e-43
E value
                  93
Match length
                  91
% identity
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi 100682 pir S21636 GOS2 protein - rice
                   >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                   >gi 3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
                  221549
Seq. No.
Seq. ID
                  LIB3165-012-P1-K1-G5
                  BLASTX
Method
NCBI GI
                  q1653089
BLAST score
                   305
                   7.0e-28
E value
                  89
Match length
                   63
% identity
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
Seq. No.
                   221550
                   LIB3165-012-P1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1170711
```

Match length

116

```
86
% identity
                  SHAGGY RELATED PROTEIN KINASE ASK-ALPHA
NCBI Description
                  >gi_541901_pir__S41596 protein kinase ASK-alpha (EC
                  2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_
                  (X75432) shaggy related kinase [Arabidopsis thaliana]
                  >gi 1769889_emb CAA48538 (X68525) serine /threonine
                  protein kinase [Arabidopsis thaliana]
                  221551
Seq. No.
                  LIB3165-012-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  q3288821
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
                  133
Match length
                  78
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  221552
Seq. No.
Seq. ID
                  LIB3165-012-P1-K1-G8
                  BLASTX
Method
                  g4468979
NCBI GI
                  278
BLAST score
                  6.0e-25
E value
                  54
Match length
                  94
% identity
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                  221553
Seq. No.
                  LIB3165-012-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  q4406530
NCBI GI
                   296
BLAST score
E value
                  2.0e-27
                  59
Match length
                   95
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   221554
Seq. No.
Seq. ID
                   LIB3165-012-P1-K1-H11
                   BLASTN
Method
                   g2687435
NCBI GI
                   262
BLAST score
                   1.0e-145
E value
Match length
                   350
                   95
% identity
NCBI Description Hamamelis virginiana large subunit 26S ribosomal RNA gene,
                   partial sequence
Seq. No.
                   221555
                   LIB3165-012-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662343
BLAST score
                   587
                   6.0e-61
E value
```

NCBI GI

BLAST score



```
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  221556
Seq. No.
                  LIB3165-012-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  q3202032
NCBI GI
BLAST score
                  263
                  4.0e-23
E value
                  96
Match length
% identity
                  41
                  (AF069319) leaf catalase [Mesembryanthemum crystallinum]
NCBI Description
                  221557
Seq. No.
                  LIB3165-012-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g1791309
NCBI GI
                  203
BLAST score
                  5.0e-16
E value
                  106
Match length
% identity
                   50
                  (U83500) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                   thaliana] >gi_2852454_dbj_BAA24699 (AB010888)
                   cystathionine gamma-synthase [Arabidopsis thaliana]
                   221558
Seq. No.
                   LIB3165-012-P1-K1-H9
Seq. ID
                   BLASTX
Method
                   g1684857
NCBI GI
BLAST score
                   596
E value
                   5.0e-62
                   120
Match length
                   40
% identity
NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]
                   221559
Seq. No.
Seq. ID
                   LIB3165-013-P1-K1-A2
                   BLASTX
Method
                   q115765
NCBI GI
BLAST score
                   734
                   4.0e-78
E value
Match length
                   143
                   65
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
NCBI Description
                   (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding
                   protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                   esculentum] >gi 170431 (M20241) chlorophyll a/b-binding
                   protein [Lycopersicon esculentum] >gi_226546_prf__1601518A
                   chlorophyll a/b binding protein II [Lycopersicon
                   esculentum]
Seq. No.
                   221560
                   LIB3165-013-P1-K1-A6
Seq. ID
Method
                   BLASTX
```

g4406530 627



```
1.0e-65
E value
                  132
Match length
                  88
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  221561
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-A7
                  BLASTX
Method
                  g1172664
NCBI GI
                  207
BLAST score
                  2.0e-16
E value
                  45
Match length
                  91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi 419791 pir S31165 photosystem I chain III precursor -
                  Flaveria trinervia >gi 298482 bbs 127083 photosystem I
                  reaction center subunit III, PSI-RC PsaF [Flaveria
                  trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem
                  I subunit III [Flaveria trinervīa]
                  221562
Seq. No.
                  LIB3165-013-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g2956717
NCBI GI
                  268
BLAST score
                  2.0e-23
E value
                  117
Match length
                  55
% identity
NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
                  221563
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-B11
                  BLASTX
Method
NCBI GI
                  q2738756
BLAST score
                   549
                   3.0e-63
E value
                   130
Match length
                   94
% identity
                  (AF016282) 5'-adenylylsulfate reductase [Arabidopsis
NCBI Description
                   thaliana]
                   221564
Seq. No.
Seq. ID
                   LIB3165-013-P1-K1-B12
                   BLASTX
Method
                   q4406530
NCBI GI
BLAST score
                   361
                   2.0e-34
E value
                   98
Match length
% identity
                   76
                 (AF126870) rubisco activase [Vigna radiata]
NCBI Description
```

LIB3165-013-P1-K1-B2 Seq. ID

BLASTX Method g487046 NCBI GI BLAST score 426



5.0e-42 E value 141 Match length 60 % identity photosystem I chain II precursor - wood tobacco NCBI Description >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris] 221566 Seq. No. LIB3165-013-P1-K1-B4 Seq. ID BLASTN Method g4519194 NCBI GI 34 BLAST score 1.0e-09 E value 194 Match length 80 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MHM17, complete sequence 221567 Seq. No. LIB3165-013-P1-K1-B5 Seq. ID BLASTX Method g3184098 NCBI GI 276 BLAST score 2.0e-24 E value 134 Match length 46 % identity (AL023777) coenzyme a synthetase [Schizosaccharomyces NCBI Description pombe] 221568 Seq. No. LIB3165-013-P1-K1-B6 Seq. ID BLASTX Method q1174162 NCBI GI 580 BLAST score 4.0e-60 E value 109 Match length 92 % identity (U44976) ubiquitin-conjugating enzyme [Arabidopsis NCBI Description thaliana] >qi 3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] 221569 Seq. No. Seq. ID LIB3165-013-P1-K1-B7 BLASTX Method q1217601 NCBI GI BLAST score 266 2.0e-23 E value 56 Match length 88 % identity (D42070) PSI-E subunit of photosystem I [Nicotiana NCBI Description sylvestris]

Seq. No. 221570

Seq. ID LIB3165-013-P1-K1-B8

Method BLASTX
NCBI GI g3033400
BLAST score 562



```
5.0e-58
E value
Match length
                  128
                  84
% identity
                  (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  221571
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-C11
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  574
                  2.0e-59
E value
                  108
Match length
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) > gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   221572
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-C2
                  BLASTX
Method
NCBI GI
                  q68200
                   528
BLAST score
                   5.0e-54
E value
                   134
Match length
                   81
% identity
NCBI Description
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >qi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                   221573
Seq. ID
                   LIB3165-013-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2664210
BLAST score
                   368
                   2.0e-40
E value
Match length
                   139
% identity
                   57
                  (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   221574
Seq. No.
                   LIB3165-013-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2244806
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
Match length
                   138
                   46
% identity
```

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 221575

 Seq. ID
 LIB3165-013-P1-K1-C6

 Method
 BLASTX

 NCBI GI
 g2894565



```
BLAST score
                  151
                  8.0e-10
E value
Match length
                  70
                  67
% identity
                  (AL021890) heat shock protein - like [Arabidopsis thaliana]
NCBI Description
                  221576
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-C7
                  BLASTX
Method
                  q115471
NCBI GI
                  625
BLAST score
                  2.0e-65
E value
                  140
Match length
                  82
% identity
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                  DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase
                  (EC 4.2.1.1) precursor - garden pea >gi 20673 emb CAA36792
                  (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
Seq. No.
                  221577
                  LIB3165-013-P1-K1-C8
Seq. ID
                  BLASTX
Method
                  q231610
NCBI GI
BLAST score
                  279
E value
                  7.0e-27
                  113
Match length
                  63
% identity
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
                  221578
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  g100616
BLAST score
                  387
                  2.0e-37
E value
Match length
                  100
                  76
% identity
NCBI Description
                  ribulose-bisphosphate carboxylase activase B precursor -
                  barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                  carboxylase activase [Hordeum vulgare] >gi 167095 (M55449)
                  ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                  vulgare]
                  221579
Seq. No.
                  LIB3165-013-P1-K1-D12
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1710112
BLAST score 423
E value 7.0e-42
Match length 101
% identity 82

NCBI Description (U53864) PRH19 [Arabidopsis thaliana]



% identity

NCBI Description

```
221580
Seq. No.
                   LIB3165-013-P1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2244954
BLAST score
                   105
                   2.0e-09
E value
                   44
Match length
                   60
% identity
                   (Z97340) strong similarity to ATsEH (EC 3.3.2.3) -
NCBI Description
                   Arabidopsis thaliana [Arabidopsis thaliana]
                   221581
Seq. No.
                   LIB3165-013-P1-K1-D8
Seq. ID
                   BLASTX
Method
                   q1946367
NCBI GI
                   164
BLAST score
                   3.0e-11
E value
Match length
                   57
% identity
                   51
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                   221582
Seq. No.
                   LIB3165-013-P1-K1-D9
Seq. ID
Method
                   BLASTX
                   g266893
NCBI GI
                   715
BLAST score
                   6.0e-76
E value
                   139
Match length
                   96
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                   PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172
                   ribulose-bisphosphate carboxylase activase - cucumber
                   >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis
                   sativus]
                   221583
Seq. No.
                   LIB3165-013-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1181599
BLAST score
                   492
                   8.0e-50
E value
Match length
                   127
                   76
% identity
                   (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
Seq. No.
                   221584
                   LIB3165-013-P1-K1-E10
Seq. ID
                   BLASTX
Method
                   g131385
NCBI GI
                   562
BLAST score
                   5.0e-58
E value
                   136
Match length
```

THYLAKOID MEMBRANE PROTEIN)

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD



Seq. No.

```
LIB3165-013-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g166834
NCBI GI
                  705
BLAST score
                  9.0e-75
E value
                  137
Match length
                  97
% identity
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
                  221586
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-E3
                  BLASTX
Method
                  g2829903
NCBI GI
                  360
BLAST score
                  3.0e-34
E value
                  75
Match length
                  89
% identity
                  (AC002311) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221587
Seq. No.
                  LIB3165-013-P1-K1-E4
Seq. ID
                  BLASTN
Method
                  g3985958
NCBI GI
                  33
BLAST score
                   6.0e-09
E value
                   97
Match length
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZN1, complete sequence [Arabidopsis thaliana]
                   221588
Seq. No.
Seq. ID
                   LIB3165-013-P1-K1-E5
Method
                   BLASTX
                   g4406530
NCBI GI
                   359
BLAST score
                   3.0e - 34
E value
Match length
                   118
% identity
                   64
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   221589
Seq. No.
                   LIB3165-013-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914435
BLAST score
                   399
                   7.0e-39
E value
Match length
                   109
% identity
                   67
                  PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
NCBI Description
                   [Glycine max]
                   221590
Seq. No.
                   LIB3165-013-P1-K1-F1
Seq. ID
                   BLASTX
Method
```



```
NCBI GI
                   g445116
BLAST score
                   142
E value
                   6.0e-15
                   73
Match length
                   57
% identity
NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]
Seq. No.
                   221591
Seq. ID
                   LIB3165-013-P1-K1-F10
Method
                   BLASTX
                   g1352821
NCBI GI
                   713
BLAST score
                   1.0e-75
E value
                   135
Match length
                   96
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carbo\overline{x}ylase (EC \overline{4.1.1.39}) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   221592
                   LIB3165-013-P1-K1-F11
```

```
Seq. No.
Seq. ID
                  BLASTX
Method
                  g3282092
NCBI GI
BLAST score
                  163
                   3.0e-11
E value
                  106
Match length
                   38
% identity
```

NCBI Description (AJ007446) hypothetical protein [Thermotoga neapolitana]

Seq. No. 221593 LIB3165-013-P1-K1-F3 Seq. ID BLASTX Method NCBI GI g1352821 BLAST score 469 5.0e-47 E value 124 Match length 79 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221594

LIB3165-013-P1-K1-F4 Seq. ID

BLASTX Method g1439609 NCBI GI BLAST score 592 E value 2.0e-61 Match length 119 % identity 55

(U62778) delta-tonoplast intrinsic protein [Gossypium NCBI Description

hirsutum]

221595 Seq. No.



```
LIB3165-013-P1-K1-F5
Seq. ID
                  BLASTX
Method
                  g100196
NCBI GI
                  473
BLAST score
E value
                  1.0e-47
                  105
Match length
                  82
% identity
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
                  221596
Seq. No.
                   _ - 5-013-P1-K1-F9
Seq. ID
                  BLA.
Method
                   q3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
Match length
                   37
% identity
                   61
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   221597
Seq. No.
                   LIB3165-013-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g479406
BLAST score
                   525
                   1.0e-53
E value
                   103
Match length
% identity
                   65
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                   >gi_2<sup>7</sup>71_emb_CAA49149 (X69215) chlorophyll a/b-binding
prot : [Pisum sativum]
                   . .598
Seq. Nc.
                   L_B3165-013-P1-K1-G11
Seq. ID
Method
                   BLASTX
                   q120663
NCBI GI
                   546
BLAST score
                   4.0e-56
E value
                   135
Match length
                   77
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE O. DROGERASE B PRECURSOR,
                   CHLOROPLAST >gi_660. DEPMNB
                   glyceraldehyde-3-gnosphale dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                   garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate
                   dehydrogenase B subunit [Pisum sativum]
                   221599
Seq. No.
                   LIB3165-013-P1-K1-G3
Seq. ID
                   BLASTX
Method
                   g1350680
NCBI GI
BLAST score
                   521
                   3.0e-53
E value
                   120
Match length
                   80
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
```

Seq. No.

% identity

91



```
LIB3165-013-P1-K1-G6
Seq. ID
                  BLASTX
Method
                  g3080390
NCBI GI
                  494
BLAST score
                  5.0e-50
E value
                  119
Match length
                  78
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  221601
Seq. No.
                  LIB3165-013-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  640
BLAST score
                   4.0e-67
E value
                  122
Match length
                   94
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   221602
Seq. No.
                   LIB3165-013-P1-K1-G9
Seq. ID
                   BLASTX
Method
                   g2088662
NCBI GI
                   227
BLAST score
                   1.0e-18
E value
                   116
Match length
                   47
% identity
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
                   221603
Seq. No.
                   LIB3165-013-P1-K1-H1
Seq. ID
                   BLASTX
Method
                   g120662
NCBI GI
                   579
BLAST score
                   5.0e-60
E value
                   119
Match length
                   89
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,
                   CHLOROPLAST >gi 81621 pir__JQ1286
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                   Arabidopsis thaliana >gi_336390 (M64115) glyceraldehyde
                   3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]
                   221604
Seq. No.
                   LIB3165-013-P1-K1-H10
Seq. ID
Method
                   BLASTN
                   g18058
NCBI GI
 BLAST score
                   187
                   1.0e-101
E value
Match length
                   311
```

NCBI Description Citrus limon cistron for 26S ribosomal RNA

BLAST score

E value Match length 555 4.0e-57

106

```
221605
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-H12
                  BLASTX
Method
                  g2832643
NCBI GI
BLAST score
                  200
                  1.0e-15
E value
                  57
Match length
                  74
% identity
                  (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  221606
Seq. No.
                  LIB3165-013-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  q625547
NCBI GI
BLAST score
                  495
                  4.0e-50
E value
                  128
Match length
                  77
% identity
                  chlorophyll a/b-binding protein type I - common tobacco
NCBI Description
                  >gi 493723 emb CAA45523 (X64198) photosystem I
                  light-harvesting chlorophyll a/b-binding protein [Nicotiana
                  tabacum]
                  221607
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-H3
Method
                  BLASTX
                  g1352821
NCBI GI
                  567
BLAST score
                  2.0e-58
E value
                  111
Match length
% identity
                  94
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581 pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221608
Seq. No.
Seq. ID
                  LIB3165-013-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q1856971
BLAST score
                  412
                  2.0e-40
E value
Match length
                   91
                   89
% identity
                  (D26058) This gene is specifically expressed at the S phase
NCBI Description
                  during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
Seq. No.
                   221609
                  LIB3165-013-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                  q1352821
```



% identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 221610 Seq. No. Seq. ID LIB3165-013-P1-K1-H6 BLASTX Method q1071913 NCBI GI 256 BLAST score 4.0e-22 E value 110 Match length 56 % identity cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial NCBI Description - spinach >gi 1066153 dbj BAA07177_ (D37963) cysteine synthase [Spinacia oleracea] Seq. No. 221611 LIB3165-013-P1-K1-H7 Seq. ID BLASTX Method q3687652 NCBI GI BLAST score 606 3.0e-63 E value 128 Match length 92 % identity NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata] Seq. No. 221612 Seq. ID LIB3165-014-P1-K1-A11 BLASTX Method q1352821 NCBI GI BLAST score 572 E value 4.0e-59 Match length 110 99 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 221613 Seq. No. LIB3165-014-P1-K1-A12 Seq. ID Method BLASTX g3913651 NCBI GI 161 BLAST score 6.0e-11 E value Match length 47 70

% identity

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR

(FNR) >gi 2225993 emb CAA74359 (Y14032)

ferredoxin--NADP(+) reductase [Nicotiana tabacum]

221614 Seq. No.

LIB3165-014-P1-K1-A2 Seq. ID



```
Method BLASTX
NCBI GI g2854153
BLAST score 196
E value 4.0e-15
Match length 91
% identity 46
NCBI Description (AF045640) No definition line found [Caenorhabditis elegans]
```

Seq. No. 221615

Seg. ID LIB3165-014-P1-K1-A5

Method BLASTX
NCBI GI g3928760
BLAST score 268
E value 2.0e-23
Match length 115
% identity 52

NCBI Description (AB011797) homolog to plastid-lipid-associated protein

[Citrus unshiu]

Seq. No. 221616

Seq. ID LIB3165-014-P1-K1-A6

Method BLASTX
NCBI GI g1168411
BLAST score 537
E value 5.0e-55
Match length 132
% identity 83

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 221617

Seq. ID LIB3165-014-P1-K1-A7

Method BLASTX
NCBI GI g2244905
BLAST score 245
E value 9.0e-22
Match length 115
% identity 50

NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 221618

Seq. ID LIB3165-014-P1-K1-B10

Method BLASTX
NCBI GI g1353352
BLAST score 325
E value 3.0e-30
Match length 91
% identity 73

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

Seq. No. 221619

Seq. ID LIB3165-014-P1-K1-B11

Method BLASTX NCBI GI g1781348 BLAST score 620



8.0e-65 E value 135 Match length 88 % identity (Y10380) homologous to plastidic aldolases [Solanum NCBI Description tuberosum] 221620 Seq. No. Seq. ID LIB3165-014-P1-K1-B12 BLASTX Method q2342674 NCBI GI 294 BLAST score 1.0e-26 E value 118 Match length 56 % identity (AC000106) Similar to ATP-dependent Clp protease NCBI Description (gb D90915). EST gb_N65461 comes from this gene. [Arabidopsis thaliana] Seq. No. 221621 LIB3165-014-P1-K1-B3 Seq. ID BLASTX Method q1168411 NCBI GI 379 BLAST score 1.0e-36 E value 99 Match length 80 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR 221622 Seq. No. Seq. ID LIB3165-014-P1-K1-B4 Method BLASTX q1771780 NCBI GI BLAST score 391 6.0e-38 E value Match length 108 78 % identity (Y10024) ubiquitin extension protein [Solanum tuberosum] NCBI Description Seq. No. 221623 Seq. ID LIB3165-014-P1-K1-B5 BLASTX Method NCBI GI g1346809 BLAST score 363 1.0e-34 E value Match length 108 % identity 64 PATHOGEN-RELATED PROTEIN >gi 499074 emb CAA34641 (X16648) NCBI Description pathogenesis related protein [Hordeum vulgare] Seq. No. 221624 LIB3165-014-P1-K1-B6 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g228403
BLAST score 247
E value 2.0e-39
Match length 130
% identity 72

```
NCBI Description glycolate oxidase [Lens culinaris]
                  221625
Seq. No.
                  LIB3165-014-P1-K1-B7
Seq. ID
Method
                  BLASTN
                  g2687434
NCBI GI
                  233
BLAST score
                  1.0e-128
E value
                  285
Match length
                  95
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                  221626
Seq. No.
                  LIB3165-014-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g2815246
NCBI GI
                  225
BLAST score
                  2.0e-18
E value
                  55
Match length
% identity
                  73
                  (X95709) class I type 2 metallothionein [Cicer arietinum]
NCBI Description
                  221627
Seq. No.
                  LIB3165-014-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g20729
                  505
BLAST score
                  2.0e-51
E value
                  122
Match length
                  81
% identity
                 (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  221628
Seq. No.
                  LIB3165-014-P1-K1-C9
Seq. ID
                  BLASTX
Method
                   g100616
NCBI GI
                   286
BLAST score
                   1.0e-25
E value
                   64
Match length
                   86
% identity
NCBI Description ribulose-bisphosphate carboxylase activase B precursor -
                  barley >qi 167093 (M55448) ribulose 1,5-bisphosphate
                   carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
                   ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                   vulgare]
                   221629
Seq. No.
Seq. ID
                   LIB3165-014-P1-K1-D1
                   BLASTX
Method
NCBI GI
                   g417103
BLAST score
                   524
                   1.0e-53
E value
Match length
                   112
% identity
                   94
NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone
                   H3.3-like protein - Arabidopsis thaliana
```



>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >qi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

```
221630
Seq. No.
                  LIB3165-014-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  527
BLAST score
                  7.0e-54
E value
                  102
Match length
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir _RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221631
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-D12
                  BLASTX
Method
NCBI GI
                  g2618686
                  142
BLAST score
                  9.0e-09
E value
                  88
Match length
% identity
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]
                   221632
Seq. No.
                  LIB3165-014-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q20733
                  515
BLAST score
                   2.0e-52
E value
```

NCBI Description (X15188) precursor C-terminal fragment (A -80 to 367) [Pisum sativum]

Seq. No. 221633

Match length

% identity

Seq. ID LIB3165-014-P1-K1-D4

118 83

Method BLASTX NCBI GI g2956717



```
169
BLAST score
                  7.0e-12
E value
                  106
Match length
                  43
% identity
NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
                  221634
Seq. No.
                  LIB3165-014-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  q131385
NCBI GI
                  570
BLAST score
                  6.0e-59
E value
                  136
Match length
                  85
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
                  221635
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-D7
                  BLASTX
Method
                  g3834306
NCBI GI
                  244
BLAST score
                  7.0e-21
E value
                  84
Match length
                  57
% identity
                  (AC005679) EST gb_R65024 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   221636
Seq. No.
                  LIB3165-014-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  g1169494
NCBI GI
                   237
BLAST score
                   7.0e-20
E value
                   70
Match length
                   71
% identity
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                   >gi_2119915_pir__S60659 EF-Tu protein precursor - soybean
                   >gi 949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine
                   max]
                   221637
Seq. No.
                   LIB3165-014-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g2119927
NCBI GI
                   612
BLAST score
                   7.0e-64
E value
Match length
                   134
                   90
 % identity
NCBI Description translation elongation factor G, chloroplast - soybean
 Seq. No.
                   221638
 Seq. ID
                   LIB3165-014-P1-K1-E11
 Method
                   BLASTX
```

g289920

704

NCBI GI BLAST score

% identity



```
1.0e-74
 E value
                    131
 Match length
                    99
 % identity
                    (L07119) chlorophyll A/B binding protein [Gossypium
 NCBI Description
                    hirsutum]
                    221639
 Seq. No.
                    LIB3165-014-P1-K1-E12
 Seq. ID
 Method
                    BLASTX
                    q585118
 NCBI GI
 BLAST score
                    636
                    1.0e-66
 E value
                    133
 Match length
                    91
 % identity
                    FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                    (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                    >gi 289367 (L15303) fructose-1,6-bisphosphate [Brassica
                    napus]
                    221640
 Seq. No.
                    LIB3165-014-P1-K1-E6
 Seq. ID
 Method
                    BLASTX
                    q2505876
 NCBI GI
                    329
 BLAST score
                    1.0e-30
 E value
                    70
 Match length
                    89
  % identity
                    (Y12776) MYB-related protein [Arabidopsis thaliana]
 NCBI Description
                    221641
  Seq. No.
                    LIB3165-014-P1-K1-E7
  Seq. ID
  Method
                    BLASTX
                    q170354
  NCBI GI
                    533
  BLAST score
                    1.0e-54
  E value
                    108
  Match length
                    21
  % identity
  NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
                    221642
  Seq. No.
                    LIB3165-014-P1-K1-E8
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q2621154
  BLAST score
                    144
                     5.0e-09
  E value
                    124
  Match length
                     30
  % identity
  NCBI Description (AE000801) unknown [Methanobacterium thermoautotrophicum]
                     221643
  Seq. No.
  Seq. ID
                     LIB3165-014-P1-K1-F10
                     BLASTX
  Method
                     q1928981
  NCBI GI
  BLAST score
                     544
                     7.0e-56
  E value
                     116
  Match length
```

% identity

```
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
                  221644
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  381
E value
                  9.0e-37
                  95
Match length
                  79
% identity
                  (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
                  barley [Medicago sativa]
                  221645
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-F3
Method
                  BLASTX
                  g2995384
NCBI GI
BLAST score
                  153
E value
                  3.0e-10
Match length
                  41
                  73
% identity
                 (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
Seq. No.
                  221646
Seq. ID
                  LIB3165-014-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g2894599
BLAST score
                  496
E value
                  3.0e-50
Match length
                  104
                  83
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  221647
                  LIB3165-014-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                  492
E value
                  9.0e-50
Match length
                  119
% identity
                  79
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  221648
                  LIB3165-014-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119748
BLAST score
                  542
E value
                  1.0e-55
Match length
                  121
```

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC

88

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi 21245 emb CAA43860 (X61690)

Sweet as bisches between [Griss also also as]

fructose-bisphosphatase [Spinacia oleracea]



```
221649
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-G1
                  BLASTX
Method
                  g3290020
NCBI GI
BLAST score
                  442
                  6.0e-44
E value
                  96
Match length
                  91
% identity
                  (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)
NCBI Description
                  lyase; cytosolic isoform [Solanum tuberosum]
                  221650
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-G11
                  BLASTX
Method
                  g4406530
NCBI GI
                  364
BLAST score
                  9.0e-35
E value
                  98
Match length
                  76
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  221651
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  g1703129
                  557
BLAST score
                  2.0e-57
E value
                  103
Match length
                  99
% identity
                  ACTIN 11 >gi_2129522 pir S68109 actin 11 - Arabidopsis
NCBI Description
                  thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                  thaliana]
                  221652
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-G5
                  BLASTN
Method
                  g18058
NCBI GI
                  57
BLAST score
                  1.0e-23
E value
Match length
                  144
                  88
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                  221653
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-G8
Method
                  BLASTX
                  g1346155
NCBI GI
BLAST score
                   611
                   9.0e-64
E value
Match length
                  133
                   89
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >qi 481942 pir S40212 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
```

>gi 437995 emb CAA81078 (Z25859) glycine



hydroxymethyltransferase [Flaveria pringlei]

```
221654
Seq. No.
                  LIB3165-014-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q994736
                  148
BLAST score
                  5.0e-10
E value
                  52
Match length
% identity
                  60
NCBI Description
                  (M18327) LacOPZ-alpha peptide from pUC9; putative [cloning
                  vectors] >gi 994738 (M18328) LacOPZ-alpha peptide from
                  pUC9; putative [cloning vectors] >gi 994740 (M18329)
                  LacOPZ-alpha peptide from pUC9; putative [cloning vectors]
Seq. No.
                  221655
Seq. ID
                  LIB3165-014-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q1353352
BLAST score
                  286
                  1.0e-25
E value
                  74
Match length
                  76
% identity
                 (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  221656
Seq. No.
                  LIB3165-014-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  517
                  1.0e-52
E value
Match length
                  127
% identity
                  83
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  221657
Seq. No.
Seq. ID
                  LIB3165-014-P1-K1-H3
Method
                  BLASTX
                  g100203
NCBI GI
BLAST score
                  241
E value
                  1.0e-20
Match length
                  66
                  71
% identity
NCBI Description cysteine proteinase (EC 3.4.22.-) precursor - tomato
                  >gi_19195_emb_CAA78403_ (Z14028) pre-p.
                  proteinase [Lycopersicon esculentum]
Seq. No.
                  221658
Seq. ID
                  LIB3165-014-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g82437
BLAST score
                  453
                  3.0e-45
E value
Match length
                  83
% identity
                  100
NCBI Description plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K
```

```
protein short form - barley chloroplast (fragment)
>gi_1617032_emb_CAA32269_ (X14107) petD [Hordeum vulgare]
221659
LIB3165-014-P1-K1-H7
```

Method BLASTX
NCBI GI g4115931
BLAST score 317
E value 3.0e-29
Match length 119
% identity 60

Seq. No. Seq. ID

NCBI Description (AF118223) contains similarity to Guillardia theta ABC

transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No. 221660

Seq. ID LIB3165-016-P1-K1-A1

Method BLASTN
NCBI GI g3128142
BLAST score 34
E value 1.0e-09
Match length 62
% identity 89

% identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

"Seq. No. 221661

Seq. ID LIB3165-016-P1-K1-A12

Method BLASTX
NCBI GI g3450842
BLAST score 190
E value 5.0e-20
Match length 90
% identity 58

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

Seq. No. 221662

Seq. ID LIB3165-016-P1-K1-A4

Method BLASTX
NCBI GI g120661
BLAST score 472
E value 8.0e-66
Match length 140
% identity 91

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate

dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 221663

Seq. ID LIB3165-016-P1-K1-A6

Method BLASTX
NCBI GI g2498629
BLAST score 181
E value 2.0e-13
Match length 99
% identity 9

NCBI Description TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869

NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens] >gi_4505387_ref_NP_002495.1_pNFX1_ nuclear transcription factor, X-box binding

Seq. No. 221664

Seq. ID LIB3165-016-P1-K1-A9

Method BLASTX
NCBI GI g927601
BLAST score 252
E value 8.0e-22
Match length 56
% identity 84

NCBI Description [2Fe-2S] ferredoxin [Datura arborea, Peptide, 97 aa] >gi 1097873_prf__2114375A ferredoxin [Datura arborea]

Seq. No. 221665

Seq. ID LIB3165-016-P1-K1-B1

Method BLASTX
NCBI GI g266892
BLAST score 258
E value 2.0e-35
Match length 99
% identity 70

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 82028_pir__S16272

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - Para rubber tree >gi_168217 (M60274)

ribulose-1,5-bisphosphate carboxylase small subunit [Hevea

brasiliensis]

Seq. No. 221666

Seq. ID LIB3165-016-P1-K1-B4

Method BLASTX
NCBI GI g100362
BLAST score 235
E value 2.0e-37
Match length 122
% identity 70

NCBI Description photosystem II oxygen-evolving complex protein 2 precursor

(clone T23-5B) - common tobacco (fragment)

>gi_1345550_emb_CAA44292_ (X62426) 23-kDa ploypeptide of photosystem II oxygen-evolving complex [Nicotiana tabacum]

Seq. No. 221667

Seq. ID LIB3165-016-P1-K1-B7

Method BLASTX
NCBI GI g3298439
BLAST score 547
E value 3.0e-56
Match length 134
% identity 81

NCBI Description (AB010878) chloroplast ribosomal protein L4 [Nicotiana

tabacum]

Seq. No. 221668

Seq. ID LIB3165-016-P1-K1-B8

Method BLASTX

```
NCBI GI g1708191
BLAST score 325
E value 2.0e-44
Match length 111
% identity 84
NCBI Description HEXOSE C carrier
```

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No. 221669

Seq. ID LIB3165-016-P1-K1-B9

Method BLASTX
NCBI GI g132091
BLAST score 308
E value 2.0e-35
Match length 87
% identity 86

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN F1 PRECURSOR

(RUBISCO SMALL SUBUNIT F1) >gi_68065_pir__RKRPF1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (gene rbcSF1) - rape >gi_17852_emb_CAA39402_
(X55937) ribulose bisphosphate carboxylase /oxygenase

small subunit [Brassica napus]

Seq. No. 221670

Seq. ID LIB3165-016-P1-K1-C1

Method BLASTX
NCBI GI g1527191
BLAST score 233
E value 1.0e-22
Match length 77
% identity 64

NCBI Description (U67861) 1-aminocyclopropane-1-carboxylate oxidase

[Pelargonium x hortorum]

Seq. No. 221671

Seq. ID LIB3165-016-P1-K1-C6

Method BLASTX
NCBI GI g118564
BLAST score 475
E value 1.0e-55
Match length 139
% identity 81

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi 65955 pir DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi_18264_emb_CAA41434_ (X58542) NADH-dependent
hydroxypyruvate reductase [Cucumis sativus]
>gi_18275_emb_CAA32764_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 221672

Seq. ID LIB3165-016-P1-K1-C7

Method BLASTX
NCBI GI 9462187
BLAST score 429
E value 1.0e-62
Match length 126



 Seq. No.
 221673

 Seq. ID
 LIB3165-016-P1-K1-C8

 Method
 BLASTX

 NCBI GI
 g2894599

 BLAST score
 429

 E value
 3.00-61

BLAST score 429 E value 3.0e-61 Match length 135 % identity 84

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 221674

Seq. ID LIB3165-016-P1-K1-D1

Method BLASTX
NCBI GI g136707
BLAST score 289
E value 7.0e-45
Match length 123
% identity 77

NCBI Description CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR

(RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397 pir S26199

plastoquinol--plastocyanin reductase (EC 1.10.99.1)

iron-sulfur protein precursor - garden pea

>gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS

protein [Pisum sativum]

Seq. No. 221675

Seq. ID LIB3165-016-P1-K1-D11

Method BLASTX
NCBI GI g2129825
BLAST score 215
E value 7.0e-37
Match length 96
% identity 79

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 221676

Seq. ID LIB3165-016-P1-K1-D7

Method BLASTX
NCBI GI g3789940
BLAST score 405
E value 9.0e-58
Match length 124
% identity 22

NCBI Description (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar

H32-8560]

Seq. No. 221677

Seq. ID LIB3165-016-P1-K1-D8

Method BLASTX

Seq. ID

```
g1168411
NCBI GI
                   203
BLAST score
                   4.0e-29
E value
                   92
Match length
                   76
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   221678
Seq. No.
                   LIB3165-016-P1-K1-E10
Seq. ID
                   BLASTX
Method
                   q3192881
NCBI GI
                   234
BLAST score
                   1.0e-19
E value
                   94
Match length
                   59
% identity
NCBI Description (AF068834) starch synthase [Ipomoea batatas]
                   221679
Seq. No.
Seq. ID
                   LIB3165-016-P1-K1-E11
                   BLASTX
Method
                   g115765
NCBI GI
BLAST score
                   285
                   3.0e-44
E value
                   112
Match length
                   74
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
NCBI Description
                   (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                   esculentum] >gi_170431 (M20241) chlorophyll a/b-binding
                   protein [Lycopersicon esculentum] >gi 226546 prf 1601518A
                   chlorophyll a/b binding protein II [Lycopersicon
                   esculentum]
                   221680
Seq. No.
Seq. ID
                   LIB3165-016-P1-K1-E2
                   BLASTX
Method
                   q3288821
NCBI GI
                   270
BLAST score
                   2.0e-42
E value
                   107
Match length
% identity
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
Seq. No.
                   221681
Seq. ID
                   LIB3165-016-P1-K1-E3
                   BLASTX
Method
                   g1168411
NCBI GI
BLAST score
                   208
E value
                   1.0e-35
Match length
                   105
                   82
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                   221682
```

LIB3165-016-P1-K1-E5



BLASTX Method NCBI GI q421826 464 BLAST score 9.0e-66 E value Match length 141 % identity chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >gi 298036 emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana] 221683 Seq. No. Seq. ID LIB3165-016-P1-K1-E6 Method BLASTX g4544427 NCBI GI 213 BLAST score 9.0e-28 E value 86 Match length 77 % identity NCBI Description (AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana] 221684 Seq. No. Seq. ID LIB3165-016-P1-K1-E7 BLASTX -Method q2501578 NCBI GI 397 BLAST score 2.0e-39 E value 116 Match length 80 % identity ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047 NCBI Description ethylene-responsive protein 1 - Para rubber tree >gi 1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis] 221685 Seq. No. LIB3165-016-P1-K1-E9 Seq. ID Method BLASTN q18058 NCBI GI BLAST score 309 E value 1.0e-173 Match length 380 % identity 96 NCBI Description Citrus limon cistron for 26S ribosomal RNA Seq. No. 221686 LIB3165-016-P1-K1-F10 Seq. ID BLASTX Method g2494299 NCBI GI

Method BLASTX
NCBI GI g2494299
BLAST score 194
E value 3.0e-29
Match length 134
% identity 58

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi 1732361 (U80269) translation initiation

factor 2 beta [Malus domestica]

Seq. No. 221687

E value

Match length

```
Seq. ID
                  LIB3165-016-P1-K1-F11
Method
                  BLASTX
                  g117290
NCBI GI
BLAST score
                  196
E value
                  6.0e - 26
Match length
                  111
                  59
% identity
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
NCBI Description
                  (P36) (E30) >qi 100071 pir S23774 triose
                  phosphate/3-phosphoglycerate/phosphate translocator
                  precursor - garden pea >gi 20691 emb CAA38451 (X54639)
                  chloroplast import receptor p36 [Pisum sativum]
                  >gi 20853 emb CAA48210 (X68077) phosphate translocator
                  [Pisum sativum] >gi 228551_prf__1805409A phosphate
                  translocator [Pisum sativum]
                  221688
Seq. No.
Seq. ID
                  LIB3165-016-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q100200
                  239
BLAST score
                  1.0e-38
E value
                  113
Match length
                  69
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  221689
Seq. No.
                  LIB3165-016-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q508304
                  171
BLAST score
                  1.0e-24
E value
                  74
Match length
% identity
                  76
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                  221690
                  LIB3165-016-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263712
BLAST score
                  234
                  6.0e-31
E value
Match length
                  91
                  76
% identity
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                  thaliana]
                  221691
Seq. No.
                  LIB3165-016-P1-K1-F5
Seq. ID
Method
                  BLASTX
                  g3831467
NCBI GI
                  143
BLAST score
```

% identity 41
NCBI Description (AC005700) putative beta-amylase [Arabidopsis thaliana]

1.0e-16



```
221692
Seq. No.
Seq. ID
                  LIB3165-016-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  418
                  3.0e-57
E value
                  111
Match length
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  221693
Seq. No.
Seq. ID
                  LIB3165-016-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g82537
                  107
BLAST score
E value
                   6.0e-11
                  58
Match length
% identity
                   61
                  hypothetical 8K protein (rps12-trnN intergenic region) -
NCBI Description
                  rice chloroplast >gi 12039 emb CAA33943 (X15901) ORF72
                   [Oryza sativa] >qi 12063 emb CAA33917
                                                          (X15901) ORF72
                   [Oryza sativa] >gi 226659 prf 1603356CK ORF 71 [Oryza
                   sativa]
                  221694
Seq. No.
                  LIB3165-016-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q289920
BLAST score
                   487
                   2.0e-69
E value
Match length
                   133
                   98
% identity
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                   221695
Seq. No.
                  LIB3165-016-P1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4545261
                   33
BLAST score
                   5.0e-09
E value
                   57
Match length
                   89
% identity
                  Gossypium hirsutum metallothionein-like protein mRNA,
NCBI Description
                   complete cds
```

Seq. No. 221696

Seq. ID LIB3165-016-P1-K1-G7

Method BLASTX
NCBI GI g2739365
BLAST score 330
E value 5.0e-44
Match length 129
% identity 64

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]



```
221697
Seq. No.
                  LIB3165-016-P1-K1-G8
Seg. ID
                  BLASTX
Method
NCBI GI
                  g1352821
                  393
BLAST score
                  4.0e-51
E value
                  109
Match length
                  95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase \overline{\text{(EC 4.1.1.39)}} small chain
                  precursor - upland cotton >gi 450505_emb CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221698
Seq. No.
                  LIB3165-016-P1-K1-G9
Seq. ID
                  BLASTN
Method
                  g18058
NCBI GI
                  311
BLAST score
                  1.0e-175
E value
                  414
Match length
                  94
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                  221699
Seq. No.
Seq. ID
                  LIB3165-016-P1-K1-H1
                  BLASTX
Method
                  g4455208
NCBI GI
                  226
BLAST score
                   1.0e-18
E value
Match length
                   124
                   36
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   221700
Seq. No.
Seq. ID
                   LIB3165-016-P1-K1-H11
                   BLASTX
Method
                   q1354515
NCBI GI
                   216
BLAST score
                   1.0e-17
E value
                   100
Match length
                   53
% identity
NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus
                   tremuloides]
Seq. No.
                   221701
                   LIB3165-016-P1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3885334
BLAST score
                   250
                   2.0e-21
E value
                   55
Match length
                   84
% identity
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
```

Seq. No. 221702

thaliana]



LIB3165-016-P1-K1-H2 Seq. ID BLASTX Method g1063400 NCBI GI 311 BLAST score 1.0e-28 E value 85 Match length 88 % identity (X92888) glycolate oxidase [Lycopersicon esculentum] NCBI Description 221703 Seq. No. LIB3165-016-P1-K1-H5 Seq. ID BLASTX Method g1168411 NCBI GI 246 BLAST score 9.0e-41 E value 124 Match length % identity 80 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR 221704 Seq. No. LIB3165-016-P1-K1-H6 Seq. ID Method BLASTX q430947 NCBI GI 312 BLAST score 1.0e-46 E value 127 Match length 74 % identity (U01103) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana] 221705 Seq. No. LIB3165-016-P1-K1-H7 Seq. ID BLASTX Method g3914605 NCBI GI 484 BLAST score 3.0e-63 E value 138 Match length 90 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica] 221706 Seq. No. LIB3165-016-P1-K1-H8 Seq. ID BLASTX Method g4325345 NCBI GI 155 BLAST score E value 3.0e-10 74 Match length % identity

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydrocrotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

```
221707
Seq. No.
                  LIB3165-017-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  487
E value
                  3.0e-49
Match length
                  122
                  81
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  221708
Seq. No.
                  LIB3165-017-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                   638
                   6.0e-67
E value
Match length
                  127
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(EC 4.1.1.39)} small chain
                   precursor - upland cotton >gi_450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   221709
Seq. No.
                   LIB3165-017-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g553107
BLAST score
                   388
                   1.0e-37
E value
                   113
Match length
% identity
                   68
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]
                   221710
Seq. No.
                   LIB3165-017-P1-K1-A2
Seq. ID
Method
                   BLASTX
                   g2213629
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
                   99
Match length
                   71
% identity
NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]
                   221711
Seq. No.
                   LIB3165-017-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g20733
NCBI GI
                   567
BLAST score
                   1.0e-58
E value
                   118
Match length
                   89
% identity
                  (X15188) precursor C-terminal fragment (AA -80 to 367)
NCBI Description
                   [Pisum sativum]
Seq. No.
                   221712
```



```
LIB3165-017-P1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2582822
                  353
BLAST score
                  2.0e-33
E value
                  102
Match length
                  37
% identity
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
                  221713
Seq. No.
                  LIB3165-017-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  g3402487
NCBI GI
                  374
BLAST score
                  3.0e-36
E value
                  87
Match length
                  83
% identity
                   (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
NCBI Description
                  thaliana]
                  221714
Seq. No.
                  LIB3165-017-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  g3914658
NCBI GI
                   404
BLAST score
                  1.0e-39
E value
                  108
Match length
                  74
% identity
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal
                  protein [Arabidopsis thaliana]
                   221715
Seq. No.
Seq. ID
                  LIB3165-017-P1-K1-B1
                   BLASTX
Method
                   q2501568
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
Match length
                   44
                   57
% identity
                  HYPOTHETICAL 28.8 KD PROTEIN SLL0506
NCBI Description
                   >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
                   221716
                   LIB3165-017-P1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2511693
BLAST score
                   389
                   8.0e-38
E value
Match length
                   110
% identity
                   71
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
```

Seq. No. 221717

Seq. ID LIB3165-017-P1-K1-B3

```
Method
                   BLASTX
NCBI GI
                   g119937
BLAST score
                   393
                   3.0e-38
E value
Match length
                   109
                   68
% identity
                   FERREDOXIN I PRECURSOR >gi_65741_pir__FESP1 ferredoxin
NCBI Description
                   [2Fe-2S] I precursor - spinach >qi 170109 (M35660)
                   ferredoxin I precursor [Spinacia oleracea]
                   >gi 227453 prf 1704156A ferredoxin I [Spinacia oleracea]
                   221718
Seq. No.
Seq. ID
                   LIB3165-017-P1-K1-B6
                   BLASTX
Method
                   g2546954
NCBI GI
BLAST score
                   437
E value
                   2.0e-48
                   113
Match length
% identity
                   88
                  (Y15108) translation elongation factor-TU [Glycine max]
NCBI Description
                   221719
Seq. No.
Seq. ID
                   LIB3165-017-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g3786001
BLAST score
                   424
                   8.0e-42
E value
Match length
                   93
% identity
                   82
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   221720
                   LIB3165-017-P1-K1-B8
Seq. ID
Method
                   BLASTX
                   g115765
NCBI GI
                   469
BLAST score
                   4.0e-47
E value
Match length
                   106
% identity
                   47
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
NCBI Description
                   (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding
                   protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                   esculentum] >gi 170431 (M20241) chlorophyll a/b-binding
                   protein [Lycopersicon esculentum] >qi 226546 prf 1601518A
                   chlorophyll a/b binding protein II [Lycopersicon
                   esculentum]
Seq. No.
                   221721
                   LIB3165-017-P1-K1-C10
Seq. ID
Method
                   BLASTX
                   g2558962
NCBI GI
BLAST score
                   280
E value
                   6.0e-25
Match length
                   60
```

(AF025667) histone H2B1 [Gossypium hirsutum]

97

% identity

NCBI Description



```
Seq. No.
                  221722
                  LIB3165-017-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3702327
                  257
BLAST score
E value
                  3.0e-22
                  126
Match length
% identity
                  50
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221723
Seq. No.
Seq. ID
                  LIB3165-017-P1-K1-C12
                  BLASTX
Method
                  g3913018
NCBI GI
                  646
BLAST score
                  7.0e-68
E value
                  135
Match length
                  90
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  221724
Seq. No.
                  LIB3165-017-P1-K1-C2
Seq. ID
                  BLASTX
Method
                   g3850111
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
Match length
                   115
                   37
% identity
                   (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                   involvement in lipid metabolism [Schizosaccharomyces pombe]
Seq. No.
                   221725
                   LIB3165-017-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g20729
BLAST score
                   595
E value
                   7.0e-62
Match length
                   137
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
Seq. No.
                   221726
                   LIB3165-017-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2582822
BLAST score
                   203
E value
                   6.0e-16
Match length
                   115
% identity
                   47
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                   Protein of 32kDa) [Solanum tuberosum]
```

221727

LIB3165-017-P1-K1-C8

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  g4056456
                  225
BLAST score
                  2.0e-18
E value
                  52
Match length
                  81
% identity
                  (AC005990) Strong similarity to gb U20808 auxin-induced
NCBI Description
                  protein from Vigna radiata and a member of the zinc-binding
                  dehydrogenase family PF 00107. ESTs gb T43674, gb H77006
                  and gb AA395179 come from this gene. [Arabidopsis thaliana]
                  221728
Seq. No.
Seq. ID
                  LIB3165-017-P1-K1-C9
                  BLASTX
Method
                  g1732511
NCBI GI
BLAST score
                  396
                  2.0e-38
E value
Match length
                  91
                  82
% identity
                  (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                  thaliana]
                  221729
Seq. No.
Seq. ID
                  LIB3165-017-P1-K1-D1
                  BLASTX
Method
NCBI GI
                  g1495366
                  338
BLAST score
                  7.0e-32
E value
Match length
                  102
% identity
                  59
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
                  221730
Seq. No.
                  LIB3165-017-P1-K1-D11
Seq. ID
```

Method BLASTX
NCBI GI g3184258
BLAST score 153
E value 5.0e-10
Match length 59
% identity 44

NCBI Description (U82130) tumor susceptibility protein [Homo sapiens]

Seq. No. 221731

Seq. ID LIB3165-017-P1-K1-D12

Method BLASTX
NCBI GI g3451068
BLAST score 413
E value 2.0e-40
Match length 120
% identity 73

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 221732

Seq. ID LIB3165-017-P1-K1-D2

Method BLASTX
NCBI GI g4220480
BLAST score 265

```
4.0e-23
E value
                  102
Match length
                  53
% identity
                 (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221733
Seq. No.
                  LIB3165-017-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
                  591
BLAST score
E value
                  2.0e-61
                  119
Match length
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221734
Seq. ID
                  LIB3165-017-P1-K1-D5
                  BLASTX
Method
                  q3548806
NCBI GI
BLAST score
                  310
E value
                  2.0e-28
                  129
Match length
                  43
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  221735
Seq. ID
                  LIB3165-017-P1-K1-D6
                  BLASTX
Method
NCBI GI
                  a166834
                   627
BLAST score
E value
                  1.0e-65
                  134
Match length
% identity
                   87
NCBI Description
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   221736
Seq. ID
                  LIB3165-017-P1-K1-D7
                   BLASTX
Method
NCBI GI
                   q3334197
BLAST score
                   470
E value
                   3.0e-47
Match length
                  117
% identity
                   76
NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T
                   PROTEIN) >gi 2894400 emb CAA94902 (Z71184) T-protein
                   [Flaveria anomala]
```

221737

BLASTX

g2565436

LIB3165-017-P1-K1-D8

Seq. No.

Seq. ID Method

NCBI GI



BLAST score 270 9.0e-24 E value Match length 115 56 % identity

(AF028842) DegP protease precursor [Arabidopsis thaliana] NCBI Description

Seq. No.

221738

Seq. ID

LIB3165-017-P1-K1-D9

Method BLASTX q1168411 NCBI GI 387 BLAST score 2.0e-37 E value 101 Match length

80 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.

221739

Seq. ID

LIB3165-017-P1-K1-E1

Method BLASTX NCBI GI q131399 BLAST score 502 6.0e-51 E value 112 Match length 84 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE NCBI Description

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411

photosystem II 10K protein precursor - potato

>gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No.

221740

Seq. ID

LIB3165-017-P1-K1-E11

Method BLASTX q2129921 NCBI GI BLAST score 194 8.0e-15 E value 51 Match length % identity 75

hypothetical protein 1 - Madagascar periwinkle >gi 758694 NCBI Description

(U12573) putative [Catharanthus roseus]

Seq. No.

221741 LIB3165-017-P1-K1-E2

Seq. ID BLASTN Method

NCBI GI q12292 BLAST score 193 E value 1.0e-104 Match length 365 % identity 88

NCBI Description Spinach chloroplast DNA homologous to ARS and ARC elements

upstream of rDNA operon

Seq. No. 221742

LIB3165-017-P1-K1-E3 Seq. ID

BLASTX Method NCBI GI g3510256 BLAST score 172

NCBI Description

nigra]

```
3.0e-12
E value
                  95
Match length
                  42
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221743
Seq. No.
                  LIB3165-017-P1-K1-E4
Seq. ID
                  BLASTX
Method
                  g419781
NCBI GI
BLAST score
                  186
                  3.0e-14
E value
                  54
Match length
                  70
% identity
                  probable cysteine proteinase precursor (clone CYP-7) -
NCBI Description
                  common tobacco >gi 19849 emb CAA78361 (Z13959) tobacco
                  pre-pro-cysteine proteinase [Nicotiana tabacum]
                  221744
Seq. No.
                  LIB3165-017-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3510256
BLAST score
                  166
                  1.0e-11
E value
                  105
Match length
                  37
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                  221745
Seq. No.
                  LIB3165-017-P1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115765
BLAST score
                  518
                  7.0e-53
E value
                  123
Match length
                  77
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
                   (CAB-7) >gi 100201 pir S07408 chlorophyll a/b-binding
                  protein type II (cab-7) - tomato >gi 19180 emb CAA32197_
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                  esculentum] >gi_170431 (M20241) chlorophyll a/b-binding
                   protein [Lycopersicon esculentum] >gi 226546_prf__1601518A
                   chlorophyll a/b binding protein II [Lycopersicon
                   esculentum]
                   221746
Seq. No.
Seq. ID
                  LIB3165-017-P1-K1-E8
Method
                  BLASTX
                   q1709651
NCBI GI
BLAST score
                   315
                   4.0e-29
E value
Match length
                   112
% identity
```

plastocyanin a precursor - black poplar

PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209

>gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus

```
Seq. No.
                  221747
Seq. ID
                  LIB3165-017-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q2864610
BLAST score
                  387
                  2.0e-37
E value
                  134
Match length
% identity
                  44
                  (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4049336 emb CAA22561 (AL034567) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  221748
                  LIB3165-017-P1-K1-F11
Seq. ID
Method
                  BLASTX
                  q1076678
NCBI GI
BLAST score
                  172
E value
                  7.0e-13
Match length
                  45
% identity
                  78
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                  221749
Seq. No.
Seq. ID
                  LIB3165-017-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4104929
BLAST score
                  190
E value
                  2.0e-14
Match length
                  118
% identity
                  42
                  (AF042195) auxin response factor 7 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  221750
Seq. ID
                  LIB3165-017-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2494415
BLAST score
                  333
E value
                   4.0e-31
Match length
                  103
% identity
                  74
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine
                  max]
                  221751
Seg. No.
                  LIB3165-017-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1771778
BLAST score
                  491
E value
                  9.0e-50
Match length
                  115
% identity
                  77
                  (X99320) 23 kDa oxygen evolving protein of photosystem II
NCBI Description
                   [Solanum tuberosum]
                  221752
Seq. No.
```



LIB3165-017-P1-K1-F7 Seq. ID BLASTX Method g1351408 NCBI GI 397 BLAST score 1.0e-38 E value 94 Match length 79 % identity VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) NCBI Description >gi 1076563_pir__S51117 cystein proteinase - sweet orange >qi 633185 emb CAA87720 (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi 1588548 prf 2208463A vascular processing protease [Citrus sinensis] 221753 Seq. No. Seq. ID LIB3165-017-P1-K1-F9 Method BLASTX g625509 NCBI GI 579 BLAST score 5.0e-60 E value 117 Match length % identity 25 NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment) 221754 Seq. No. LIB3165-017-P1-K1-G12 Seq. ID BLASTX Method NCBI GI q1709846 293 BLAST score 2.0e-26 E value 126 Match length 45 % identity PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) NCBI Description 22 kDa component of photosystem II [Lycopersicon esculentum] 221755 Seq. No. Seq. ID LIB3165-017-P1-K1-G6 BLASTX Method g433970 NCBI GI BLAST score 653 E value 1.0e-68 Match length 140 18 % identity NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii] 221756 Seq. No. LIB3165-017-P1-K1-G7 Seq. ID Method BLASTX g1172664 NCBI GI BLAST score 308 E value 3.0e-28

Match length 132 % identity 59

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_419791_pir__S31165 photosystem I chain III precursor Flaveria trinervia >gi_298482_bbs_127083 photosystem I

reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No. 221757 LIB3165-017-P1-K1-H1 Seq. ID Method BLASTX NCBI GI q3288821 BLAST score 406 1.0e-39 E value 99 Match length 79 % identity (AF063901) alanine:glyoxylate aminotransferase; NCBI Description transaminase [Arabidopsis thaliana] 221758 Seq. No. Seq. ID LIB3165-017-P1-K1-H10 Method BLASTX NCBI GI g2493144 BLAST score 431 1.0e-42 E value 121 Match length 53 % identity VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE NCBI Description 16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] 221759 Seq. No. LIB3165-017-P1-K1-H11 Seq. ID Method BLASTX a3063392 NCBI GI BLAST score 431 1.0e-42E value Match length 115 76 % identity NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No. 221760

Seq. ID LIB3165-017-P1-K1-H2

Method BLASTX NCBI GI q68200 BLAST score 524 2.0e-53 E value Match length 129 % identity 82

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 221761

LIB3165-017-P1-K1-H3 Seq. ID

BLASTX Method NCBI GI q121080 BLAST score 454

```
2.0e-45
E value
                   105
Match length
                   86
% identity
                   GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                   >gi_1070638_pir__GCPMH glycine cleavage system protein H
                   precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H
protein [Pisum sativum] >gi_169093 (J05164) H-protein of
                   glycine decarboxylase precursor (EC 2.1.2.10) [Pisum
                   sativum] >gi 287815_emb_CAA37704_ (X53656) H-protein [Pisum
                   sativum]
                   221762
Seq. No.
Seq. ID
                   LIB3165-017-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   667
                   3.0e-70
E value
                   124
Match length
                   100
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   221763
Seq. No.
Seq. ID
                   LIB3165-017-P1-K1-H6
                   BLASTX
Method
NCBI GI
                   g2765081
BLAST score
                   494
                   5.0e-50
E value
                   132
Match length
                   74
% identity
NCBI Description
                  (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                   221764
Seq. ID
                   LIB3165-017-P1-K1-H7
                   BLASTX
Method
NCBI GI
                   g4406530
BLAST score
                   359
E value
                   3.0e-34
Match length
                   97
                   76
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   221765
Seq. No.
                   LIB3165-017-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   a68200
BLAST score
                   381
                   9.0e-37
E value
Match length
                   98
                   82
% identity
NCBI Description
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
```

Seq. No. 221766

Seq. ID LIB3165-017-P1-K1-H9

Method BLASTX



q1352821 NCBI GI BLAST score 559 1.0e-57 E value 108 Match length 99 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221767

LIB3165-018-P1-K1-A1 Seq. ID

BLASTX Method q115765 NCBI GI 445 BLAST score E value 2.0e-44 105 Match length 77 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR NCBI Description

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

221768 Seq. No.

LIB3165-018-P1-K1-A10 Seq. ID

Method BLASTX NCBI GI g1352821 625 BLAST score 2.0e-65 E value 123 Match length 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC $\overline{4.1.1.39}$) small chain precursor - upland cotton >gi_450505_emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221769

LIB3165-018-P1-K1-A11 Seq. ID

BLASTX Method g231610 NCBI GI 356 BLAST score 8.0e - 34E value 118 Match length 65 % identity

ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR NCBI Description

>gi 67880 pir PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >qi 19785 emb CAA45152 (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

221770 Seq. No.

Method

NCBI GI

BLASTX

g2505865

```
LIB3165-018-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   g4164576
NCBI GI
BLAST score
                   341
                   4.0e-32
E value
                   94
Match length
                   76
% identity
                   (AF098946) CTF2A [Arabidopsis thaliana]
NCBI Description
                   221771
Seq. No.
                   LIB3165-018-P1-K1-A2
Seq. ID
                   {\tt BLASTX}
Method
                   g2494415
NCBI GI
                   295
BLAST score
                   1.0e-26
E value
                   97
Match length
                   71
% identity
                   FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine
                   max]
                   221772
Seq. No.
                   LIB3165-018-P1-K1-A5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q468770
                   36
BLAST score
                   1.0e-10
E value
                   72
Match length
                   34
% identity
                   A.thaliana genes for chloroplast ribosomal protein L12 and
NCBI Description
                   tRNA-Pro
                   221773
Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-A6
                   BLASTX
Method
                   g4097547
NCBI GI
BLAST score
                   311
                   2.0e-28
E value
                   123
Match length
                   33
 % identity
 NCBI Description
                  (U64906) ATFP3 [Arabidopsis thaliana]
                   221774
 Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-A7
 Method
                   BLASTX
                   g20729
 NCBI GI
 BLAST score
                   404
                   2.0e-39
 E value
 Match length
                   112
 % identity
                   74
 NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
 Seq. No.
                   221775
                   LIB3165-018-P1-K1-A9
 Seg. ID
```

```
269
BLAST score
E value
                  1.0e-23
                  124
Match length
                  19
% identity
                  (Y12227) putative topoisomerase [Arabidopsis thaliana]
NCBI Description
                  221776
Seq. No.
Seq. ID
                  LIB3165-018-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  592
                  2.0e-61
E value
                  122
Match length
                  94
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221777
Seq. No.
                  LIB3165-018-P1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1703478
BLAST score
                  613
                   5.0e-64
E value
                  125
Match length
% identity
                  (U40566) ubiquitin activating enzyme 2 [Arabidopsis
NCBI Description
                  thaliana]
                   221778
Seq. No.
                  LIB3165-018-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1352821
BLAST score
                   566
                   2.0e-58
E value
                   107
Match length
% identity
                   100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
 Seq. No.
                   221779
                   LIB3165-018-P1-K1-B4
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501578
BLAST score
                   524
                   2.0e-53
E value
Match length
                   113
                   95
 % identity
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913 pir S60047
                   ethylene-responsive protein 1 - Para rubber tree
```

31349

brasiliensis]

>gi 1209317 (M88254) ethylene-inducible protein [Hevea

```
221780
Seq. No.
Seq. ID
                  LIB3165-018-P1-K1-B5
                  BLASTX
Method
                  g2435511
NCBI GI
BLAST score
                  149
                  1.0e-10
E value
                  80
Match length
                  49
% identity
                  (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
                  221781
Seq. No.
Seq. ID
                  LIB3165-018-P1-K1-B6
                  BLASTX
Method
                  g4510363
NCBI GI
                  545
BLAST score
                  5.0e-56
E value
                  113
Match length
                  89
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  221782
Seq. No.
                  LIB3165-018-P1-K1-B7
Seq. ID
                  BLASTX
Method
                  g3080428
NCBI GI
BLAST score
                  372
                  1.0e-35
E value
                  98
Match length
                  69
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  221783
Seq. No.
Seq. ID
                  LIB3165-018-P1-K1-B8
Method
                  BLASTX
                  q100616
NCBI GI
BLAST score
                  589
                  3.0e-61
E value
Match length
                  117
% identity
NCBI Description ribulose-bisphosphate carboxylase activase B precursor -
                  barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                  carboxylase activase [Hordeum vulgare] >gi 167095 (M55449)
                  ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                   vulgare]
                   221784
Seq. No.
                  LIB3165-018-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                   345
                   1.0e-32
E value
Match length
                  70
% identity
                   96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
```

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221785 Seq. ID LTB316

Seq. ID LIB3165-018-P1-K1-C10

Method BLASTX
NCBI GI g430947
BLAST score 496
E value 3.0e-50
Match length 120
% identity 82

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 221786

Seq. ID LIB3165-018-P1-K1-C12

Method BLASTX
NCBI GI g2275219
BLAST score 497
E value 2.0e-50
Match length 133
% identity 70

NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]

Seq. No. 221787

Seq. ID LIB3165-018-P1-K1-C2

Method BLASTX
NCBI GI g2435406
BLAST score 233
E value 2.0e-19
Match length 135
% identity 44

NCBI Description (U83490) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 221788

Seq. ID LIB3165-018-P1-K1-C5

Method BLASTX
NCBI GI g3915022
BLAST score 307
E value 3.0e-30
Match length 135
% identity 53

NCBI Description SUCROSE-PHOSPHATE SYNTHASE 2

(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2) >gi_2190350_emb_CAA72491_ (Y11795) sucrose-phosphate

synthase [Craterostigma plantagineum]

Seq. No. 221789

Seq. ID LIB3165-018-P1-K1-C6

Method BLASTX
NCBI GI g400890
BLAST score 162
E value 1.0e-20
Match length 117
% identity 43

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR



>gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274
aa] [Spinacia oleracea]

 Seq. No.
 221790

 Seq. ID
 LIB3165-018-P1-K1-C8

 Method
 BLASTX

Method BLASTX
NCBI GI g1063400
BLAST score 488
E value 2.0e-49
Match length 112
% identity 88

NCBI Description (X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No. 221791

Seq. ID LIB3165-018-P1-K1-C9

Method BLASTX
NCBI GI g3885511
BLAST score 391
E value 5.0e-38
Match length 99
% identity 79

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 221792

Seq. ID LIB3165-018-P1-K1-D1

Method BLASTX
NCBI GI g461501
BLAST score 599
E value 9.0e-67
Match length 140
% identity 92

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE 2, CHLOROPLAST

>gi 418803 pir S29048 fructose-bisphosphate aldolase (EC

4.1.2.13) - garden pea (fragment)

Seq. No. 221793

Seq. ID LIB3165-018-P1-K1-D10

Method BLASTX
NCBI GI g1351279
BLAST score 308
E value 4.0e-32
Match length 110
% identity 68

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi 602590 emb CAA58230 (X83227) triosephosphate isomerase

[Petunia x hybrida]

Seq. No. 221794

Seq. ID LIB3165-018-P1-K1-D12

Method BLASTX
NCBI GI g115765
BLAST score 442
E value 6.0e-44



Match length 122
% identity 66
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding
protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
(X14036) chlorophyll a/b-binding protein [Lycopersicon
esculentum] >gi_170431 (M20241) chlorophyll a/b-binding
protein [Lycopersicon esculentum] >gi_226546_prf__1601518A
chlorophyll a/b binding protein II [Lycopersicon

 Seq. No.
 221795

 Seq. ID
 LIB3165-018-P1-K1-D2

 Method
 BLASTX

 NCBI GI
 g886100

 BLAST score
 325

esculentum]

BLAST score 325 E value 2.0e-50 Match length 132 % identity 79

NCBI Description (U27347) putative water channel protein; plasmalemma

intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No. 221796

Seq. ID LIB3165-018-P1-K1-D3

Method BLASTX
NCBI GI g2511693
BLAST score 389
E value 1.0e-37
Match length 107
% identity 71

NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 221797

Seq. ID LIB3165-018-P1-K1-D4

Method BLASTX
NCBI GI g118564
BLAST score 473
E value 1.0e-47
Match length 101
% identity 89

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi_18264_emb_CAA41434_ (X58542) NADH-dependent
hydroxypyruvate reductase [Cucumis sativus]
>gi_18275_emb_CAA32764_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 221798

Seq. ID LIB3165-018-P1-K1-D5

Method BLASTX
NCBI GI g2246625
BLAST score 220
E value 7.0e-18
Match length 121
% identity 40



NCBI Description (AF004947) protein kinase [Oryza sativa]

Seq. No. 221799

Seq. ID LIB3165-018-P1-K1-D6

Method BLASTX
NCBI GI g1352821
BLAST score 594
E value 1.0e-61
Match length 111
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221800

Seq. ID LIB3165-018-P1-K1-D7

Method BLASTX
NCBI GI g2582822
BLAST score 239
E value 4.0e-20
Match length 126
% identity 51

NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress

Protein of 32kDa) [Solanum tuberosum]

Seq. No. 221801

Seq. ID LIB3165-018-P1-K1-D9

Method BLASTX
NCBI GI g2129538
BLAST score 504
E value 3.0e-51
Match length 105
% identity 91

NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No. 221802

Seq. ID LIB3165-018-P1-K1-E10

Method BLASTX
NCBI GI g131194
BLAST score 368
E value 3.0e-35
Match length 115
% identity 69

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_72686_pir__F1SP5

photosystem I chain V precursor - spinach

>gi_21299_emb_CAA31524_ (X13134) PSI subunit V preprotein (AA -69 to 98) [Spinacia oleracea] >gi_226167_prf__1413236B

photosystem I reaction center V [Spinacia oleracea]

Seq. No. 221803

Seq. ID LIB3165-018-P1-K1-E11

Method BLASTX NCBI GI g4406530

```
375
BLAST score
                   5.0e-36
E value
Match length
                   126
% identity
                   64
                   (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                   221804
Seq. No.
                   LIB3165-018-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g3202042
NCBI GI
                   488
BLAST score
                   2.0e-49
E value
                   114
Match length
                   82
% identity
                   (AF069324) 26S proteasome regulatory subunit S5A
NCBI Description
                   [Mesembryanthemum crystallinum]
                   221805
Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-E5
Method
                   BLASTX
                   a3914603
NCBI GI
BLAST score
                   532
                   2.0e-54
E value
                   130
Match length
                   76
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                   PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Oryza sativa]
                   221806
Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-E6
                   BLASTX
Method
NCBI GI
                   q132808
BLAST score
                   440
                   1.0e-43
E value
                   93
Match length
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L23 >gi_71299_pir__R5NT23
NCBI Description
                   ribosomal protein L23 - common tobacco chloroplast
                   >gi_11868_emb_CAA77385_ (Z00044) ribosomal protein L23
[Nicotiana tabacum] >gi_1223690_emb_CAA77408_ (Z00044)
                   ribosomal protein L23 [Nicotiana tabacum]
                   >gi_225239_prf__1211235BX ribosomal protein L23 [Nicotiana
                   tabacum] >qi 227679 prf 1709206A ribosomal protein CL23
                    [Nicotiana tabacum]
                   221807
Seq. No.
                   LIB3165-018-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158476
BLAST score
                   417
E value
                   4.0e-41
                   94
Match length
                   83
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
```



```
221808
Seq. No.
                   LIB3165-018-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g586004
BLAST score
                   618
                   1.0e-64
E value
                   128
Match length
% identity
                   SUPEROXIDE DISMUTASE [CU-ZN] >gi 421962 pir S34267
NCBI Description
                   superoxide dismutase (EC 1.15.1.\overline{1}) (Cu-\overline{Z}n) \overline{-} sweet potato
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
(Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
                   superoxide dismutase [Ipomoea batatas]
                   221809
Seq. No.
                   LIB3165-018-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131399
BLAST score
                   363
                   8.0e-35
E value
                   97
Match length
% identity
                   70
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                   TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411
                   photosystem II 10K protein precursor - potato
                    >qi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                    tuberosum]
                    221810
Seq. No.
                   LIB3165-018-P1-K1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q730850
BLAST score
                    143
                    7.0e-09
E value
                    123
Match length
                    28
% identity
                   SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2)
NCBI Description
                    >qi 626942 pir S48533 SUR2 protein - yeast (Saccharomyces
                    cerevisiae) >gi_458718 (U07171) Sur2p [Saccharomyces
                    cerevisiae] >gi_849215 (U28374) Sur2p: syringomycin
                    response protein 2 [Saccharomyces cerevisiae] >gi_1786173
                    (U10427) Syr2p [Saccharomyces cerevisiae]
                    221811
Seq. No.
                    LIB3165-018-P1-K1-F10
Seq. ID
                    BLASTX
Method
NCBI GI
                    g1673344
BLAST score
                    166
                    1.0e-11
E value
                    53
Match length
                    55
% identity
NCBI Description (D64002) hypothetical protein [Synechocystis sp.]
                    221812
Seq. No.
Seq. ID
                    LIB3165-018-P1-K1-F12
```

31356

BLASTX

q3935184

Method NCBI GI

Seq. ID Method

NCBI GI

```
304
BLAST score
E value
                   9.0e-28
                   77
Match length
                   71
% identity
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]
                   221813
Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-F2
Method
                   BLASTX
                   g2924262
NCBI GI
                   576
BLAST score
                   1.0e-59
E value
Match length
                   139
                   77
% identity
NCBI Description (Z00044) PSII 44kd protein [Nicotiana tabacum]
                   221814
Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q3150412
                   327
BLAST score
                   2.0e-30
E value
                   101
Match length
                   64
% identity
                   (ACO04165) putative Fe(II) transport protein [Arabidopsis
NCBI Description
                   thaliana] >gi 3420044 (AC004680) putative Fe(II) transport
                   protein [Arabidopsis thaliana]
Seq. No.
                   221815
Seq. ID
                   LIB3165-018-P1-K1-F4
                   BLASTX
Method
                   q3808101
NCBI GI
                   278
BLAST score
                   1.0e-24
E value
Match length
                   97
                   59
% identity
NCBI Description
                   (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                   221816
Seq. ID
                   LIB3165-018-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g131276
BLAST score
                   485
                   5.0e-49
E value
Match length
                   91
% identity
                   96
                   PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
NCBI Description
                   PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll
                   a-binding protein psbB - common tobacco chloroplast
                   >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein
[Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem
                   II P680 apoprotein [Nicotiana tabacum]
Seq. No.
                   221817
```

31357

LIB3165-018-P1-K1-F7

BLASTX

g1352821

641 BLAST score 3.0e-67 E value Match length 121 99 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC $\overline{4.1.1.39}$) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 221818 Seq. No. LIB3165-018-P1-K1-F8 Seq. ID BLASTX Method NCBI GI g3176076 260 BLAST score 1.0e-22 E value 60 Match length 82 % identity (AJ002487) protein phosphatase 1 catalitic subunit NCBI Description [Medicago sativa] 221819 Seq. No. LIB3165-018-P1-K1-G10 Seq. ID BLASTX Method NCBI GI g1170567 691 BLAST score 4.0e-73 E value 143 Match length 93 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi 1085960 pir S52648 INO1 protein - Citrus paradisi >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi] 221820 Seq. No. Seq. ID LIB3165-018-P1-K1-G12 BLASTX Method g3282092 NCBI GI BLAST score 170

Method BLASTX
NCBI GI g3282092
BLAST score 170
E value 5.0e-12
Match length 116
% identity 36

NCBI Description (AJ007446) hypothetical protein [Thermotoga neapolitana]

Seq. No. 221821

Seq. ID LIB3165-018-P1-K1-G2

Method BLASTX
NCBI GI 91449179
BLAST score 153
E value 1.0e-14
Match length 78
% identity 60

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

Seq. No. 221822

Seq. ID LIB3165-018-P1-K1-G3

Method BLASTX



NCBI GI g2262116 BLAST score 252 E value 2.0e-28 Match length 110 % identity 62

NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 221823

Seq. ID LIB3165-018-P1-K1-G4

Method BLASTX
NCBI GI g68200
BLAST score 519
E value 6.0e-53
Match length 128
% identity 83

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi 22633_emb_CAA47293_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 221824

Seq. ID LIB3165-018-P1-K1-G5

Method BLASTX
NCBI GI g3914605
BLAST score 665
E value 5.0e-70
Match length 140
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 221825

Seq. ID LIB3165-018-P1-K1-G7

Method BLASTN
NCBI GI g2687432
BLAST score 42
E value 1.0e-14
Match length 102
% identity 85

NCBI Description Plumbago auriculata large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 221826

Seq. ID LIB3165-018-P1-K1-G9

Method BLASTX
NCBI GI g2493694
BLAST score 257
E value 3.0e-22
Match length 112
% identity 54

NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II

protein - spinach >gi_728716 emb CAA59409 (X85038) protein

of photosystem II [Spinacia oleracea]

Seq. No.

221832

```
221827
Seq. No.
                  LIB3165-018-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  q68200
NCBI GI
BLAST score
                  438
                  1.0e-43
E value
                  109
Match length
% identity
                  82
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
                  221828
Seq. No.
                  LIB3165-018-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  g1709825
NCBI GI
                  398
BLAST score
                  9.0e-39
E value
                  120
Match length
                   68
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   221829
Seq. No.
                  LIB3165-018-P1-K1-H11
Seq. ID
Method
                  BLASTX
                   g1353352
NCBI GI
                   440
BLAST score
                   1.0e-43
E value
                   135
Match length
% identity
                   57
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   221830
Seq. No.
                   LIB3165-018-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   q1354517
NCBI GI -
BLAST score
                   292
                   3.0e-26
E value
                   133
Match length
                   53
% identity
NCBI Description (U55838) carbonic anhydrase [Populus tremula x Populus
                   tremuloides]
                   221831
Seq. No.
                   LIB3165-018-P1-K1-H2
Seq. ID
                   BLASTX
Method
                   q1181599
NCBI GI
BLAST score
                   324
                   4.0e-30
E value
                   131
Match length
% identity
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
```

```
LIB3165-018-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g1172664
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
Match length
                  48
                   92
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi 419791 pir S31165 photosystem I chain III precursor -
                   Flaveria trinervia >gi 298482 bbs 127083 photosystem I
                  reaction center subunit III, PSI-RC PsaF [Flaveria
                   trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                   I subunit III [Flaveria trinervia]
                   221833
Seq. No.
Seq. ID
                  LIB3165-018-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   q4545262
BLAST score
                   160
                   7.0e-11
E value
                   44
Match length
                   64
% identity
                   (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                   hirsutum]
                   221834
Seq. No.
Seq. ID
                   LIB3165-018-P1-K1-H7
                   BLASTX
Method
NCBI GI
                   q4325041
                   246
BLAST score
                   7.0e-35
E value
                   118
Match length
% identity
                   69
                   (AF117339) FtsH-like protein Pftf precursor [Nicotiana
NCBI Description
                   tabacum]
                   221835
Seq. No.
Seq. ID
                   LIB3165-019-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   q421826
BLAST score
                   148
                   2.0e-17
E value
                   69
Match length
                   66
% identity
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi 298036 emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
Seq. No.
                   221836
                   LIB3165-019-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3212610
                   287
BLAST score
                   1.0e-25
E value
                   108
Match length
```

31361

54

% identity



NCBI Description Chain A, Sulfite Oxidase From Chicken Liver

>gi 3212611_pdb_1SOX_B Chain B, Sulfite Oxidase From

Chicken Liver

Seq. No. 221837

Seq. ID LIB3165-019-P1-K1-A6

Method BLASTX
NCBI GI g1351411
BLAST score 323
E value 3.0e-30
Match length 77

Match length 77 % identity 75

NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B)

>gi_1076553_pir__S49175 cysteine proteinase precursor spring vetch >gi_2129906_pir_S68984 cysteine proteinase
precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899)

cysteine proteinase [Vicia sativa]

Seq. No. 221838

Seq. ID LIB3165-019-P1-K1-A7

Method BLASTX
NCBI GI g1644427
BLAST score 313
E value 9.0e-29
Match length 77
% identity 79

NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 221839

Seq. ID LIB3165-019-P1-K1-A8

Method BLASTX
NCBI GI g418854
BLAST score 617
E value 2.0e-64
Match length 124
% identity 18

NCBI Description ubiquitin precursor - parsley >gi_288112_emb_CAA45621_

(X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin

[Petroselinum crispum]

Seq. No. 221840

Seq. ID LIB3165-019-P1-K1-B11

Method BLASTX
NCBI GI g3912953
BLAST score 197
E value 4.0e-15
Match length 77
% identity 51

NCBI Description PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC

DEAMINASE)

Seq. No. 221841

Seq. ID LIB3165-019-P1-K1-B3

Method BLASTX NCBI GI g4263711 BLAST score 293

BLAST score

Match length

E value

645

125

1.0e-67



```
2.0e-26
E value
                   108
Match length
                   56
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   221842
Seq. No.
                   LIB3165-019-P1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2104951
BLAST score
                   311
                   1.0e-28
E value
                   129
Match length
                   57
% identity
                  (U96717) MAP kinase-like protein [Selaginella lepidophylla]
NCBI Description
Seq. No.
                   221843
                   LIB3165-019-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3292814
BLAST score
                   158
                   1.0e-10
E value
                   96
Match length
                   44
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   221844
                   LIB3165-019-P1-K1-B9
Seq. ID
Method
                   BLASTX
                   g20739
NCBI GI
BLAST score
                   348
E value
                   6.0e-33
                   69
Match length
                   90
% identity
                   (X54377) P-protein subunit of glycine decarboxylase enzyme
NCBI Description
                   complex [Pisum sativum]
                   221845
Seq. No.
                   LIB3165-019-P1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1172437
BLAST score
                   528
                   5.0e-54
E value
Match length
                   99
                   100
% identity
NCBI Description
                   CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)
                   >gi_1363524_pir__S58582 plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K protein - maize chloroplast
                   >gi 902252 emb CAA60316 (X86563) cytochrome b/f [Zea mays]
Seq. No.
                   221846
Seq. ID
                   LIB3165-019-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g266893
```

```
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >qi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                  sativus]
Seq. No.
                  221847
                  LIB3165-019-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q289920
BLAST score
                  673
E value
                  5.0e-71
                  127
Match length
                  99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  221848
Seq. ID
                  LIB3165-019-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1707008
BLAST score
                  209
E value
                  1.0e-16
Match length
                  86
% identity
                  51
                  (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  221849
                  LIB3165-019-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  592
                  1.0e-61
E value
                  128
Match length
                  87
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Oryza sativa]
                  221850
Seq. No.
                  LIB3165-019-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643608
BLAST score
                  266
                  3.0e-23
E value
                  101
Match length
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 221851

Seq. ID LIB3165-019-P1-K1-D2

Method BLASTX NCBI GI g2262170 BLAST score 204



E value 5.0e-16 Match length 114 % identity 44

NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis

thaliana]

Seq. No. 221852

Seq. ID LIB3165-019-P1-K1-D3

Method BLASTX
NCBI GI g1352821
BLAST score 546
E value 4.0e-56
Match length 104
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221853

Seq. ID LIB3165-019-P1-K1-D6

Method BLASTX
NCBI GI g2827548
BLAST score 258
E value 3.0e-22
Match length 85
% identity 56

NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis

thaliana]

Seq. No. 221854

Seq. ID LIB3165-019-P1-K1-D9

Method BLASTX
NCBI GI g1168411
BLAST score 332
E value 5.0e-31
Match length 88
% identity 80

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 221855

Seq. ID LIB3165-019-P1-K1-E10

Method BLASTX
NCBI GI g3914603
BLAST score 546
E value 4.0e-56
Match length 131
% identity 79

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

Seq. No. 221856

Seq. ID LIB3165-019-P1-K1-E12

Method BLASTX

```
g289920
NCBI GI
BLAST score
                   723
                   7.0e-77
E value
                   136
Match length
                   99
 % identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   221857
 Seq. No.
                   LIB3165-019-P1-K1-E4
 Seq. ID
                   BLASTX
 Method
                   g480082
 NCBI GI
                   169
 BLAST score
                   7.0e-12
 E value
                   139
 Match length
                   33
 % identity
                   catechol O-methyltransferase (EC 2.1.1.6) - common tobacco
 NCBI Description
                   >gi 396589 emb CAA52461_ (X74452) catechol
                   O-methyltransferase [Nicotiana tabacum]
                   221858
 Seq. No.
                   LIB3165-019-P1-K1-E5
· Seq. ID
                   BLASTX
 Method
                   g3687652
 NCBI GI
 BLAST score
                   180
                   4.0e-13
 E value
                   96
 Match length
                   48
 % identity
                   (AF047352) rubisco activase precursor [Datisca glomerata]
 NCBI Description
                   221859
 Seq. No.
 Seq. ID
                   LIB3165-019-P1-K1-E7
 Method
                   BLASTX
                   q1352821
 NCBI GI
 BLAST score
                    593
                    1.0e-61
 E value
                    111
 Match length
                    100
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                    ribulose bisphosphate carboxylase [Gossypium hirsutum]
 Seq. No.
                    221860
                    LIB3165-019-P1-K1-E8
 Seq. ID
 Method
                    BLASTX
                    q100203
 NCBI GI
 BLAST score
                    141
                    8.0e-09
 E value
                    104
 Match length
                    40
 % identity
                    cysteine proteinase (EC 3.4.22.-) precursor - tomato
 NCBI Description
```

Seq. No. 221861

proteinase [Lycopersicon esculentum]

>gi 19195_emb_CAA78403_ (Z14028) pre-pro-cysteine

```
LIB3165-019-P1-K1-E9
Seq. ID
Method
                  BLASTX
                  g2853087
NCBI GI
BLAST score
                  401
E value
                  4.0e-39
                  126
Match length
                  41
% identity
                  (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  221862
                  LIB3165-019-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1181599
BLAST score
                  381
                  5.0e-37
E value
                  105
Match length
% identity
                  72
                 (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                  221863
Seq. No.
                  LIB3165-019-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4574320
BLAST score
                  208
                  2.0e-16
E value
Match length
                  61
% identity
                  67
                  (AF117224) wound-induced protein WI12 [Mesembryanthemum
NCBI Description
                  crystallinum]
                   221864
Seq. No.
                  LIB3165-019-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174162
                  528
BLAST score
E value
                   4.0e-54
Match length
                  101
                   91
% identity
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                   thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   221865
Seq. No.
Seq. ID
                  LIB3165-019-P1-K1-F12
Method
                  BLASTX
NCBI GI
                   q3913018
BLAST score
                   518
E value
                   5.0e-53
Match length
                   108
% identity
                   91
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj_BAA02730_ (D13513) chloroplastic
                   aldolase [Oryza sativa]
```

Seq. No. 221866

Seq. ID LIB3165-019-P1-K1-F2

Method BLASTX

NCBI GI

BLAST score

g548774

207

```
NCBI GI
                   g4406530
BLAST score
                   206
E value
                   2.0e-16
Match length
                   63
                   71
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
Seq. No.
                   221867
                   LIB3165-019-P1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2477521
BLAST score
                   49
                   2.0e-18
E value
Match length
                   65
% identity
                   94
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F22K20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   221868
                   LIB3165-019-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334320
_BLAST score
                   448
                   9.0e-45
E value
                   99
Match length
                   92
% identity
                   40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
Seq. No.
                   221869
Seq. ID
                   LIB3165-019-P1-K1-F8
Method
                   BLASTX
                   g1439609
NCBI GI
                   556
BLAST score
                   2.0e-57
E value
Match length
                   112
                   53
 % identity
NCBI Description
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
                   hirsutum]
                   221870
Seq. No.
                   LIB3165-019-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131385
                   496
BLAST score
E value
                   2.0e-50
Match length
                   130
 % identity
                   78
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
Seq. No.
                   221871
Seq. ID
                   LIB3165-019-P1-K1-G1
Method
                   BLASTX
```

```
E value
                  7.0e-17
                  40
Match length
                  95
% identity
                  60S RIBOSOMAL PROTEIN L7A >qi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
                  221872
Seq. No.
                  LIB3165-019-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                  274
                  3.0e-24
E value
Match length
                  131
% identity
                  52
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
Seq. No.
                  221873
                  LIB3165-019-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g508304
BLAST score
                  353
                  2.0e-33
E value
                  79
Match length
% identity
                  80
NCBI Description
                  (L22305) corC [Medicago sativa]
Seq. No.
                  221874
Seq. ID
                  LIB3165-019-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  641
E value
                  3.0e-67
Match length
                  124
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221875
                  LIB3165-019-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160782
BLAST score
                  324
E value
                  3.0e-30
Match length
                  75
% identity
                  84
NCBI Description
                  (AF001505) putative ammonium transporter OsAMT1p [Oryza
```

Seq. No. 221876

Seq. ID LIB3165-019-P1-K1-G7

sativa]

Method BLASTX NCBI GI g1168411



```
BLAST score
                  264
E value
                  3.0e-23
                  75
Match length
                  75
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  221877
Seq. No.
Seq. ID
                  LIB3165-019-P1-K1-G9
                  BLASTX
Method
                  g1709651
NCBI GI
                  353
BLAST score
                  1.0e-33
E value
Match length
                  107
% identity
                  64
                  PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >gi 929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus
                  nigra]
                  221878
Seq. No.
                  LIB3165-019-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q445613
NCBI GI
BLAST score
                  494
                  4.0e-50
E value
                  123
Match length
                  75
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                  221879
Seq. ID
                  LIB3165-019-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q729051
BLAST score
                  551
                  1.0e-56
E value
Match length
                  115
                  59
% identity
NCBI Description CALTRACTIN (CENTRIN) >gi 444342 prf 1906390A
                  caltractin-like protein [Atriplex nummularia]
Seq. No.
                  221880
                  LIB3165-019-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  g2708749
NCBI GI
BLAST score
                  244
                  1.0e-20
E value
                  76
Match length
                  58
```

% identity

NCBI Description (AC003952) putative senescence-assoc. rhodanese-like

protein [Arabidopsis thaliana]

Seq. No. 221881

LIB3165-019-P1-K1-H3 Seq. ID

Method BLASTX g4262181 NCBI GI BLAST score 144 5.0e-09 E value



Match length 101 % identity 43

NCBI Description (AC005508) 37496 [Arabidopsis thaliana]

Seq. No. 221882

Seq. ID LIB3165-019-P1-K1-H5

Method BLASTX
NCBI GI g1352821
BLAST score 552
E value 7.0e-57
Match length 116
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC $\overline{4.1.1.39}$) small chain precursor - upland cotton >gi $\underline{450505}$ emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221883

Seq. ID LIB3165-019-P1-K1-H6

Method BLASTX
NCBI GI g4406530
BLAST score 207
E value 2.0e-16
Match length 77
% identity 58

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221884

Seq. ID LIB3165-019-P1-K1-H7

Method BLASTX
NCBI GI g3928760
BLAST score 176
E value 7.0e-13
Match length 75
% identity 48

NCBI Description (AB011797) homolog to plastid-lipid-associated protein

[Citrus unshiu]

Seq. No. 221885

Seq. ID LIB3165-019-P1-K1-H9

Method BLASTX
NCBI GI g82263
BLAST score 236
E value 7.0e-20
Match length 93
% identity 62

NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome

c1 precursor (clone pC(1)3II) - potato

Seq. No. 221886

Seq. ID LIB3165-020-P1-K1-A1

Method BLASTX
NCBI GI g1181599
BLAST score 162
E value 2.0e-11
Match length 83

```
% identity
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                  221887
Seq. No.
Seq. ID
                  LIB3165-020-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q1168411
BLAST score
                  327
                  2.0e-30
E value
                  87
Match length
                  79
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  221888
Seq. No.
Seq. ID
                  LIB3165-020-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1354515
BLAST score
                  318
E value
                  2.0e-29
Match length
                  140
                  50
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
Seq. No.
                  221889
                  LIB3165-020-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  612
E value
                  8.0e-64
                  114
Match length
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221890
Seq. ID
                  LIB3165-020-P1-K1-A5
Method
                  BLASTX
                  q3869088
NCBI GI
BLAST score
                  618
                  2.0e-64
E value
Match length
                  119
% identity
                  99
                 (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                  221891
Seq. No.
                  LIB3165-020-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1181599
BLAST score
                  288
                  3.0e-26
E value
                  83
Match length
                  69
% identity
NCBI Description
                 (D83007) subunit of photosystem I [Cucumis sativus]
```

NCBI GI

```
Seq. No.
                  221892
Seq. ID
                  LIB3165-020-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g266893
BLAST score
                  654
E value
                  8.0e-69
Match length
                  127
% identity
                  98
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi_18284_emb_CAA47906 (X67674) rubisco activase [Cucumis
                  sativus]
Seq. No.
                  221893
Seq. ID
                  LIB3165-020-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q399082
BLAST score
                  199
E value
                  2.0e-15
Match length
                  128
% identity
                  39
NCBI Description
                 ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
                  >gi 322713 pir S28171 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain, chloroplast - garden pea >gi 169045
                  (M94558) ATP synthase delta subunit [Pisum sativum]
Seq. No.
                  221894
                  LIB3165-020-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2661021
BLAST score
                  592
                  1.0e-61
E value
Match length
                  112
% identity
                  98
NCBI Description
                 (AF035255) catalase [Glycine max]
Seq. No.
                  221895
                  LIB3165-020-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g400890
BLAST score
                  316
                  4.0e-29
E value
Match length
                  128
                  45
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                  >gi_282837_pir__S26953 photosystem II 22K protein precursor
                  - spinach > gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
                  PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
                  photosystem II 22 kda polypeptide [spinach, Peptide, 274
                  aa] [Spinacia oleracea]
                  221896
Seq. No.
Seq. ID
                  LIB3165-020-P1-K1-B3
Method
                  BLASTX
```

31373

q1352821

BLAST score 627 E value 1.0e-65 Match length 119 % identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221897

Seq. ID LIB3165-020-P1-K1-B4

Method BLASTX
NCBI GI 94406530
BLAST score 363
E value 1.0e-34
Match length 119
% identity 65

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221898

Seq. ID LIB3165-020-P1-K1-B5

Method BLASTX
NCBI GI g100200
BLAST score 437
E value 3.0e-43
Match length 114
% identity 75

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 221899

Seq. ID LIB3165-020-P1-K1-B7

Method BLASTX
NCBI GI g992706
BLAST score 527
E value 7.0e-54
Match length 100
% identity 92

NCBI Description (U33758) UBC13 [Arabidopsis thaliana]

Seq. No. 221900

Seq. ID LIB3165-020-P1-K1-B8

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 221901

Seq. ID LIB3165-020-P1-K1-C10

Method BLASTX
NCBI GI g2914706
BLAST score 355
E value 1.0e-33
Match length 94



% identity (AC003974) putative homeobox protein [Arabidopsis thaliana] NCBI Description 221902 Seq. No. LIB3165-020-P1-K1-C2 Seq. ID BLASTN Method g2687442 NCBI GI 94 BLAST score 8.0e-46 E value 146 Match length 91 % identity Mitella pentandra large subunit 26S ribosomal RNA gene, NCBI Description partial sequence Seq. No. 221903 LIB3165-020-P1-K1-C5 Seq. ID Method BLASTX NCBI GI g2191191 BLAST score 242 2.0e-20 E value 114 Match length 54 % identity (AF007271) A TM021B04.14 gene product [Arabidopsis NCBI Description thaliana] 221904 Seq. No. LIB3165-020-P1-K1-C8 Seq. ID Method BLASTX NCBI GI g2791834 BLAST score 511 5.0e-52E value Match length 97 100 % identity NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta] 221905 Seq. No. Seq. ID LIB3165-020-P1-K1-C9 Method BLASTX NCBI GI q2738949 547 BLAST score 3.0e-56 E value Match length 114 % identity 89 (AF022213) cytosolic ascorbate peroxidase [Fragaria x NCBI Description ananassa] Seq. No. 221906 Seq. ID LIB3165-020-P1-K1-D1 Method BLASTX NCBI GI g289920 BLAST score 695 1.0e-73E value

Match length 135 98 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

% identity

94



```
Seq. No.
                  221907
                  LIB3165-020-P1-K1-D10
Seq. ID
Method
                  BLASTX
                  g1304227
NCBI GI
                  501
BLAST score
                  8.0e-51
E value
Match length
                  128
                  70
% identity
                  (D63781) Epoxide hydrolase [Glycine max]
NCBI Description
                  >gi 2764804_emb_CAA55293_ (X78547) epoxide hydrolase
                  [Glycine max]
                  221908
Seq. No.
                  LIB3165-020-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  246
                  3.0e-21
E value
Match length
                  72
                  74
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221909
Seq. No.
Seq. ID
                  LIB3165-020-P1-K1-D5
Method
                  BLASTX
                  q4406530
NCBI GI
                  392
BLAST score
                  5.0e-38
E value
Match length
                  111
% identity
                  74
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   221910
Seq. No.
                  LIB3165-020-P1-K1-D8
Seq. ID
Method
                  BLASTX
                   g2266992
NCBI GI
                   392
BLAST score
                   5.0e-38
E value
                   131
Match length
                   51
% identity
                  (U77412) O-linked GlcNAc transferase [Caenorhabditis
NCBI Description
                   elegans]
                   221911
Seq. No.
                   LIB3165-020-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g1345698
NCBI GI
                   637
BLAST score
                   9.0e-67
E value
Match length
                   126
```

(CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR



a/b-binding protein - upland cotton >gi 452314 emb CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 221912

Seq. ID LIB3165-020-P1-K1-E10

Method BLASTX
NCBI GI g289920
BLAST score 451
E value 2.0e-45
Match length 84
% identity 100

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221913

Seq. ID LIB3165-020-P1-K1-E12

Method BLASTX
NCBI GI g1352821
BLAST score 597
E value 4.0e-62
Match length 113
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221914

Seq. ID LIB3165-020-P1-K1-E2

Method BLASTX
NCBI GI g289920
BLAST score 719
E value 2.0e-76
Match length 136
% identity 99

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221915

Seq. ID LIB3165-020-P1-K1-E3

Method BLASTX
NCBI GI g289920
BLAST score 723
E value 8.0e-77
Match length 136
% identity 99

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221916

Seq. ID LIB3165-020-P1-K1-E5

Method BLASTX NCBI GI g3510256 BLAST score 258 E value 3.0e-22



Match length 125 % identity 44

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 221917

Seq. ID LIB3165-020-P1-K1-F10

Method BLASTX
NCBI GI g1352821
BLAST score 590
E value 3.0e-61
Match length 110
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221918

Seq. ID LIB3165-020-P1-K1-F12

Method BLASTX
NCBI GI g2815246
BLAST score 225
E value 2.0e-18
Match length 55
% identity 73

NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No. 221919

Seq. ID LIB3165-020-P1-K1-F3

Method BLASTX
NCBI GI g11638
BLAST score 219
E value 9.0e-38
Match length 107
% identity 81

NCBI Description (X01647) open reading frame (ORF701) pot. membrane protein

(aa 1-487) [Marchantia polymorpha]

Seq. No. 221920

Seq. ID LIB3165-020-P1-K1-F5

Method BLASTX
NCBI GI g289920
BLAST score 727
E value 3.0e-77
Match length 138
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221921

Seq. ID LIB3165-020-P1-K1-F6

Method BLASTX
NCBI GI g2244916
BLAST score 215
E value 3.0e-17
Match length 133

```
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  221922
Seq. No.
                  LIB3165-020-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  g945081
NCBI GI
                  535
BLAST score
                  8.0e-55
E value
                  134
Match length
                  78
% identity
                  (U31094) P21 [Petunia hybrida]
NCBI Description
                  221923
Seq. No.
                  LIB3165-020-P1-K1-F8
Seq. ID
                  BLASTX
Method
                  q285317
NCBI GI
                   463
BLAST score
                  2.0e-46
E value
                  141
Match length
                   70
% identity
                  dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea
NCBI Description
                  221924
Seq. No.
                  LIB3165-020-P1-K1-G11
Seq. ID
                  BLASTX
Method
                   g1354515
NCBI GF
BLAST score
                   343
                   2.0e-32
E value
                   146
Match length
                   53
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   221925
Seq. No.
                   LIB3165-020-P1-K1-G12
Seq. ID
Method
                   BLASTX
                   q289920
NCBI GI
                   718
BLAST score
                   3.0e-76
E value
                   134
Match length
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   221926
Seq. No.
                   LIB3165-020-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1168408
                   597
BLAST score
                   4.0e-62
E value
Match length
                   132
% identity
                   89
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                   >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
```

31379

4.1.2.13) - garden pea >gi 927507 emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

E value

Match length

% identity

9.0e-28

```
221927
Seq. No.
                   LIB3165-020-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   613
                   6.0e-64
E value
                   115
Match length
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   221928
                   LIB3165-020-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1694621
BLAST score
                   369
E value
                   2.0e-35
                   114
Match length
                   68
% identity
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
NCBI Description
                   221929
Seq. No.
                   LIB3165-020-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3063444
                   529
BLAST score
E value
                   4.0e-54
Match length
                   142
% identity
                   68
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
Seq. No.
                   221930
Seq. ID
                   LIB3165-020-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   q1352821
BLAST score
                   608
E value
                   2.0e-63
Match length
                   124
                   95
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   221931
Seq. ID
                   LIB3165-020-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g2995384
BLAST score
                   286
```

```
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seg No. 221932
```

Seq. No. 221932 LIB3165-020-P1-K1-H4 Seq. ID Method BLASTX g2351846 NCBI GI BLAST score 208 2.0e-16 E value 105 Match length 46 % identity (U93050) poly(A) binding protein II [Mus musculus] NCBI Description Seq. No. 221933 LIB3165-020-P1-K1-H5 Seq. ID Method BLASTX NCBI GI g3738285 BLAST score 506 2.0e-51 E value 127 Match length 75 % identity (AC005309) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 221934 LIB3165-020-P1-K1-H6 Seq. ID Method BLASTX NCBI GI g548437 BLAST score 179 4.0e-13 E value Match length 133 % identity 36 OSH1 PROTEIN >qi 1078479 pir S53463 SWH1 protein (version NCBI Description 1) - yeast (Saccharomyces cerevisiae) >gi_456143 (L28920) Oshlp [Saccharomyces cerevisiae] 221935 Seq. No. LIB3165-020-P1-K1-H8 Seq. ID BLASTX Method NCBI GI g231688 BLAST score 668 2.0e-70 E value Match length 126 100 % identity NCBI Description CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi 18488 emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum] 221936 Seq. No. LIB3165-020-P1-K1-H9 Seq. ID Method BLASTX NCBI GI q2760834 BLAST score 495 E value 4.0e-50

Match length 132

% identity 74
NCBI Description (AC003105) putative nitrate transporter [Arabidopsis thaliana]

```
Seq. No.
                  221937
Seq. ID
                  LIB3165-021-P1-K1-A10
Method
                  BLASTX
                  q289920
NCBI GI
BLAST score
                  702
                  2.0e-74
E value
                  133
Match length
% identity
                  98
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  221938
Seq. No.
Seq. ID
                  LIB3165-021-P1-K1-A11
Method
                  BLASTX
                  q231688
NCBI GI
BLAST score
                  298
E value
                  5.0e-27
Match length
                  57
% identity
                  100
                  CATALASE ISOZYME 2 > gi 99599 pir S17493 catalase (EC
NCBI Description
                  1.11.1.6) - upland cotton >qi 18488 emb CAA39998 (X56675)
                  subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. No.
                  221939
                  LIB3165-021-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  q487046
NCBI GI
BLAST score
                  368
E value
                  3.0e-35
Match length
                  130
% identity
                  62
NCBI Description
                  photosystem I chain II precursor - wood tobacco
                  >gi 407769 dbj BAA02871 (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
                  221940
Seq. No.
                  LIB3165-021-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  698
                  6.0e-74
E value
Match length
                  133
% identity
                  97
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  221941
Seq. No.
                  LIB3165-021-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
                  364
BLAST score
                  9.0e-35
E value
Match length
                  104
% identity
                   74
```

Seq. No. 221942

NCBI Description

(AF126870) rubisco activase [Vigna radiata]

```
Seq. ID LIB3165-021-P1-K1-A8 Method BLASTX
```

NCBI GI g166834
BLAST score 539
E value 2.0e-55
Match length 134
% identity 75

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi 2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 221943

Seq. ID LIB3165-021-P1-K1-B11

Method BLASTX
NCBI GI g1352821
BLAST score 544
E value 7.0e-56
Match length 103
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221944

Seq. ID LIB3165-021-P1-K1-B2

Method BLASTX
NCBI GI g2501578
BLAST score 477
E value 5.0e-48
Match length 110
% identity 89

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047

ethylene-responsive protein 1 - Para rubber tree

>gi_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 221945

Seq. ID LIB3165-021-P1-K1-B3

Method BLASTX
NCBI GI g3158474
BLAST score 240
E value 2.0e-24
Match length 70
% identity 88

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 221946

Seq. ID LIB3165-021-P1-K1-B4

Method BLASTX
NCBI GI g548653
BLAST score 176
E value 1.0e-12
Match length 94
% identity 45

NCBI Description 50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)

>gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast
- Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046)
ribosomal protein L12 [Arabidopsis thaliana]

Seq. No. 221947 Seq. ID LIB3165-021-P1-K1-B8 Method BLASTX NCBI GI g1076724 BLAST score 554 3.0e-57 E value Match length 109 91 % identity

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 221948

Seq. ID LIB3165-021-P1-K1-B9

Method BLASTX
NCBI GI g100196
BLAST score 494
E value 4.0e-50
Match length 109
% identity 83

NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No. 221949

Seq. ID LIB3165-021-P1-K1-C12

Method BLASTX
NCBI GI g3650033
BLAST score 155
E value 3.0e-10
Match length 81
% identity 41

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 221950

Seq. ID LIB3165-021-P1-K1-C7

Method BLASTX
NCBI GI g4105697
BLAST score 446
E value 2.0e-44
Match length 113
% identity 69

NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 221951

Seq. ID LIB3165-021-P1-K1-C9

Method BLASTX
NCBI GI g1777312
BLAST score 461
E value 4.0e-46
Match length 118
% identity 74

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No.

221957

```
Seq. No.
                  221952
                  LIB3165-021-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
                  369
BLAST score
E value
                  2.0e-35
                  139
Match length
                  57
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  221953
Seq. No.
                  LIB3165-021-P1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  510
                  7.0e-52
E value
                  100
Match length
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221954
                  LIB3165-021-P1-K1-D3
Seq. ID
Method
                  BLASTX
                  g1354515
NCBI GI
                   274
BLAST score
                   3.0e-24
E value
Match length
                  134
                   48
% identity
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
Seq. No.
                   221955
                  LIB3165-021-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2317910
BLAST score
                   340
                   6.0e-32
E value
Match length
                  130
% identity
                  (U89959) CER1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   221956
Seq. ID
                  LIB3165-021-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q4538959
BLAST score
                   436
E value
                   3.0e-43
Match length
                   120
% identity
                  (AL049488) putative protein [Arabidopsis thaliana]
NCBI Description
```

BLAST score

% identity

E value Match length 497 2.0e-50

99 93

```
Seq. ID
                  LIB3165-021-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  704
E value
                  1.0e-74
Match length
                  133
                  98
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  221958
Seq. No.
Seq. ID
                  LIB3165-021-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g131399
BLAST score
                  214
                  1.0e-17
E value
Match length
                  87
                  55
% identity
NCBI Description
                 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411
                  photosystem II 10K protein precursor - potato
                  >qi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                  tuberosum]
Seq. No.
                  221959
Seq. ID
                  LIB3165-021-P1-K1-D9
                  BLASTX
Method
NCBI GI
                  q121353
BLAST score
                  443
E value
                  5.0e-44
Match length
                  115
                  76
% identity
                  GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)
NCBI Description
                  (GLUTAMATE-AMMONIA LIGASE) > gi 68596 pir AJFBQD
                  glutamate--ammonia ligase (EC 6.3.1.2) delta precursor,
                  chloroplast - kidney bean >gi 21005 emb CAA31234 (X12738)
                  GS precursor protein [Phaseolus vulgaris]
Seq. No.
                  221960
Seq. ID
                  LIB3165-021-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q231496
BLAST score
                  313
                  3.0e-36
E value
                  87
Match length
                  92
% identity
NCBI Description ACTIN 58 >gi_100421_pir__S20094 actin - potato
                  >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]
                  221961
Seq. No.
                  LIB3165-021-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  g120669
NCBI GI
```

```
NCBI Description
                 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >qi 19566 emb CAA42905 (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  221962
                  LIB3165-021-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115833
BLAST score
                  419
                  3.0e-41
E value
Match length
                  117
                  71
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                  (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
Seq. No.
                  221963
Sea. ID
                  LIB3165-021-P1-K1-E5
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  597
                  4.0e-62
E value
                  111
Match length
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >qi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221964
                  LIB3165-021-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  g3047064
NCBI GI
BLAST score
                  359
E value
                  4.0e - 34
Match length
                  134
% identity
                  61
                  (AF058825) contains similarity to peptidyl-prolyl cis-trans
NCBI Description
                  isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41
                  [Arabidopsis thaliana]
                  221965
Seq. No.
                  LIB3165-021-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  615
E value
                  3.0e-64
Match length
                  122
```

% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)



ribulose bisphosphate carboxylase [Gossypium hirsutum]

221966 Seq. No. LIB3165-021-P1-K1-F11 Seq. ID Method BLASTX q125576 NCBI GI BLAST score 625 2.0e-65 E value Match length 123 98 % identity PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) NCBI Description (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana] 221967 Seq. No. Seq. ID LIB3165-021-P1-K1-F2 Method BLASTX NCBI GI g1707943 BLAST score 613 E value 6.0e-64Match length 126 % identity 94 GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT NCBI Description PRECURSOR 1 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi 541977 pir S41293 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) fava bean >gi 440593 emb CAA54259 (X76940) ADP-glucose pyrophosphorylase [Vicia faba] Seq. No. 221968 LIB3165-021-P1-K1-F3 Seq. ID BLASTX Method q1352821 NCBI GI BLAST score 616 E value 3.0e-64 Match length 124 97 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 221969 Seq. No. Seq. ID LIB3165-021-P1-K1-F6 Method BLASTX NCBI GI g3914940 BLAST score 423 E value 1.0e-41

Match length 140 % identity 64

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase

BLAST score

E value

240 3.0e-20



[Spinacia oleracea]

```
221970
Seq. No.
Seq. ID
                  LIB3165-021-P1-K1-F8
Method
                  BLASTX
                  g285317
NCBI GI
BLAST score
                  307
                  4.0e-28
E value
Match length
                  103
% identity
                  65
NCBI Description dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea
                  221971
Seq. No.
                  LIB3165-021-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  546
BLAST score
                  4.0e-56
E value
                  104
Match length
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  221972
Seq. No.
                  LIB3165-021-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g68200
BLAST score
                  467
                  8.0e-47
E value
                  127
Match length
                  76
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                  chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                  221973
Seq. ID
                  LIB3165-021-P1-K1-G10
                  BLASTX
Method
NCBI GI
                  q1709651
BLAST score
                  450
                  7.0e-45
E value
                  139
Match length
% identity
                  65
NCBI Description
                 PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209
                  plastocyanin a precursor - black poplar
                  >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
                  221974
Seq. No.
Seq. ID
                  LIB3165-021-P1-K1-G2
Method
                  BLASTX
                  q3451463
NCBI GI
```



Match length 126 % identity 40

NCBI Description (AL031349) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 221975

LIB3165-021-P1-K1-G3 Seq. ID

Method BLASTX NCBI GI q1781348 BLAST score 286 E value 1.0e-25 Match length 71 % identity 75

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 221976

Seq. ID LIB3165-021-P1-K1-G5

Method BLASTX NCBI GI q81850 BLAST score 417 E value 5.0e-41 Match length 86 99 % identity

NCBI Description histone H3 (clone pH3c-1) - alfalfa (fragment)

>gi_829279_emb_CAA31967 (X13676) histone H3 (AA 1-120)

[Medicago sativa]

Seq. No. 221977

Seq. ID LIB3165-021-P1-K1-G6

Method BLASTX NCBI GI q68200 BLAST score 566 E value 2.0e-58 139 Match length 82 % identity

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,

> chloroplast - spinach >gi 22633 emb CAA47293 (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 221978

Seq. ID LIB3165-021-P1-K1-G7

Method BLASTN NCBI GI g18511 BLAST score 377 E value 0.0e + 00Match length 409 98 % identity

NCBI Description G.hirsutum light regulated unknown reading frame DNA

Seq. No. 221979

Seq. ID LIB3165-021-P1-K1-G8

Method BLASTX NCBI GI g4049399 BLAST score 160 7.0e-11 E value Match length 108 % identity 33

```
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
                  221980
Seq. No.
                  LIB3165-021-P1-K1-G9
Seq. ID
Method
                  BLASTX
                  g4406530
NCBI GI
                  341
BLAST score
                  4.0e-32
E value
                  104
Match length
                  71
% identity
                 (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  221981
Seq. No.
                  LIB3165-021-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2252824
BLAST score
                  211
                  3.0e-17
E value
Match length
                  86
                  56
% identity
                 (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                  221982
Seq. No.
                  LIB3165-021-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  605
BLAST score
                  5.0e-63
E value
                  113
Match length
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221983
                  LIB3165-021-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2564237
BLAST score
                  440
E value
                  1.0e-43
Match length
                  103
% identity
NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]
Seq. No.
                  221984
Seq. ID
                  LIB3165-021-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3914605
```

Method BLASTX
NCBI GI g3914605
BLAST score 517
E value 1.0e-52
Match length 121
% identity 83

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir_ S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -



apple tree >gi 415852 emb CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

221985 Seq. No.

Seq. ID LIB3165-021-P1-K1-H7

Method BLASTX NCBI GI g3914603 BLAST score 358 4.0e-34 E value Match length 88 % identity 77

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

221986 Seq. No.

LIB3165-021-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI g973313 BLAST score 549 2.0e-56 E value Match length 113 % identity 91

NCBI Description (U30250) myo-inositol 1-phosphate synthase isozyme-2

[Arabidopsis thaliana]

Seq. No. 221987

LIB3165-022-P1-K1-A10 Seq. ID

Method BLASTX NCBI GI g2980770 BLAST score 165 E value 2.0e-11 Match length 51

% identity 59

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 221988

Seq. ID LIB3165-022-P1-K1-A12

Method BLASTX NCBI GI q100200 BLAST score 352 E value 2.0e-33 Match length 99 70 % identity

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 221989

Seq. ID LIB3165-022-P1-K1-A3

Method BLASTX NCBI GI q1352821 BLAST score 645 E value 1.0e-67 Match length 119 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
Seq. No.
                  221990
                  LIB3165-022-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  g1653089
NCBI GI
                  305
BLAST score
                  8.0e-28
E value
Match length
                  89
                  63
% identity
                 (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  221991
                  LIB3165-022-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q125578
BLAST score
                  341
                  4.0e-32
E value
Match length
                  99
% identity
                  68
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                  (PRK) >gi_167266 (M73707) phosphoribulokinase
                  [Mesembryanthemum crystallinum]
Seq. No.
                  221992
                  LIB3165-022-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2218141
BLAST score
                  294
E value
                  1.0e-26
Match length
                  112
                  51
% identity
NCBI Description (AF004914) E8 protein homolog [Lycopersicon esculentum]
Seq. No.
                  221993
                  LIB3165-022-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  412
E value
                  1.0e-40
                  83
Match length
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  221994
Seq. ID
                  LIB3165-022-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g119150
BLAST score
                  631
```

4.0e-66

E value



Match length 124 % identity 95

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_82081_pir__S10507 translation elongation factor eEF-1
alpha chain - tomato >gi 19273 emb CAA32618 (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No. 221995

Seq. ID LIB3165-022-P1-K1-B5

Method BLASTX
NCBI GI g289920
BLAST score 704
E value 1.0e-74
Match length 134
% identity 97

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 221996

Seq. ID LIB3165-022-P1-K1-B6

Method BLASTX
NCBI GI g131392
BLAST score 291
E value 2.0e-33
Match length 105
% identity 70

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >qi 81479 pir S00005 photosystem II oxygen-evolving

complex protein 2 precursor - spinach

>gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein
[Spinacia oleracea] >gi_225596_prf__1307179A luminal

protein 23kD [Spinacia oleracea]

Seq. No. 221997

Seq. ID LIB3165-022-P1-K1-B7

Method BLASTX
NCBI GI g2499710
BLAST score 623
E value 4.0e-65
Match length 132
% identity 84

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 221998

Seq. ID LIB3165-022-P1-K1-B8

Method BLASTX
NCBI GI g2281633
BLAST score 189
E value 2.0e-20
Match length 135
% identity 51

NCBI Description (AF003097) AP2 domain containing protein RAP2.4



[Arabidopsis thaliana]

Seq. No. 221999 Seq. ID

LIB3165-022-P1-K1-B9

Method BLASTX g4406530 NCBI GI BLAST score 346 1.0e-32 E value Match length 119 % identity 62

(AF126870) rubisco activase [Vigna radiata] NCBI Description

Seq. No. 222000

LIB3165-022-P1-K1-C1 Seq. ID

Method BLASTX NCBI GI g289920 BLAST score 601 1.0e-62 E value Match length 117 95 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

222001 Seq. No.

LIB3165-022-P1-K1-C10 Seq. ID

Method BLASTX g2924521 NCBI GI BLAST score 179 E value 4.0e-13 Match length 109 42 % identity

(AL022023) putative protein [Arabidopsis thaliana] NCBI Description

222002 Seq. No.

LIB3165-022-P1-K1-C12 Seq. ID

Method BLASTX NCBI GI g231610 BLAST score 291 3.0e-26E value 105 Match length 62 % identity

ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR NCBI Description

>gi 67880 pir PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 222003

Seq. ID LIB3165-022-P1-K1-C2

Method BLASTX NCBI GI q4103324 367 BLAST score E value 8.0e-37 Match length 88 % identity 93

(AF022716) GDP-mannose pyrophosphorylase [Solanum NCBI Description

tuberosum]

```
222004
Seq. No.
                   LIB3165-022-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g1666234
NCBI GI
                   324
BLAST score
                   4.0e-30
E value
Match length
                   66
                   95
% identity
                   (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
NCBI Description
                   [Pisum sativum]
                   222005
Seq. No.
                   LIB3165-022-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   g4510354
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
Match length
                   70
                   50
% identity
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   222006
Seq. No.
                   LIB3165-022-P1-K1-C8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3510339
BLAST score
                   34
                   1.0e-09
E value
Match length
                   157
                   83
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   222007
Seq. No.
                   LIB3165-022-P1-K1-C9
Seq. ID
                   BLASTX
Method
                   g1172664
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
                   56
Match length
                   93
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                   >gi_419791_pir__S31165 photosystem I chain III precursor -
                   Flaveria trinervia >gi_298482_bbs_127083 photosystem I
                   reaction center subuni\overline{t} III, \overline{P}SI-\overline{R}C PsaF [Flaveria
                   trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                   I subunit III [Flaveria trinervia]
                   222008
Seq. No.
                   LIB3165-022-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   -q3024020
BLAST score
                   620
                   8.0e-65
E value
                   124
Match length
                   94
% identity
```



NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 222009

Seq. ID LIB3165-022-P1-K1-D12

Method BLASTX
NCBI GI g2735766
BLAST score 181
E value 3.0e-13
Match length 118
% identity 37

NCBI Description (AF008652) MADS transcriptional factor; STMADS11 [Solanum

tuberosum]

Seq. No. 222010

Seq. ID LIB3165-022-P1-K1-D2

Method BLASTX
NCBI GI g461812
BLAST score 333
E value 4.0e-31
Match length 114
% identity 50

NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE

GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi_445604_prf__1909351A cytochrome P450 [Catharanthus

roseus]

Seq. No. 222011

Seq. ID LIB3165-022-P1-K1-D6

Method BLASTX
NCBI GI g1362017
BLAST score 179
E value 4.0e-13
Match length 78
% identity 51

NCBI Description zinc finger protein 4 - Arabidopsis thaliana >gi_790679

(L39647) zinc finger protein [Arabidopsis thaliana]

Seq. No. 222012

Seq. ID LIB3165-022-P1-K1-D8

Method BLASTX
NCBI GI g3738261
BLAST score 209
E value 1.0e-16
Match length 52
% identity 85

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 222013

Seq. ID LIB3165-022-P1-K1-D9

Method BLASTX
NCBI GI g1352821
BLAST score 580
E value 4.0e-60



```
Match length
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222014
Seq. No.
Seq. ID
                  LIB3165-022-P1-K1-E1
Method
                  BLASTX
                  q113240
NCBI GI
BLAST score
                  129
                  1.0e-10
E value
                  60
Match length
                  62
% identity
                  ACTIN 2 >qi 71636 pir ATRZ2 actin 2 - rice
NCBI Description
                  >gi 20329 emb CAA33873 (X15864) actin [Oryza sativa]
Seq. No.
                  222015
Seq. ID
                  LIB3165-022-P1-K1-E11
                  BLASTX
Method
                  q119931
NCBI GI
BLAST score
                  382
                  7.0e-37
E value
                  109
Match length
                  69
% identity
NCBI Description FERREDOXIN I PRECURSOR >gi 65740 pir FEPM1 ferredoxin
                  [2Fe-2S] I precursor - garden pea >gi 169087 (M31713)
                  ferredoxin I precursor [Pisum sativum]
                  222016
Seq. No.
                  LIB3165-022-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  520
                  4.0e-53
E value
Match length
                  102
                  99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222017
                  LIB3165-022-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  q1168411
NCBI GI
BLAST score
                  154
                  4.0e-10
E value
```

Match length 72 % identity 49

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 222018

LIB3165-022-P1-K1-E5 Seq. ID

```
Method
                  BLASTX
                  g4406530
NCBI GI
                  351
BLAST score
                  3.0e-33
E value
                  94
Match length
                  77
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  222019
Seq. No.
                  LIB3165-022-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1769905
                  390
BLAST score
                  7.0e-38
E value
                  96
Match length
% identity
                  77
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
                  222020
Seq. No.
                  LIB3165-022-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829892
BLAST score
                  219
                  9.0e-18
E value
Match length
                  109
                  51
% identity
                  (AC002311) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  222021
Seq. No.
                  LIB3165-022-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g3776572
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
                   99
Match length
                   70
% identity
                  (AC005388) ESTs gb_R65052, gb_AA712146, gb_H76533,
NCBI Description
                   gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383,
                   gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis
                   thaliana]
                   222022
Seq. No.
                  LIB3165-022-P1-K1-F1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1354517
BLAST score 175
E value 1.0e-12
Match length 39
% identity 85

NCBI Description (U55838) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 222023

Seq. ID LIB3165-022-P1-K1-F10

Method BLASTX NCBI_GI g1724102



```
BLAST score
                   277
                   6.0e-25
E value
Match length
                  63
% identity
                  87
                   (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                  222024
                  LIB3165-022-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2129651
BLAST score
                   558
                   2.0e-57
E value
                  139
Match length
% identity
                  77
NCBI Description
                  myosin heavy chain ATM2 - Arabidopsis thaliana (fragment)
                  >gi 499045 emb CAA84065 (Z34292) myosin [Arabidopsis
                   thaliana]
Seq. No.
                   222025
                  LIB3165-022-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1439609
BLAST score
                   321
                   1.0e-29
E value
                   79
Match length
                   80
% identity
NCBI Description
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
                  hirsutum]
                   222026
Seq. No.
                   LIB3165-022-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g1514977
NCBI GI
                   375
BLAST score
                   2.0e-36
E value
                   93
Match length
                   74
% identity
NCBI Description
                  (D84669) VM23 [Raphanus sativus]
                   222027
Seq. No.
                   LIB3165-022-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1199772
BLAST score
                   298
                   5.0e-27
E value
                   123
Match length
                   55
% identity
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
Seq. No.
                   222028
```

LIB3165-022-P1-K1-F9 Seq. ID

Method BLASTX NCBI GI g20729 BLAST score 444



E value 4.0e-44 Match length 123 % identity 74

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 222029

Seq. ID LIB3165-022-P1-K1-G10

Method BLASTX
NCBI GI g430947
BLAST score 420
E value 2.0e-41
Match length 104
% identity 81

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 222030

Seq. ID LIB3165-022-P1-K1-G11

Method BLASTX
NCBI GI g1709846
BLAST score 312
E value 1.0e-28
Match length 129
% identity 47

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq. No. 222031

Seq. ID LIB3165-022-P1-K1-G12

Method BLASTX
NCBI GI g131399
BLAST score 547
E value 3.0e-56
Match length 129
% identity 82

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411

photosystem II 10K protein precursor - potato

>gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No. 222032

Seq. ID LIB3165-022-P1-K1-G3

Method BLASTX
NCBI GI g3913661
BLAST score 296
E value 8.0e-27
Match length 80
% identity 70

NCBI Description FERREDOXIN B (FD B) >gi_322807_pir__S28199 ferredoxin

[2Fe-2S] B - giant taro >gi_264602_bbs_123934 ferredoxin B

isoprotein, Fd B [Alocasia macrorrhiza=elephant ear,

Schott, Peptide, 98 aa]

Seq. No. 222033

Seq. ID LIB3165-022-P1-K1-G4



```
Method
                  BLASTX
NCBI GI
                  g166834
BLAST score
                  170
                  2.0e-12
E value
                  39
Match length
                  74
% identity
NCBI Description
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
                  222034
Seq. No.
Seq. ID
                  LIB3165-022-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g228403
BLAST score
                  625
E value
                  2.0e-65
                  138
Match length
% identity
                  90
                  glycolate oxidase [Lens culinaris]
NCBI Description
Seq. No.
                  222035
                  LIB3165-022-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
                  346
BLAST score
                  1.0e-32
E value
Match length
                  120
% identity
                  62
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  222036
Seq. No.
                  LIB3165-022-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g886100
                  559
BLAST score
E value
                  1.0e-57
Match length
                  124
                  86
% identity
                  (U27347) putative water channel protein; plasmalemma
NCBI Description
                  intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
Seq. No.
                  222037
Seq. ID
                  LIB3165-022-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                  314
E value
                  6.0e-29
Match length
                  138
% identity
                  51
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
```

Seq. No. 222038

Seq. ID LIB3165-022-P1-K1-H11

Method BLASTX



NCBI GI g119905 BLAST score 662 E value 1.0e-69 Match length 135 % identity 90

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

> gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC

1.18.1.2) precursor - garden pea > gi_20722_emb_CAA30978_

(X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to

308) [Pisum sativum] > gi_226545_prf__1601517A ferredoxin

NADP reductase [Arachis hypogaea]

Seq. No. 222039

Seq. ID LIB3165-022-P1-K1-H3

Method BLASTX
NCBI GI g3850111
BLAST score 240
E value 3.0e-20
Match length 112
% identity 42

NCBI Description (AL033388) hypothetical integral membrane protein, putative

involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No. 222040

Seq. ID LIB3165-022-P1-K1-H6

Method BLASTX
NCBI GI g1352821
BLAST score 577
E value 1.0e-60
Match length 118
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222041

Seq. ID LIB3165-022-P1-K1-H7

Method BLASTX
NCBI GI g1352821
BLAST score 558
E value 2.0e-57
Match length 112
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222042

Seq. ID LIB3165-023-P1-K1-A1

Method BLASTN
NCBI GI g2656026
BLAST score 60
E value 5.0e-25



Match length 188 % identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MDF20

Seq. No. 222043

Seq. ID LIB3165-023-P1-K1-A12

Method BLASTX
NCBI GI g1352821
BLAST score 743
E value 3.0e-79
Match length 138
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222044

Seq. ID LIB3165-023-P1-K1-A2

Method BLASTX
NCBI GI 9400198
BLAST score 217
E value 2.0e-17
Match length 85
% identity 55

NCBI Description PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)

(LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)

>gi_99604_pir__S21023 hypothetical protein - upland cotton
>gi_1361978_pir__A57500 photosystem II protein psbT upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown

reading frame [Gossypium hirsutum]

Seq. No. 222045

Seq. ID LIB3165-023-P1-K1-A4

Method BLASTX
NCBI GI g289920
BLAST score 211
E value 9.0e-22
Match length 99
% identity 66

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222046

Seq. ID LIB3165-023-P1-K1-A6

Method BLASTX
NCBI GI g3776572
BLAST score 168
E value 8.0e-12
Match length 131
% identity 46

NCBI Description (AC005388) ESTs gb R65052, gb_AA712146, gb_H76533,

gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383, gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis

thaliana]

E value Match length

```
222047
Seq. No.
Seq. ID
                    LIB3165-023-P1-K1-A7
Method
                    BLASTX
NCBI GI
                    q3335350
BLAST score
                    265
E value
                    3.0e-23
Match length
                    119
% identity
                    31
                    (AC004512) Similar to gb Z84386 anthranilate
NCBI Description
                    N-hydroxycinnamoyl/benzoyltransferase from Dianthus
                    caryophyllus. [Arabidopsis thaliana]
                    222048
Seq. No.
Seq. ID
                    LIB3165-023-P1-K1-A9
Method
                    BLASTX
NCBI GI
                    g4406530
BLAST score
                    366
E value
                    6.0e-35
Match length
                    107
                    73
% identity
NCBI Description
                    (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                    222049
                    LIB3165-023-P1-K1-B1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g544437
BLAST score
                    386
E value
                    2.0e-37
                    90
Match length
                    83
% identity
                    GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
NCBI Description
                    >gi 296358 emb CAA47018 (X66377) CIT-SAP [Citrus sinensis]
                    222050
Seq. No.
                    LIB3165-023-P1-K1-B10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3183454
                    247
BLAST score
                    5.0e-21
E value
                    110
Match length
                    45
% identity
                    HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION
NCBI Description
                    \label{eq:capprox} $$ \geq_2632217\_emb\_CAA10859\_ (AJ222587) $$ YkwC protein [Bacillus subtilis] $$ \geq_{G1}2633767\_emb\_CAB13269\_ (Z99111) $$ similar to
                    3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]
                    222051
Seq. No.
                    LIB3165-023-P1-K1-B11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q131399
BLAST score
                    520
```

% identity 79
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411

5.0e-53



photosystem II 10K protein precursor - potato
>gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No. 222052

Seq. ID LIB3165-023-P1-K1-B3

Method BLASTX
NCBI GI g4415908
BLAST score 334
E value 5.0e-47
Match length 109
% identity 83

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 222053

Seq. ID LIB3165-023-P1-K1-B6

Method BLASTX
NCBI GI g289920
BLAST score 711
E value 2.0e-75
Match length 136
% identity 97

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222054

Seq. ID LIB3165-023-P1-K1-B9

Method BLASTX
NCBI GI g4415908
BLAST score 258
E value 2.0e-22
Match length 63
% identity 81

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 222055

Seq. ID LIB3165-023-P1-K1-C1

Method BLASTX
NCBI GI g3402684
BLAST score 402
E value 3.0e-39
Match length 114
% identity 52

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 222056

Seq. ID LIB3165-023-P1-K1-C12

Method BLASTX
NCBI GI g1168411
BLAST score 385
E value 9.0e-44
Match length 122
% identity 82

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 222057

Seq. ID LIB3165-023-P1-K1-C2

Seq. ID

Method



```
BLASTX
Method
NCBI GI
                  q3023752
                  237
BLAST score
                  6.0e-20
E value
                  95
Match length
% identity
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
                  222058
Seq. No.
Seq. ID
                  LIB3165-023-P1-K1-C3
                  BLASTX
Method
NCBI GI
                  q3913649
                   149
BLAST score
                   1.0e-15
E value
                   83
Match length
                   58
% identity
                  FERREDOXIN >gi_404374_bbs_135503 [2Fe-2S] ferredoxin,
NCBI Description
                   [2Fe-2S] Fd [Datura stramonium, var. stramonium and var.
                   tatula, Peptide, 97 aa] >gi_1174327_bbs_171862 [2Fe-2S]
                   ferredoxin [Datura fastuosa, leaves, Peptide, 97 aa]
                   >gi 742379 prf__2009392A ferredoxin [Datura stramonium]
                   222059
Seq. No.
                   LIB3165-023-P1-K1-C8
Seq. ID
                   BLASTX
Method
                   q3309086
NCBI GI
                   375
BLAST score
                   8.0e-37
E value
Match length
                   87
                   90
% identity
                   (AF076253) calcineurin B-like protein 3 [Arabidopsis
NCBI Description
                   thaliana]
                   222060
Seq. No.
                   LIB3165-023-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2791834
BLAST score
                   268
                   9.0e-35
E value
Match length
                   105
% identity
                   77
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   222061
Seq. No.
                   LIB3165-023-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   g1168411
NCBI GI
                   449
BLAST score
                   2.0e-45
E value
Match length
                   121
                   84
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAŞT PRECURSOR
NCBI Description
                   222062
Seq. No.
```

31407

LIB3165-023-P1-K1-D12

BLASTX



```
q3935185
NCBI GI
BLAST score
                  412
                  2.0e-40
E value
                  137
Match length
                  67
% identity
                  (AC004557) F17L21.28 [Arabidopsis thaliana]
NCBI Description
                  222063
Seq. No.
                  LIB3165-023-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3201969
NCBI GI
                   416
BLAST score
                  7.0e-41
E value
                  122
Match length
                   61
% identity
NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]
                   222064
Seq. No.
Seq. ID
                  LIB3165-023-P1-K1-D5
                  BLASTX
Method
                   g289920
NCBI GI
                   647
BLAST score
                   6.0e-68
E value
                   124
Match length
                   98
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   222065
Seq. No.
Seq. ID
                   LIB3165-023-P1-K1-D6
                   BLASTX
Method
                   q1488043
NCBI GI
BLAST score
                   267
                   2.0e-23
E value
Match length
                   83
                   67
% identity
                  (U63784) PAPS-reductase-like protein [Catharanthus roseus]
NCBI Description
Seq. No.
                   222066
                   LIB3165-023-P1-K1-D9
Seq. ID
Method
                   BLASTX
                   g4262239
NCBI GI
                   395
BLAST score
                   2.0e-45
E value
Match length
                   143
                   66
% identity
                   (AC006200) putative membrane transporter [Arabidopsis
NCBI Description
                   thaliana]
                   222067
Seq. No.
                   LIB3165-023-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g417820
NCBI GI
                   155
BLAST score
                   7.0e-27
E value
```

96

Match length

```
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi_167536 (M59858)
                  stearoyl-acyl-carrier protein desaturase [Cucumis sativus]
                  222068
Seq. No.
                  LIB3165-023-P1-K1-E10
Seq. ID
                  BLASTN
Method
                  g3241924
NCBI GI
                  40
BLAST score
                  4.0e-13
E value
                  147
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC6, complete sequence [Arabidopsis thaliana]
                  222069
Seq. No.
Seq. ID
                  LIB3165-023-P1-K1-E12
                  BLASTX
Method
                  g3293031
NCBI GI
BLAST score
                   452
                   4.0e-45
E value
                  116
Match length
                   79
% identity
                  (AJ007574) amino acid carrier [Ricinus communis]
NCBI Description
                   222070
Seq. No.
Seq. ID
                  LIB3165-023-P1-K1-E2
                   BLASTX
Method
NCBI GI
                   q4091806
BLAST score
                   274
                   3.0e-24
E value
                   88
Match length
                   44
% identity
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
NCBI Description
                   222071
Seq. No.
                   LIB3165-023-P1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1352821
BLAST score
                   566
                   2.0e-58
E value
                   127
Match length
                   87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222072
 Seq. No.
                   LIB3165-023-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   a4567202
NCBI GI
BLAST score
                   456
                   1.0e-45
E value
```

99

91

Match length



```
(AC007168) putative myo-inositol 1-phosphate synthase
NCBI Description
                  [Arabidopsis thaliana]
                  222073
Seq. No.
Seq. ID
                  LIB3165-023-P1-K1-E7
                  BLASTX
Method
                  a1679658
NCBI GI
BLAST score
                  212
                  6.0e-17
E value
                  91
Match length
                  53
% identity
NCBI Description (U63726) gamma glutamyl hydrolase [Glycine max]
                  222074
Seq. No.
Seq. ID
                  LIB3165-023-P1-K1-F10
                  BLASTX
Method
                  q2641638
NCBI GI
                  569
BLAST score
E value
                  2.0e-63
                  140
Match length
                  89
% identity
NCBI Description (AF032883) AtJ3 [Arabidopsis thaliana]
                  222075
Seq. No.
                  LIB3165-023-P1-K1-F11
Seq. ID
                  BLASTX
Method
                  g3121825
NCBI GI
BLAST score
                  177
                  2.0e-13
E value
Match length
                  87
                   64
% identity
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)
                   bas1 protein [Spinacia oleracea]
                   222076
Seq. No.
                   LIB3165-023-P1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2499946
BLAST score
                   143
                   4.0e-09
E value
Match length
                   31
                   84
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana
                   tabacum]
                   222077
Seq. No.
                   LIB3165-023-P1-K1-F3
Seq. ID
                   BLASTX
Method
                   g421826
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   103
Match length
```



>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
thaliana]

Seq. No. 222078

Seq. ID LIB3165-023-P1-K1-F4

Method BLASTX
NCBI GI g2078386
BLAST score 246
E value 6.0e-21
Match length 129
% identity 30

% identity 30
NCBI Description (U96623) glyceraldehyde-3-phosphate-dehydrogenase

[Selaginella lepidophylla]

Seq. No. 222079

Seq. ID LIB3165-023-P1-K1-F8

Method BLASTX
NCBI GI g1352821
BLAST score 579
E value 6.0e-60
Match length 109
% identity 100

NCBI Description RIBULOSÉ BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222080

Seq. ID LIB3165-023-P1-K1-G5

Method BLASTX
NCBI GI g3860272
BLAST score 262
E value 1.0e-46
Match length 108
% identity 90

NCBI Description (AC005824) putative suppressor protein [Arabidopsis

thaliana] >gi 4314399 gb AAD15609_ (AC006232) putative skdl

protein [Arabidopsis thaliana]

Seq. No. 222081

Seq. ID LIB3165-023-P1-K1-G7

Method BLASTX
NCBI GI 94406530
BLAST score 231
E value 3.0e-31
Match length 98
% identity 73

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 222082

Seq. ID LIB3165-023-P1-K1-H10

Method BLASTX
NCBI GI g1488043
BLAST score 235
E value 1.0e-19
Match length 73

Match length

% identity

117 44



```
% identity
                  68
                  (U63784) PAPS-reductase-like protein [Catharanthus roseus]
NCBI Description
                  222083
Seq. No.
                  LIB3165-023-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  q3676818
NCBI GI
                  190
BLAST score
                  2.0e-14
E value
                  54
Match length
                  69
% identity
                  (AF091514) metallothionein homolog [Elaeagnus umbellata]
NCBI Description
                  222084
Seq. No.
                  LIB3165-023-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  g2435518
NCBI GI
BLAST score
                  146
                  3.0e-09
E value
                  80
Match length
                  44
% identity
                  (AF024504) contains similarity to C3HC4-type zinc fingers
NCBI Description
                   [Arabidopsis thaliana]
                  222085
Seq. No.
                  LIB3165-023-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
                   456
BLAST score
                   3.0e-47
E value
                  139
Match length
                   66
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   222086
Seq. No.
                  LIB3165-024-P1-K1-A1
Seq. ID
Method
                  BLASTX
                   g120026
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   87
Match length
                   55
% identity
                  FERREDOXIN PRECURSOR >gi_65746_pir__FEQH ferredoxin
NCBI Description
                   [2Fe-2S] precursor - white campion >gi_21362_emb_CAA26281
                   (X02432) ferredoxin precursor [Silene latifolia ssp. alba]
Seq. No.
                   222087
Seq. ID
                   LIB3165-024-P1-K1-A10
Method
                   BLASTX
                   q2832669
NCBI GI
BLAST score
                   196
E value
                   4.0e-15
```

NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]



[Pisum sativum]

% identity

NCBI Description

```
222088
Seq. No.
                  LIB3165-024-P1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2754849
BLAST score
                  585
                  1.0e-60
E value
                  133
Match length
                  83
% identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
                  222089
Seq. No.
Seq. ID
                  LIB3165-024-P1-K1-A5
                  BLASTX
Method
                  q3063392
NCBI GI
                   436
BLAST score
                  3.0e-43
E value
                  116
Match length
                   76
% identity
                  (AB012932) Ca2+/H+ exchanger [Vigna radiata]
NCBI Description
                   222090
Seq. No.
                  LIB3165-024-P1-K1-A6
Seq. ID
                   BLASTX
Method
                   q4091810
NCBI GI
                   379
BLAST score
                   2.0e-36
E value
                   140
Match length
                   49
% identity
                   (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1
NCBI Description
                   [Arabidopsis thaliana]
                   222091
Seq. No.
                   LIB3165-024-P1-K1-A8
Seq. ID
Method
                   BLASTX
                   g1352821
NCBI GI
BLAST score
                   617
                   2.0e-64
E value
Match length
                   120
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222092
Seq. No.
                   LIB3165-024-P1-K1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g20733
                   492
BLAST score
                   9.0e-50
E value
Match length
                   122
```

(X15188) precursor C-terminal fragment (AA -80 to 367)



```
Seq. No.
                  222093
                  LIB3165-024-P1-K1-B12
Seq. ID
Method
                  BLASTN
                  g3985958
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
Match length
                  49
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZN1, complete sequence [Arabidopsis thaliana]
                  222094
Seq. No.
                  LIB3165-024-P1-K1-B2
Seq. ID
                  BLASTX
Method
                   q70644
NCBI GI
BLAST score
                   616
                   2.0e-64
E value
                   125
Match length
% identity
                   19
                  ubiquitin precursor - common sunflower (fragment)
NCBI Description
                   222095
Seq. No.
                   LIB3165-024-P1-K1-B3
Seq. ID
Method
                   BLASTX
                   q3242704
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
                   45
Match length
% identity
                   64
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   222096
Seq. No.
                   LIB3165-024-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129879
BLAST score
                   619
                   8.0e-65
E value
                   117
Match length
% identity
                   64
                   chlorophyll a/b-binding protein type II precursor,
NCBI Description
                   photosystem I - garden pea >gi_602359_emb_CAA57492
                   (X81962) Type II chlorophyll a/b binding protein from
                   photosystem I [Pisum sativum]
                   222097
Seq. No.
                   LIB3165-024-P1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1352821
                   492
BLAST score
                   7.0e-50
E value
Match length
                   94
                   99
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
- 1 A
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
```

ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
222098
Seq. No.
                  LIB3165-024-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  q3913651
NCBI GI
BLAST score
                  476
                  7.0e-48
E value
Match length
                  112
                  79
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                  (FNR) >gi_2225993 emb_CAA74359_ (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                  222099
Seq. No.
                  LIB3165-024-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  563
                   4.0e-58
E value
Match length
                  107
                   99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222100
Seq. No.
Seq. ID
                   LIB3165-024-P1-K1-C3
Method
                   BLASTX
                   g421826
NCBI GI
                   393
BLAST score
                   3.0e-38
E value
Match length
                   120
% identity
                   63
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   222101
Seq. No.
                   LIB3165-024-P1-K1-C6
Seq. ID
                   BLASTX
Method
                   q4538897
NCBI GI
                   493
BLAST score
                   7.0e-50
E value
                   135
Match length
                   68
% identity
                  (AL049482) AX110P-like protein [Arabidopsis thaliana]
NCBI Description
                   222102
Seq. No.
                   LIB3165-024-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   q1928981
NCBI GI
                   455
BLAST score
                   2.0e-45
E value
                   112
Match length
                   81
```

Seq. ID



```
(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                  222103
Seq. No.
Seq. ID
                  LIB3165-024-P1-K1-C8
                  BLASTX
Method
                  q2754849
NCBI GI
BLAST score
                  416
                  2.0e-45
E value
                  120
Match length
                  80
% identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
                  222104
Seq. No.
                  LIB3165-024-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  q1353352
NCBI GI
BLAST score
                   429
                   2.0e-42
E value
                   136
Match length
                   57
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   222105
Seq. No.
Seq. ID
                   LIB3165-024-P1-K1-D10
                   BLASTX
Method
NCBI GI
                   q398992
BLAST score
                   432
                   8.0e-43
E value
                   100
Match length
                   76
% identity
                  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                   (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN PTOM13)
                   >gi 100205 pir__S16591 ethylene-forming enzyme - tomato
                   >gi 19207 emb CAA41212 (X58273)
                   1-Aminocyclopropane-1-carboxylic acid oxidase [Lycopersicon
                   esculentum]
Seq. No.
                   222106
                   LIB3165-024-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   q398992
NCBI GI
BLAST score
                   452
                   4.0e-45
E value
                   105
Match length
                   75
 % identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                   (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN PTOM13)
                   >gi_100205_pir__S16591 ethylene-forming enzyme - tomato
                   >gi_19207_emb_CAA41212_ (X58273)
                   1-Aminocyclopropane-1-carboxylic acid oxidase [Lycopersicon
                   esculentum]
                   222107
 Seq. No.
                   LIB3165-024-P1-K1-D2
```



```
Method
                   BLASTX
                   g2055230
NCBI GI
                   339
BLAST score
                   7.0e-32
E value
                   114
Match length
                   56
% identity
NCBI Description (AB000130) SRC2 [Glycine max]
                   222108
Seq. No.
                   LIB3165-024-P1-K1-D4
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
                   512
BLAST score
                   4.0e-52
E value
                   109
Match length
                   89
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222109
Seq. No.
                   LIB3165-024-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g131166
NCBI GI
                   557
BLAST score
                   1.0e-59
E value
                   125
Match length
                   89
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir__S00449
                   photosystem I chain II precursor - tomato >gi_170492
                   (M21344) photosystem I subunit II protein precursor
                   [Lycopersicon esculentum] >gi_226544_prf__1601516A
                   photosystem I reaction center II [Lycopersicon esculentum]
Seq. No.
                   222110
                   LIB3165-024-P1-K1-D7
Seq. ID
                   BLASTN
Method
                   q289919
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
Match length
                   83
                   82
% identity
NCBI Description Gossypium hirsutum chloroplast photosystem II chlorophyll
                   A/B-binding protein gene, complete cds
Seq. No.
                   222111
                   LIB3165-024-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1352821
BLAST score
                   574
                   2.0e-59
E value
Match length
                   108
                   98
% identity
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222112 Seq. No. LIB3165-024-P1-K1-E12 Seq. ID BLASTN Method q18058 NCBI GI BLAST score 82 E value 3.0e-38 270 Match length 83 % identity NCBI Description Citrus limon cistron for 26S ribosomal RNA 222113 Seq. No.

Seq. ID LIB3165-024-P1-K1-E2

Method BLASTX
NCBI GI g224293
BLAST score 410
E value 3.0e-40
Match length 86
% identity 97

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 222114

Seq. ID LIB3165-024-P1-K1-E3

Method BLASTX
NCBI GI g1168408
BLAST score 627
E value 1.0e-65
Match length 134
% identity 92

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 222115

Seq. ID LIB3165-024-P1-K1-E4

Method BLASTX
NCBI GI g1172664
BLAST score 234
E value 1.0e-19
Match length 51
% identity 90

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_419791_pir__S31165 photosystem I chain III precursor Flaveria trinervia >gi_298482_bbs_127083 photosystem I
reaction center subunit III, PSI-RC PsaF [Flaveria

trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem

I subunit III [Flaveria trinervia]

Seq. No. 222116

Seq. ID LIB3165-024-P1-K1-E6

Method BLASTX

77

% identity

```
q4406530
NCBI GI
BLAST score
                  311
                  1.0e-28
E value
Match length
                  109
                  66
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  222117
Seq. No.
Seq. ID
                  LIB3165-024-P1-K1-E8
                  BLASTX
Method
                  g2956690
NCBI GI
BLAST score
                  176
                  1.0e-12
E value
Match length
                  104
                  29
% identity
                  (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928
NCBI Description
                   (AF079800) PsbY precursor [Arabidopsis thaliana]
Seq. No.
                   222118
                  LIB3165-024-P1-K1-E9
Seq. ID
                  BLASTX
Method
                   g1730635
NCBI GI
                   152
BLAST score
E value
                   6.0e-10
                   103
Match length
                   38
% identity
                   HYPOTHETICAL 40.7 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION
NCBI Description
                   >gi 2132777_pir__S60917 probable membrane protein YNL264c -
                   yeast (Saccharomyces cerevisiae) >gi_1045245_emb_CAA63233_
                   (X92494) ORF NO815 [Saccharomyces cerevisiae]
                   >gi 1302321 emb_CAA96171_ (Z71540) ORF YNL264c
                   [Saccharomyces cerevisiae]
Seq. No.
                   222119
                   LIB3165-024-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
                   733
BLAST score
E value
                   5.0e-78
                   136
Match length
                   99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222120
Seq. No.
                   LIB3165-024-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   g4406530
NCBI GI
                   340
BLAST score
                   5.0e-32
E value
                   91
Match length
```

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Sea. No.

Seq. ID

222126

LIB3165-024-P1-K1-G10



```
222121
 Seq. No.
                   LIB3165-024-P1-K1-F4
 Seq. ID
                   BLASTX
 Method
                   g3928760
 NCBI GI
                   322
 BLAST score
                   8.0e-30
 E value
                   131
 Match length
 % identity
                   (AB011797) homolog to plastid-lipid-associated protein
 NCBI Description
                   [Citrus unshiu]
                   222122
 Seq. No.
                   LIB3165-024-P1-K1-F5
 Seq. ID
                   BLASTX
 Method
                   g217909
 NCBI GI
                   606
 BLAST score
                   3.0e-63
 E value
                   128
 Match length
                   93
 % identity
 NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]
                   222123
 Seq. No.
                   LIB3165-024-P1-K1-F6
 Seq. ID
                   BLASTX
Method
                    g4538944
 NCBI GI
                    154
 BLAST score
                    4.0e-10
 E value
                    45
 Match length
                    67
 % identity
                   (AL049483) putative transcription factor [Arabidopsis
 NCBI Description
                    thaliana]
                    222124
 Seq. No.
                    LIB3165-024-P1-K1-F9
 Seq. ID
                    BLASTX
 Method
                    g2443878
 NCBI GI
                    186
 BLAST score
                    6.0e-14
 E value
                    80
 Match length
 % identity
                   (AC002294) Unknown protein [Arabidopsis thaliana]
 NCBI Description
                    222125
 Seq. No.
                    LIB3165-024-P1-K1-G1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g115833
 BLAST score
                    507
                    1.0e-51
 E value
                    126
 Match length
                    78
  % identity
                    CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
 NCBI Description
                    (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                    a/b-binding protein Cab10A - tomato >gi_170394 (M32605)
                    a-binding protein [Lycopersicon esculentum]
```



```
Method
                  BLASTX
NCBI GI
                  g2494415
BLAST score
                  498
                  2.0e-50
E value
Match length
                  134
                  76
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine
Seq. No.
                  222127
                  LIB3165-024-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  g3377517
NCBI GI
BLAST score
                  380
                  1.0e-36
E value
Match length
                  112
% identity
                   67
                  (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  222128
Seq. ID
                  LIB3165-024-P1-K1-G4
Method
                  BLASTX
NCBI GI
                   g1352821
BLAST score
                   596
                   6.0e-62
E value
Match length
                   119
% identity
                   97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222129
Seq. No.
                   LIB3165-024-P1-K1-G5
Seq. ID
Method
                   BLASTX
                   g2129538
NCBI GI
                   504
BLAST score
                   3.0e-51
E value
                   105
Match length
% identity
                   91
NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                   AT103 [Arabidopsis thaliana]
Seq. No.
                   222130
Seq. ID
                   LIB3165-024-P1-K1-G7
Method
                   BLASTX
                   g4406530
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
Match length
                   91
```

Seq. No. 222131

% identity

NCBI Description

(AF126870) rubisco activase [Vigna radiata]



LIB3165-024-P1-K1-G8 Seq. ID Method BLASTX NCBI GI q3128217 BLAST score 244 9.0e-21 E value 87 Match length 64 % identity (AC004077) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 3337374 (AC004481) hypothetical protein [Arabidopsis thaliana] 222132 Seq. No. LIB3165-024-P1-K1-H1 Seq. ID BLASTX Method NCBI GI q558925 BLAST score 433 E value 6.0e-43Match length 123 % identity 70 (U15778) geranylgeranyl pyrophosphate synthase [Lupinus NCBI Description albus] Seq. No. 222133 LIB3165-024-P1-K1-H10 Seq. ID BLASTX Method NCBI GI q1352821 BLAST score 513 3.0e-52E value Match length 125 82 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 222134 Seq. No. LIB3165-024-P1-K1-H2 Seq. ID Method BLASTX g2501578 NCBI GI 577 BLAST score 9.0e-60 E value 122 Match length 96 % identity ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047 NCBI Description ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis] 222135 Seq. No. LIB3165-024-P1-K1-H3 Seq. ID

Method BLASTX
NCBI GI g1061040
BLAST score 603
E value 8.0e-63
Match length 127
% identity 85



```
NCBI Description
                  (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
                  >gi 1587694_prf__2207220A sterol C-methyltransferase
                  [Arabidopsis thaliana]
                  222136
Seq. No.
                  LIB3165-024-P1-K1-H4
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  33
BLAST score
                  5.0e-09
E value
                  48
Match length
                  51
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  222137
Seq. No.
                  LIB3165-024-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  g4467115
NCBI GI
                  213
BLAST score
                  3.0e-21
E value
                  70
Match length
                  77
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  222138
Seq. No.
                  LIB3165-024-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q231496
                   581
BLAST score
                   3.0e-60
E value
                  129
Match length
                   89
% identity
                  ACTIN 58 >gi_100421_pir__S20094 actin - potato
NCBI Description
                   >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]
Seq. No.
                   222139
Seq. ID
                  LIB3165-024-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q2244734
                   439
BLAST score
                   8.0e-44
E value
Match length
                   98
                   90
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
                   222140
Seq. No.
Seq. ID
                   LIB3165-025-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q3687652
BLAST score
                   407
                   3.0e-44
E value
Match length
                   98
% identity
                  (AF047352) rubisco activase precursor [Datisca glomerata]
NCBI Description
```

31423

222141

LIB3165-025-P1-K1-A3

Seq. No. Seq. ID



```
BLASTX
Method
NCBI GI
                  q120663
                  329
BLAST score
                  6.0e-51
E value
                  135
Match length
                  75
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,
NCBI Description
                  CHLOROPLAST >qi 66027 pir DEPMNB
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                  garden pea >gi 309671 (M55147) glyceraldehyde-3-phosphate
                  dehydrogenase B subunit [Pisum sativum]
                  222142
Seq. No.
                  LIB3165-025-P1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2129921
                   167
BLAST score
E value
                   1.0e-11
Match length
                   51
                   67
% identity
                  hypothetical protein 1 - Madagascar periwinkle >gi 758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
                   222143
Seq. No.
                   LIB3165-025-P1-K1-A7
Seq. ID
Method
                   BLASTX
                   q4468813
NCBI GI
BLAST score
                   281
E value
                   4.0e-25
Match length
                   68
                   75
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   222144
Seq. No.
                   LIB3165-025-P1-K1-B1
Seq. ID
                   BLASTX
Method
                   q68200
NCBI GI
BLAST score
                   517
                   1.0e-52
E value
                   128
Match length
                   82
% identity
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   222145
Seq. No.
                   LIB3165-025-P1-K1-B12
Seq. ID
Method
                   BLASTX
                   g1352821
NCBI GI
                   399
BLAST score
E value
                   6.0e-39
                   87
Match length
 % identity
                   92
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
```

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Seq. ID Method



precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222146 LIB3165-025-P1-K1-B2 Seq. ID Method BLASTX NCBI GI q1168411 BLAST score 448 1.0e-44 E value Match length 120 78 % identity FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description 222147 Seq. No. LIB3165-025-P1-K1-B5 Seq. ID BLASTX Method NCBI GI q4102703 BLAST score 400 5.0e-39 E value 117 Match length % identity 73 (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis NCBI Description thaliana] 222148 Seq. No. LIB3165-025-P1-K1-C11 Seq. ID BLASTX Method NCBI GI q3694872 BLAST score 441 7.0e-44E value Match length 107 79 % identity (AF092547) profilin [Ricinus communis] NCBI Description 222149 Seq. No. LIB3165-025-P1-K1-C2 Seq. ID BLASTX Method q1130682 NCBI GI BLAST score 447 2.0e-44E value Match length 86 100 % identity NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum] 222150 Seq. No. LIB3165-025-P1-K1-C3 Seq. ID Method BLASTX g4106696 NCBI GI BLAST score 241 2.0e-20 E value 70 Match length 73 % identity (AB021872) ribosome-sedimenting protein [Pisum sativum] NCBI Description 222151 Seq. No.

31425

LIB3165-025-P1-K1-D1

BLASTX



```
NCBI GI
                  g1352821
                  620
BLAST score
                  8.0e-65
E value
                  121
Match length
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222152
Seq. No.
Seq. ID
                  LIB3165-025-P1-K1-D10
                  BLASTN
Method
                  g18511
NCBI GI
BLAST score
                  162
                  5.0e-86
E value
                  250
Match length
                  91
% identity
NCBI Description G.hirsutum light regulated unknown reading frame DNA
Seq. No.
                  222153
                  LIB3165-025-P1-K1-D12
Seq. ID
                  BLASTN
Method
                  g2264318
NCBI GI
                   34
BLAST score
                  1.0e-09
E value
                  192
Match length
                   83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
                   222154
Seq. No.
                  LIB3165-025-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4454459
BLAST score
                   190
E value
                   1.0e-14
                   58
Match length
                   60
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   222155
Seq. No.
                  LIB3165-025-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2493494
BLAST score
                   443
                   5.0e-44
E value
Match length
                   110
                   75
% identity
```

NCBI Description

SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >qi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase

[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436

aa]

Seq. No. 222156

Seq. ID LIB3165-025-P1-K1-D9



```
Method BLASTX
NCBI GI g4056456
BLAST score 467
E value 7.0e-47
Match length 112
% identity 81
NCBI Description (AC005990) Strong
```

(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

 Seq. No.
 222157

 Seq. ID
 LIB3165-025-P1-K1-E10

 Method
 BLASTX

 NCBI GI
 g20729

 BLAST score
 183

 E value
 5.0e-14

Match length 61 % identity 62

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 222158

Seq. ID LIB3165-025-P1-K1-E11

Method BLASTX
NCBI GI g1055130
BLAST score 186
E value 6.0e-14
Match length 95
% identity 37

NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for

by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA

yk78c2.3

Seq. No. 222159

Seq. ID LIB3165-025-P1-K1-E6

Method BLASTX
NCBI GI g120663
BLAST score 417
E value 5.0e-41
Match length 116
% identity 72

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi_66027_pir__DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]

Seq. No. 222160

Seq. ID LIB3165-025-P1-K1-F1

Method BLASTX
NCBI GI g1872544
BLAST score 285
E value 1.0e-25
Match length 122

% identity

NCBI Description

59



```
% identity
                  (U89014) early light-induced protein; ELIP [Arabidopsis
NCBI Description
                  thaliana]
                  222161
Seq. No.
                  LIB3165-025-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  33
                  5.0e-09
E value
                  37
Match length
                  97
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  222162
Seq. No.
Seq. ID
                  LIB3165-025-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  q450504
BLAST score
                   75
E value
                   3.0e - 34
Match length
                   178
                   85
% identity
NCBI Description
                  G.hirsutum rbcS gene for ribulose-1,5-bisphosphate
                  carboxylase, small subunit
                   222163
Seq. No.
                  LIB3165-025-P1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1209703
                   332
BLAST score
                   5.0e - 31
E value
                  126
Match length
                   45
% identity
NCBI Description (U40489) maize gl1 homolog [Arabidopsis thaliana]
                   222164
Seq. No.
                  LIB3165-025-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3334115
BLAST score
                   326
                   2.0e-30
E value
                   90
Match length
                   76
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
                   222165
Seq. No.
                   LIB3165-025-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4567249
BLAST score
                   295
E value
                   1.0e-26
                   103
Match length
```

(AC007070) hypothetical protein [Arabidopsis thaliana]

NCBI GI

BLAST score

```
Seq. No.
                  222166
                  LIB3165-025-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2292917
BLAST score
                  441
E value
                  8.0e-44
Match length
                  129
                  67
% identity
                  (X99851) galactokinase [Arabidopsis thaliana]
NCBI Description
                  222167
Seq. No.
Seq. ID
                  LIB3165-025-P1-K1-G9
                  BLASTX
Method
                  g3915873
NCBI GI
BLAST score
                  404
E value
                  1.0e-39
                  98
Match length
% identity
                  78
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   (NODULIN-100) >qi 2606081 (AF030231) sucrose synthase
                  [Glycine max]
                  222168
Seq. No.
                  LIB3165-025-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q1352821
NCBI GI
                  596
BLAST score
E value
                  5.0e-62
Match length
                  119
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222169
Seq. No.
Seq. ID
                  LIB3165-025-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g132091
BLAST score
                  245
                  4.0e-33
E value
                  96
Match length
                  75
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN F1 PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT F1) >gi_68065_pir__RKRPF1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (gene rbcSF1) - rape >gi_17852_emb_CAA39402
                   (X55937) ribulose bisphosphate carboxylase /oxygenase
                  small subunit [Brassica napus]
                  222170
Seq. No.
Seq. ID
                  LIB3165-025-P1-K1-H7
Method
                  BLASTX
```

g1354515

335

BLAST score

Match length

E value

5.0e-13

48



```
E value
                  2.0e-31
Match length
                  130
                  58
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   222171
Seq. No.
Seq. ID
                  LIB3165-026-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  g2388583
BLAST score
                  195
                   5.0e-15
E value
Match length
                   87
                   55
% identity
                   (AC000098) Similar to Synechocystis hypothetical protein
NCBI Description
                   (gb D90908). [Arabidopsis thaliana]
                   222172
Seq. No.
                   LIB3165-026-P1-K1-A4
Seq. ID
                   BLASTN
Method
                   q3985958
NCBI GI
BLAST score
                   41
                   1.0e-13
E value
Match length
                   49
                   96
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   222173
                   LIB3165-026-P1-K1-A6
Seq. ID
                   BLASTX
Method
                   g3153902
NCBI GI
                   321
BLAST score
                   4.0e-30
E value
                   79
Match length
                   82
% identity
                   (AF066076) 14-3-3-like protein [Helianthus annuus]
NCBI Description
Seq. No.
                   222174
                   LIB3165-026-P1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g125578
BLAST score
                   609
                   1.0e-63
E value
                   126
Match length
                   93
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                   222175
Seq. No.
                   LIB3165-026-P1-K1-A9
Seq. ID
Method
                   BLASTX
                   q1001135
NCBI GI
                   178
```

Seq. ID

```
% identity
                  (D64001) acetolactate synthase [Synechocystis sp.]
NCBI Description
                  222176
Seq. No.
Seq. ID
                  LIB3165-026-P1-K1-B10
                  BLASTX
Method
                  q487046
NCBI GI
BLAST score
                  389
                  1.0e-37
E value
                  131
Match length
                  61
% identity
                  photosystem I chain II precursor - wood tobacco
NCBI Description
                  >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
                  222177
Seq. No.
Seq. ID
                  LIB3165-026-P1-K1-B11
                  BLASTX
Method
NCBI GI
                  q4406530
                   608
BLAST score
                  2.0e-63
E value
                  127
Match length
                  87
% identity
NCBI Description
                  (AF126870) rubisco activase [Vigna radiata]
                  222178
Seq. No.
                  LIB3165-026-P1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2414160
BLAST score
                   283
                   3.0e-25
E value
Match length
                   90
                   53
% identity
NCBI Description
                  (Z99266) F15C11.2 [Caenorhabditis elegans]
                   222179
Seq. No.
                   LIB3165-026-P1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3183640
BLAST score
                   268
                   1.0e-23
E value
                   52
Match length
                   96
% identity
                  (AJ005869) transmembrane channel protein [Cicer arietinum]
NCBI Description
                   222180
Seq. No.
                   LIB3165-026-P1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g20729
                   368
BLAST score
E value
                   2.0e-35
Match length
                   103
                   73
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
Seq. No.
                   222181
```

31431

LIB3165-026-P1-K1-B6



Method BLASTX
NCBI GI g1352821
BLAST score 593
E value 1.0e-61
Match length 118
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222182

Seq. ID LIB3165-026-P1-K1-B7

Method BLASTX
NCBI GI g1172811
BLAST score 460
E value 3.0e-46
Match length 87
% identity 97

NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)

>gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
- rice >gi 575355 emb CAA57339 (X81691) putative tumor

suppresser [Oryza sativa]

Seq. No. 222183

Seq. ID LIB3165-026-P1-K1-B9

Method BLASTX
NCBI GI g3738299
BLAST score 363
E value 1.0e-34
Match length 90
% identity 81

NCBI Description (AC005309) putative glutaredoxin [Arabidopsis thaliana]

>gi 4249395 (AC006072) putative glutaredoxin [Arabidopsis

50° 0° 10 10 10 10 10

thaliana]

Seq. No. 222184

Seq. ID LIB3165-026-P1-K1-C10

Method BLASTX
NCBI GI g2194137
BLAST score 391
E value 6.0e-38
Match length 125
% identity 68

NCBI Description (AC002062) ESTs gb_R29947,gb_H76702 come from this gene.

[Arabidopsis thaliana]

Seq. No. 222185

Seq. ID LIB3165-026-P1-K1-C11

Method BLASTX
NCBI GI g131385
BLAST score 473
E value 1.0e-47
Match length 127
% identity 78

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

NCBI Description

esculentum]



SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

```
Seq. No.
                   222186
 Seq. ID
                   LIB3165-026-P1-K1-C3
                   BLASTX
Method
                   q3193298
 NCBI GI
 BLAST score
                   319
                   2.0e-29
 E value
                   93
 Match length
                   65
 % identity
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
 NCBI Description
                   222187
 Seq. No.
 Seq. ID
                   LIB3165-026-P1-K1-C4
                   BLASTX
 Method
 NCBI GI
                   q3721926
                   244
 BLAST score
 E value
                   1.0e-20
 Match length
                    91
                    63
 % identity
                   (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
 NCBI Description
                    222188
 Seq. No.
 Seq. ID
                   LIB3165-026-P1-K1-C5
                   BLASTX
 Method
                    q2146797
 NCBI GI
                    557
 BLAST score
                    2.0e-57
 E value
 Match length
                    134
                    43
 % identity
                   protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
 NCBI Description
                    >gi 1134968 (U41385) protein disulphide isomerase PDI
                    [Ricinus communis] >gi 1587210 prf 2206331A protein
                    disulfide isomerase [Ricinus communis]
                    222189
 Seq. No.
Seq. ID
                    LIB3165-026-P1-K1-C9
 Method
                    BLASTX
 NCBI GI
                    q4454480
 BLAST score
                    328
                    1.0e-30
 E value
                    73
 Match length
                    78
 % identity
                    (AC006234) putative (1-4)-beta-mannan endohydrolase
 NCBI Description
                    [Arabidopsis thaliana]
                    222190
 Seq. No.
                    LIB3165-026-P1-K1-D3
 Seq. ID
 Method
                    BLASTX
                    g441457
 NCBI GI
                    513
 BLAST score
                    3.0e-52
 E value
                    95
 Match length
                    98
 % identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
```



68

% identity

```
Seq. No.
                  222191
                  LIB3165-026-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709825
                  332
BLAST score
E value
                  4.0e-31
Match length
                  122
% identity
                  66
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >qi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  222192
                  LIB3165-026-P1-K1-D8
Seq. ID
Method
                  BLASTX
                  q2739365
NCBI GI
BLAST score
                  531
                  2.0e-54
E value
Match length
                  118
% identity
                  79
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  222193
Seq. No.
Seq. ID
                  LIB3165-026-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1352821
                  531
BLAST score
                  2.0e-54
E value
Match length
                  103
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222194
Seq. No.
                  LIB3165-026-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4325041
BLAST score
                  635
                  1.0e-66
E value
Match length
                  128
                  95
% identity
                  (AF117339) FtsH-like protein Pftf precursor [Nicotiana
NCBI Description
                  tabacum]
                  222195
Seq. No.
                  LIB3165-026-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953471
                  238
BLAST score
                  5.0e-20
E value
Match length
                  68
```

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

```
Seq. No.
                  222196
                  LIB3165-026-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  q1781348
NCBI GI
                  209
BLAST score
                  7.0e-17
E value
Match length
                  46
                  91
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
                  222197
Seq. No.
                  LIB3165-026-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q289920
BLAST score
                   696
                   1.0e-73
E value
Match length
                   130
                   99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   222198
Seq. No.
                   LIB3165-026-P1-K1-F11
Seq. ID
Method
                   BLASTX
                   q131399
NCBI GI
BLAST score
                   441
E value
                   3.0e-45
Match length
                   110
                   84
% identity
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                   TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277_pir__S00411
                   photosystem II 10K protein precursor - potato
                   >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum
                   tuberosum]
                   222199
Seq. No.
Seq. ID
                   LIB3165-026-P1-K1-F3
Method
                   BLASTX
                   g3158474
NCBI GI
                   539
BLAST score
                   3.0e-55
E value
```

Match length 114 % identity 91

(AF067184) aquaporin 1 [Samanea saman] NCBI Description

222200 Seq. No.

LIB3165-026-P1-K1-F4 Seq. ID

BLASTX Method NCBI GI g4091806 BLAST score 520 4.0e-53 E value Match length 117 % identity 85

(AF052585) CONSTANS-like protein 2 [Malus domestica] NCBI Description

222201 Seq. No.

```
Seq. ID
                   LIB3165-026-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q82426
- BLAST score
                   559
                   1.0e-57
E value
Match length
                   116
                   45
 % identity
                   ubiquitin precursor - barley (fragment)
NCBI Description
                   >qi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                   (171 aa) [Hordeum vulgare]
                   222202
 Seq. No.
                   LIB3165-026-P1-K1-F7
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   g1651736
 BLAST score
                   199
                   2.0e-15
 E value
 Match length
                   52
 % identity
                   71
 NCBI Description
                   (D90899) cysteine synthase [Synechocystis sp.]
                   222203
 Seq. No.
                   LIB3165-026-P1-K1-F8
 Seq. ID
 Method
                   BLASTX
                   q1352821
 NCBI GI
                   575
 BLAST score
                   2.0e-59
 E value
                   116
 Match length
 % identity
                   96
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222204
 Seq. No.
                   LIB3165-026-P1-K1-F9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g3785995
 BLAST score
                   153
 E value
                    5.0e-10
                   71
 Match length
                    46
 % identity
                   (AC005499) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   222205
 Seq. No.
                   LIB3165-026-P1-K1-G10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g100616
 BLAST score
                    256
                    4.0e-22
 E value
 Match length
                    60
                    82
 % identity
                   ribulose-bisphosphate carboxylase activase B precursor -
 NCBI Description
                   barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
```

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
ribulose 1,5-bisphosphate carboxylase activase [Hordeum

Seq. No.

Seq. ID

222211

LIB3165-026-P1-K1-H10



vulgare]

Seq. No. 222206 LIB3165-026-P1-K1-G12 Seq. ID Method BLASTX NCBI GI q430947 BLAST score 421 E value 2.0e-41 Match length 103 82 % identity NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana] 222207 Seq. No. Seq. ID LIB3165-026-P1-K1-G2 Method BLASTX NCBI GI g1532135 BLAST score 279 E value 8.0e-25 57 Match length 91 % identity (U49442) chloroplast mRNA-binding protein CSP41 precursor NCBI Description [Spinacia oleracea] Seq. No. 222208 Seq. ID LIB3165-026-P1-K1-G5 Method BLASTX NCBI GI g1354515 BLAST score 287 E value 9.0e-26 Match length 132 % identity 48 NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus tremuloides] 222209 Seq. No. LIB3165-026-P1-K1-G7 Seq. ID Method BLASTX NCBI GI g1168411 BLAST score 363 1.0e-34 E value Match length 94 81 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR Seq. No. 222210 LIB3165-026-P1-K1-G8 Seq. ID Method BLASTX NCBI GI g2827076 BLAST score 278 E value 1.0e-24 Match length 109 54 % identity NCBI Description (AF020269) malate dehydrogenase precursor [Medicago sativa]

31437



```
BLASTX
Method
NCBI GI
                  g3024126
                  537
BLAST score
                  4.0e-55
E value
                  105
Match length
                  97
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 1655576 emb CAA95856 (Z71271) S-adenosyl-L-methionine
                  synthetase 1 [Catharanthus roseus]
                  222212
Seq. No.
Seq. ID
                  LIB3165-026-P1-K1-H11
                  BLASTX
Method
                  g3063392
NCBI GI
BLAST score
                  418
                  4.0e-41
E value
                  113
Match length
                  75
% identity
NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]
                  222213
Seq. No.
Seq. ID
                  LIB3165-026-P1-K1-H2
                  BLASTX
Method
                  g2499967
NCBI GI
                  186
BLAST score
E value
                  6.0e-14
                  110
Match length
                  43
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E
NCBI Description
                  B) >qi 632724 bbs 151002 (S72358) photosystem I subunit
                  PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,
                  143 aa] [Nicotiana sylvestris]
Seq. No.
                  222214
                  LIB3165-026-P1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3023752
BLAST score
                  309
                  2.0e-28
E value
Match length
                  109
% identity
                  61
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                  222215
                  LIB3165-026-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  g282833
NCBI GI
BLAST score
                  481
                  2.0e-48
E value
                  110
Match length
% identity
                  89
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
```

Seq. ID LIB3165-026-P1-K1-H7

222216

Seq. No.

```
BLASTX
Method
NCBI GI
                   q166834
                   641
BLAST score
                   3.0e-67
E value
Match length
                   134
% identity
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                   activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
                   222217
Seq. No.
                   LIB3165-026-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   g2213597
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   61
Match length
                   72
% identity
                   (AC000348) T7N9.17 [Arabidopsis thaliana]
NCBI Description
                   222218
Seq. No.
Seq. ID
                   LIB3165-026-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   g1545804
                   33
BLAST score
                   4.0e-09
E value
                   85
Match length
% identity
                   Nicotiana tabacum mRNA for cytochrome P450 like_TBP,
NCBI Description
                   complete cds
                   222219
Seq. No.
                   LIB3165-027-P1-K1-A1
Seq. ID
                   BLASTX
Method
                   g2388578
NCBI GI
BLAST score
                   456
                   1.0e-45
E value
Match length
                   109
                   79
% identity
                   (AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs
NCBI Description
                   gb_T75785,gb_R30580,gb_T04698 come from this gene.
                   [Arabidopsis thaliana]
                   222220
Seq. No.
                   LIB3165-027-P1-K1-A10
Seq. ID
                   BLASTX
Method
                   g2708749
NCBI GI
                   278
BLAST score
                   8.0e-25
E value
Match length
                   85
                   59
 % identity
                   (AC003952) putative senescence-assoc. rhodanese-like
NCBI Description
                   protein [Arabidopsis thaliana]
```

Seq. No. 222221

Seq. ID LIB3165-027-P1-K1-A11

Method BLASTX

Method

NCBI GI BLAST score BLASTX g4406530

315

```
NCBI GI
                  g1172558
BLAST score
                  256
                  2.0e-22
E value
Match length
                  85
% identity
                  60
NCBI Description
                  OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
                  ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >gi 480122 pir S36454 porin porl - garden pea
                  >gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]
                  222222
Seq. No.
Seq. ID
                  LIB3165-027-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                  541
                  1.0e-55
E value
Match length
                  109
                  96
% identity
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  222223
Seq. ID
                  LIB3165-027-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2191191
BLAST score
                  215
E value
                  2.0e-17
Match length
                  100
% identity
                  54
NCBI Description
                  (AF007271) A TM021B04.14 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  222224
Seq. ID
                  LIB3165-027-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4468812
BLAST score
                  426
                  3.0e-42
E value
Match length
                  112
% identity
                  37
NCBI Description
                  (AL035601) putative protein [Arabidopsis thaliana]
                  222225
Seq. No.
                  LIB3165-027-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539324
                  264
BLAST score
                  2.0e-25
E value
Match length
                  124
% identity
                  55
NCBI Description
                 (AL035679) kinesin like protein [Arabidopsis thaliana]
                  222226
Seq. No.
Seq. ID
                  LIB3165-027-P1-K1-A9
```

31440

4.0e-29 E value 87 Match length 75 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] 222227 Seq. No. LIB3165-027-P1-K1-B1 Seq. ID BLASTX Method NCBI GI q2623960 BLAST score 140 E value 7.0e-09 48 Match length 58 % identity NCBI Description (Y12599) histone H1 [Apium graveolens] 222228 Seq. No. Seq. ID LIB3165-027-P1-K1-B2 Method BLASTX NCBI GI q131399 BLAST score 457 9.0e-46 E value 105 Match length 82 % identity NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411 photosystem II 10K protein precursor - potato >gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum tuberosum] 222229 Seq. No. LIB3165-027-P1-K1-B4 Seq. ID Method BLASTN

NCBI GI g3869069
BLAST score 44
E value 1.0e-15
Match length 115
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 222230

Seq. ID LIB3165-027-P1-K1-B6

Method BLASTX
NCBI GI g2499931
BLAST score 233
E value 1.0e-19
Match length 66
% identity 74

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)

>gi_2129534_pir__S71272 adenine phosphoribosyltransferase

(EC 2.4.2.7) - Arabidopsis thaliana

>qi 1321681 emb CAA65609 (X96866) adenine

phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No. 222231

Seq. ID LIB3165-027-P1-K1-B7

Method BLASTX

```
g100200
NCBI GI
                   332
BLAST score
                   4.0e-31
E value
                   95
Match length
                   68
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                   222232
Seq. No.
                   LIB3165-027-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   g3024126
NCBI GI
                   444
BLAST score
                   3.0e-44
E value
                   87
Match length
                   97
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
                   222233
Seq. No.
                   LIB3165-027-P1-K1-C10
Seq. ID
                   BLASTX
Method
                   q1181599
NCBI GI
                   412
BLAST score
                   2.0e-40
E value
                   111
Match length
                   73
% identity
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                   222234
                   LIB3165-027-P1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1361983
BLAST score
                   268
                   4.0e-35
E value
                   111
Match length
                   73
% identity
NCBI Description ARP protein - Arabidopsis thaliana >gi 886434 emb_CAA89858
                   (Z49776) ARP protein [Arabidopsis thaliana]
Seq. No.
                   222235
                   LIB3165-027-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   g132086
NCBI GI
BLAST score
                   159
                   4.0e-11
E value
Match length
                   30
                   97
 % identity
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR
                    (RUBISCO SMALL SUBUNIT 1) >gi_68053_pir__RKSYS
                    ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor SRS1 - soybean >gi_18742_emb_CAA23736_ (V00458)
                    rubpcase [Glycine max]
```

31442

222236

LIB3165-027-P1-K1-C3

Seq. No.

Seq. ID

Method BLASTX
NCBI GI g1352821
BLAST score 391
E value 4.0e-38
Match length 76
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222237

Seq. ID LIB3165-027-P1-K1-C5

Method BLASTX
NCBI GI g710626
BLAST score 261
E value 6.0e-23
Match length 77
% identity 65

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] $>gi_3241941$

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 222238

Seq. ID LIB3165-027-P1-K1-C6

Method BLASTX
NCBI GI g131392
BLAST score 342
E value 2.0e-32
Match length 86
% identity 84

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81479_pir__S00005 photosystem II oxygen-evolving

complex protein 2 precursor - spinach

>gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein
[Spinacia oleracea] >gi_225596_prf__1307179A luminal

protein 23kD [Spinacia oleracea]

Seq. No. 222239

Seq. ID LIB3165-027-P1-K1-C7

Method BLASTX
NCBI GI g1174498
BLAST score 362
E value 1.0e-34
Match length 86
% identity 76

NCBI Description SYNAPTOBREVIN-RELATED PROTEIN >gi 600710 (M90418) formerly

called HAT24; synaptobrevin-related protein [Arabidopsis

thaliana]

Seq. No. 222240

Seq. ID LIB3165-027-P1-K1-D1

Method BLASTX NCBI GI g3913651



```
237
BLAST score
                  4.0e-20
E value
                  69
Match length
                  70
% identity
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
                  (FNR) >gi 2225993 emb CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                  222241
                  LIB3165-027-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2580440
BLAST score
                  271
                  5.0e-24
E value
Match length
                  68
% identity
                  75
NCBI Description (D87261) PCF2 [Oryza sativa]
                  222242
Seq. No.
Seq. ID
                  LIB3165-027-P1-K1-D2
Method
                 BLASTX
NCBI GI
                 g1345698
BLAST score
                  641
                  2.0e-67
E value
                  121
Match length
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                  (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi 452314 emb CAA38025 (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
Seq. No.
                  222243
                  LIB3165-027-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4539422
BLAST score
                  233
                  2.0e-19
E value
Match length
                  88
                  62
% identity
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
                  222244
Seq. No.
                  LIB3165-027-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539543
BLAST score
                  565
                  2.0e-58
E value
Match length
                 118
% identity
NCBI Description (AJ133422) glyceraldehyde-3-phosphate dehydrogenase
                  [Nicotiana tabacum]
Seq. No.
                  222245
                  LIB3165-027-P1-K1-D7
Seq. ID
```

31444

BLASTN

g3510339

Method NCBI GI

Match length

116



```
BLAST score
                  38
                  5.0e-12
E value
Match length
                  128
                  86
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K3K7, complete sequence [Arabidopsis thaliana]
                  222246
Seq. No.
Seq. ID
                  LIB3165-027-P1-K1-D8
                  BLASTX
Method
                  q1694976
NCBI GI
                  384
BLAST score
                  3.0e-37
E value
                  85
Match length
                  81
% identity
NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]
                  >gi 2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                  thaliana]
                  222247
Seq. No.
Seq. ID
                  LIB3165-027-P1-K1-D9
                  BLASTX
Method
                  q289920
NCBI GI
BLAST score
                  608
                  2.0e-63
E value
Match length
                  115
                  97
% identity
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  222248
Seq. No.
                  LIB3165-027-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2970051
BLAST score
                  303
E value
                  9.0e-28
Match length
                  82
% identity
                  68
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  222249
                  LIB3165-027-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  192
E value
                  8.0e-15
                  65
Match length
                  65
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  222250
Seq. ID
                  LIB3165-027-P1-K1-E2
                  BLASTX
Method
NCBI GI
                  q4406530
BLAST score
                  582
E value
                  2.0e-60
```



% identity 96 NCBI Description (AF126870) rubisco activase [Vigna radiata] 222251 Seq. No. LIB3165-027-P1-K1-E3 Seq. ID BLASTX Method q1352821 NCBI GI 453 BLAST score 2.0e-45 E value 87 Match length % identity 98 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 222252 Seq. No. LIB3165-027-P1-K1-E4 Seq. ID BLASTX Method g1168411 NCBI GI BLAST score 454 2.0e-45 E value 113 Match length 82 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR 222253 Seq. No. LIB3165-027-P1-K1-E6 Seq. ID BLASTX Method g441457 NCBI GI 462 BLAST score 2.0e-46 E value 88 Match length 97 % identity NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum] 222254 Seq. No. Seq. ID LIB3165-027-P1-K1-E8 BLASTX Method q1353352 NCBI GI 379 BLAST score 1.0e-36 E value 111 Match length % identity NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii] 222255 Seq. No. LIB3165-027-P1-K1-F1 Seq. ID BLASTX Method g3738324 NCBI GI BLAST score 217 1.0e-17 E value 65 Match length

31446

55

% identity

BLAST score

E value

1.0e-56



```
NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
                  222256
Seq. No.
                  LIB3165-027-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  q2499497
NCBI GI
                  465
BLAST score
                  7.0e-47
E value
                  96
Match length
                  96
% identity
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase
                  [Nicotiana tabacum]
                  222257
Seq. No.
                  LIB3165-027-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  a266893
BLAST score
                   573
                   2.0e-59
E value
                   114
Match length
                   96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                   PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172
                   ribulose-bisphosphate carboxylase activase - cucumber
                   >gi 18284 emb_CAA47906 (X67674) rubisco activase [Cucumis
                   satīvus]
                   222258
Seq. No.
                   LIB3165-027-P1-K1-F12
Seq. ID
                   BLASTN
Method
                   q1669584
NCBI GI
                   43
BLAST score
                   5.0e-15
E value
                   83
Match length
 % identity
                   Cucumis sativus mRNA for cytosolic ascorbate peroxidase,
NCBI Description
                   complete cds
 Seq. No.
                   222259
 Seq. ID
                   LIB3165-027-P1-K1-F3
 Method
                   BLASTX
                   q4206195
 NCBI GI
                   202
 BLAST score
                   7.0e-16
 E value
 Match length
                   39
                   87
 % identity
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
                    [Arabidopsis thaliana]
                   222260
 Seq. No.
                   LIB3165-027-P1-K1-F4
 Seq. ID
                   BLASTX
 Method
                   q289920
 NCBI GI
                    549
```

31447



100 Match length % identity 99 (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 222261 Seq. No. LIB3165-027-P1-K1-F5 Seq. ID Method BLASTX NCBI GI q629733 BLAST score 403 2.0e - 39E value 98 Match length 78 % identity sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato NCBI Description >gi_2130000_pir__S67498 sulfate adenylyltransferase (EC 2.7.7.4) (clone StMet3-2) - potato >gi_479090_emb_CAA55655_ (X79053) sulfate adenylyltransferase [Solanum tuberosum] Seq. No. 222262 LIB3165-027-P1-K1-F6 Seq. ID BLASTX Method NCBI GI g1352821 BLAST score 474 E value 9.0e-48 Match length 91 98 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 222263 Seq. No. LIB3165-027-P1-K1-G1 Seq. ID Method BLASTX NCBI GI q832876 BLAST score 255 E value 4.0e-22 Match length 100 % identity 40 NCBI Description (L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum] Seq. No. 222264 Seq. ID LIB3165-027-P1-K1-G12 Method BLASTX NCBI GI q1352821 BLAST score 485 E value 5.0e-49

Match length 92 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

Seq. ID Method

NCBI GI

222269

BLASTX

g400890

LIB3165-027-P1-K1-G9

```
Seq. No.
                  222265
                  LIB3165-027-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462273
BLAST score
                  181
                  2.0e-13
E value
Match length
                  42
% identity
                  88
                  IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi 437213
NCBI Description
                  (U02689) imidazoleglycerolphosphate dehydratase
                  [Arabidopsis thaliana]
Seq. No.
                  222266
Seq. ID
                  LIB3165-027-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  584
E value
                  1.0e-60
Match length
                  112
                  95
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222267
                  LIB3165-027-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120661
BLAST score
                  570
E value
                  5.0e-59
Match length
                  118
                  93
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi 170237 (M14417) qlyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                  222268
Seq. ID
                  LIB3165-027-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g266893
BLAST score
                  624
E value
                  2.0e-65
Match length
                  121
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__$28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                  sativus]
```

31449



BLAST score 217 E value 1.0e-17 Match length 107 % identity 54 PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR NCBI Description >gi 282837_pir S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea] Seq. No. 222270 Seq. ID LIB3165-027-P1-K1-H1 Method BLASTX NCBI GI q70644 BLAST score 238 4.0e-20 E value Match length 60 % identity 14 NCBI Description ubiquitin precursor - common sunflower (fragment) 222271 Seq. No. LIB3165-027-P1-K1-H4 Seq. ID Method BLASTX NCBI GI q289920 BLAST score 262 E value 4.0e-23 Match length 58 % identity 90 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum] Seq. No. 222272 LIB3165-028-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g2894599 BLAST score 375 E value 3.0e-36 80 Match length % identity NCBI Description (AL021889) putative protein [Arabidopsis thaliana] Seq. No. 222273 Seq. ID LIB3165-028-P1-K1-A10 Method BLASTX NCBI GI q4406530 BLAST score 255 E value 7.0e-23

83 Match length % identity 66

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 222274

LIB3165-028-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI g121902 BLAST score 163



```
3.0e-11
E value
Match length
                   36
% identity
                   89
                   HISTONE H1.1 >gi 1070594 pir HSMU11 histone H1.1 -
NCBI Description
                   Arabidopsis thaliana >gi_16317_emb_CAA44314_ (X62458)
                   Histone H1 [Arabidopsis thaliana]
                   222275
Seq. No.
                   LIB3165-028-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   q4234955
NCBI GI
                   175
BLAST score
                   1.0e-12
E value
                   92
Match length
                   23
% identity
NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
Seq. No.
                   222276
Seq. ID
                   LIB3165-028-P1-K1-A3
Method
                   BLASTX
                   q2880043
NCBI GI
                   376
BLAST score
                   2.0e-36
E value
Match length
                   101
                   73
% identity
NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
                   hydrolase [Arabidopsis thaliana]
Seq. No.
                   222277
                   LIB3165-028-P1-K1-A7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346155
                   286
BLAST score
                   6.0e-26
E value
                   66
Match length
                   83
% identity
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481942_pir__S40212 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                   >gi_437995_emb_CAA81078_ (Z25859) glycine
hydroxymethyltransferase [Flaveria pringlei]
                   222278
Seq. No.
Seq. ID
                   LIB3165-028-P1-K1-A8
```

Method BLASTX
NCBI GI g549063
BLAST score 375
E value 3.0e-36
Match length 91
% identity 79

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi 1072464 pir A38958 IgE-dependent histamine-releasing

factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 222279



LIB3165-028-P1-K1-B1 Seq. ID

Method BLASTX g2129511 NCBI GI 367 BLAST score 2.0e-40 E value 98 Match length 82 % identity

glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, NCBI Description

microbody - cucurbit >gi 1304042 dbj BAA08410 (D49432)

hydroxypyruvate reductase [Cucurbita sp.]

222280 Seq. No.

Seq. ID LIB3165-028-P1-K1-B10

Method BLASTX NCBI GI q115765 BLAST score 498 2.0e-50 E value Match length 110 % identity 48

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 222281

LIB3165-028-P1-K1-B12 Seq. ID

BLASTX Method NCBI GI g1778095 233 BLAST score 2.0e-19 E value Match length 113 44 % identity

NCBI Description (U64903) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 222282

Seq. ID LIB3165-028-P1-K1-B3

Method BLASTX NCBI GI g131385 BLAST score 518 E value 6.0e-53 Match length 126 % identity 84

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 222283

Seq. ID LIB3165-028-P1-K1-B4

Method BLASTX NCBI GI g1352821 BLAST score 535

BLAST score

E value

246

6.0e-21



E value 7.0e-55 Match length 102 98 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505_emb_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 222284 Seq. No. LIB3165-028-P1-K1-B5 Seq. ID BLASTX Method q3063451 NCBI GI 304 BLAST score 9.0e-28 E value 94 Match length 59 % identity NCBI Description (AC003981) F22013.13 [Arabidopsis thaliana] Seq. No. 222285 Seq. ID LIB3165-028-P1-K1-B8 BLASTX Method NCBI GI q130283 BLAST score . 365 6.0e-35 E value 78 Match length 87 % identity NCBI Description PLASTOCYANIN >gi 65839 pir CUUA plastocyanin - Chilean potato-tree >gi 223147 prf 0512261A plastocyanin [Solanum crispum] 222286 Seq. No. LIB3165-028-P1-K1-B9 Seq. ID Method BLASTX g1181599 NCBI GI 454 BLAST score E value 2.0e-45 Match length 119 75 % identity NCBI Description (D83007) subunit of photosystem I [Cucumis sativus] Seq. No. 222287 Seq. ID LIB3165-028-P1-K1-C1 Method BLASTX NCBI GI g2598589 BLAST score 281 E value 4.0e-25 91 Match length 57 % identity NCBI Description (Y15367) MtN19 [Medicago truncatula] 222288 Seq. No. Seq. ID LIB3165-028-P1-K1-C10 Method BLASTX NCBI GI q400890



```
Match length
                     112
% identity
                     PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                     >gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_(X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
                     photosystem II 22 kda polypeptide [spinach, Peptide, 274
                     aa] [Spinacia oleracea]
                     222289
Seq. No.
Seq. ID
                     LIB3165-028-P1-K1-C3
                     BLASTX
Method
NCBI GI
                     q2494415
                     323
BLAST score
E value
                     5.0e-30
                     101
Match length
                     73
% identity
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                     (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                     >qi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine
                     maxl
Seq. No.
                     222290
Seq. ID
                     LIB3165-028-P1-K1-C4
Method
                     BLASTX
                     g3928543
NCBI GI
BLAST score
                     220
                     6.0e-18
E value
Match length
                     127
% identity
                     35
                    (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                     thaliana]
                     222291
Seq. No.
                     LIB3165-028-P1-K1-C5
Seq. ID
Method
                     BLASTX
                     g115471
NCBI GI
                     526
BLAST score
                     8.0e-54
E value
Match length
                     127
                     76
% identity
NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                     DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792
                      (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
Seq. No.
                     222292
                     LIB3165-028-P1-K1-C7
Seq. ID
Method
                     BLASTX
NCBI GI
                     q121953
BLAST score
                     167
```

E value 6.0e-12
Match length 38
% identity 87

NCBI Description HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >qi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263)

[Pisum sativum]

```
222293
Seq. No.
                  LIB3165-028-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914605
                  361
BLAST score
                  2.0e-34
E value
                  122
Match length
                  60
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857_ (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Malus domestica]
                  222294
Seq. No.
                  LIB3165-028-P1-K1-D10
Seq. ID
Method
                  BLASTX
                  q4097547
NCBI GI
                  172
BLAST score
E value
                   3.0e-12
Match length
                   34
                   44
% identity
                  (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
                   222295
Seq. No.
                   LIB3165-028-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g3482925
NCBI GI
BLAST score
                   238
E value
                   5.0e-20
                   77
Match length
                   62
% identity
                  (AC003970) Highly similar to cinnamyl alcohol
NCBI Description
                   dehydrogenase, gi_1143445 [Arabidopsis thaliana]
                   222296
Seq. No.
                   LIB3165-028-P1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662343
                   420
BLAST score
                   2.0e-41
E value
                   82
Match length
 % identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   222297
Seq. No.
                   LIB3165-028-P1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g100616
                   387
 BLAST score
                   1.0e-37
 E value
 Match length
                   113
 % identity
                   66
 NCBI Description ribulose-bisphosphate carboxylase activase B precursor -
                   barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
```



carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
ribulose 1,5-bisphosphate carboxylase activase [Hordeum
vulgare]

222298 Seq. No. LIB3165-028-P1-K1-D6 Seq. ID BLASTX Method g4455787 NCBI GI 296 BLAST score 8.0e-27 E value Match length 120 % identity 42 (AL035536) putative DNA polymerase accessory protein NCBI Description [Schizosaccharomyces pombe] 222299 Seq. No. LIB3165-028-P1-K1-D9 Seq. ID BLASTN Method g2687434 NCBI GI 327 BLAST score E value 0.0e + 00Match length 395 % identity 96 Eucryphia lucida large subunit 26S ribosomal RNA gene, NCBI Description partial sequence 222300 Seq. No. LIB3165-028-P1-K1-E10 Seq. ID BLASTX Method g228403 NCBI GI BLAST score 475 7.0e-48 E value 104 Match length 88 % identity NCBI Description glycolate oxidase [Lens culinaris] 222301 Seq. No.

Seq. ID LIB3165-028-P1-K1-E11

Method BLASTX
NCBI GI g2493689
BLAST score 340
E value 5.0e-32
Match length 73
% identity 90

NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN

>gi_1070377_emb_CAA63670_ (X93203) 10 kDa phosphoprotein
[Populus deltoides] >gi_2143326_emb_CAA73768_ (Y13328)

10kDa phosphoprotein [Populus deltoides]

Seq. No. 222302

Seq. ID LIB3165-028-P1-K1-E4

Method BLASTX
NCBI GI 9441457
BLAST score 577
E value 8.0e-60
Match length 110
% identity 97



```
(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  222303
Seq. No.
                  LIB3165-028-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
                  353
BLAST score
                  1.0e-33
E value
                  94
Match length
                  77
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  222304
Seq. No.
                  LIB3165-028-P1-K1-E8
Seq. ID
                  {\tt BLASTX}
Method
                  g131397
NCBI GI
                  224
BLAST score
                  2.0e-18
E value
                  111
Match length
                  50
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 81480_pir__S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi 225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
                   222305
Seq. No.
                  LIB3165-028-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  q2244965
NCBI GI
BLAST score
                   262
                   7.0e-23
E value
                   86
Match length
                   60
% identity
NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]
                   222306
Seq. No.
Seq. ID
                   LIB3165-028-P1-K1-F11
                   BLASTX
Method
                   q3763916
NCBI GI
BLAST score
                   356
E value
                   7.0e - 34
                   127
Match length
                   50
```

% identity

(AC004450) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown

protein [Arabidopsis thaliana]

Seq. No. 222307

LIB3165-028-P1-K1-F12 Seq. ID

Method BLASTX NCBI GI q3702327 195 BLAST score

```
4.0e-15
E value
Match length
                  57
% identity
                  63
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  222308
Seq. No.
                  LIB3165-028-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  a2244906
BLAST score
                  294
                  1.0e-26
E value
                  108
Match length
                  57
% identity
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  222309
Seq. No.
                  LIB3165-028-P1-K1-F5
Seq. ID
Method
                  BLASTX
                  g399082
NCBI GI
BLAST score
                  140
                  1.0e-08
E value
                  89
Match length
                  38
% identity
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 322713 pir S28171 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain, chloroplast - garden pea >gi 169045
                  (M94558) ATP synthase delta subunit [Pisum sativum]
Seq. No.
                  222310
                  LIB3165-028-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172494
BLAST score
                  142
E value
                  9.0e-09
Match length
                  113
                  30
% identity
NCBI Description PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE (PHS)
                  (4-ALPHA-HYDROXY-TETRAHYDROPTERIN DEHYDRATASE)
                   (PHENYLALANINE HYDROXYLASE-STIMULATING PROTEIN) (PCD)
                  >qi 476742 (M88627) phenylalanine hydroxylase [Pseudomonas
                  aeruginosa]
Seq. No.
                  222311
Seq. ID
                  LIB3165-028-P1-K1-F8
Method
                  BLASTX
                  g1694976
NCBI GI
BLAST score
                  370
                  2.0e-35
E value
Match length
                  103
                  68
% identity
                  (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                  thaliana]
```

31458

222312

LIB3165-028-P1-K1-F9

Seq. No.

Seq. ID



```
Method
                   BLASTX
                   q4544399
 NCBI GI
 BLAST score
                   457
                   1.0e-45
 E value
 Match length
                   107
                   77
 % identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
 NCBI Description
                   thaliana]
                   222313
 Seq. No.
                   LIB3165-028-P1-K1-G1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3885328
 BLAST score
                   578
                   7.0e-60
 E value
                   130
 Match length
                    76
 % identity
                    (AC005623) putative serine/threonine protein kinase
 NCBI Description
                    [Arabidopsis thaliana]
                    222314
 Seq. No.
                    LIB3165-028-P1-K1-G10
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1352821
                    531
BLAST score
                    2.0e-54
 E value
                    100
 Match length
                    100
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor - upland cotton >gi 450505 emb_CAA38026_ (X54091)
                    ribulose bisphosphate carboxylase [Gossypium hirsutum]
                    222315
 Seq. No.
                    LIB3165-028-P1-K1-G11
 Seq. ID
                    BLASTX
 Method
                    g1168411
 NCBI GI
 BLAST score
                    327
                    2.0e-30
 E value
                    87
 Match length
                    79
 % identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
 NCBI Description
                    222316
 Seq. No.
                    LIB3165-028-P1-K1-G12
 Seq. ID
                    BLASTX
 Method
                    g131773
 NCBI GI
                    363
 BLAST score
                    1.0e-34
 E value
                    114
 Match length
                    71
  % identity
                    40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
 NCBI Description
                    >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
```

Seq. No. 222317

maize

Seq. ID

NCBI GI

BLAST score

Method

```
LIB3165-028-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1871577
                  237
BLAST score
                  6.0e-20
E value
                  87
Match length
                  54
% identity
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  222318
Seq. No.
                  LIB3165-028-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  g3850778
NCBI GI
                  414
BLAST score
                  1.0e-40
E value
                  99
Match length
                  79
% identity
NCBI Description (Y18346) gluaredoxin [Lycopersicon esculentum]
                   222319
Seq. No.
                  LIB3165-028-P1-K1-G5
Seq. ID
                  BLASTX
Method
                   g3236240
NCBI GI
                   227
BLAST score
                   2.0e-32
E value
                   86
Match length
                   76
% identity
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                   222320
Seq. No.
                   LIB3165-028-P1-K1-G7
Seq. ID
                   BLASTX
Method
                   q128188
NCBI GI
                   298
BLAST score
E value
                   5.0e-27
                   115
Match length
                   59
% identity
NCBI Description NITRATE REDUCTASE 2 (NR2) >gi_66202_pir__RDMUNH nitrate
                   reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis thaliana
                   >qi 166782 (J03240) nitrate reductase (EC 1.6.6.1)
                   [Arabidopsis thaliana]
                   222321
Seq. No.
                   LIB3165-028-P1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q508304
                   352
BLAST score
                   2.0e-33
E value
                   79
Match length
                   80
% identity
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                   222322
```

31460

LIB3165-028-P1-K1-G9

BLASTX

242

q1354515



```
1.0e-20
E value
Match length
                  120
                  53
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  222323
Seq. No.
Seq. ID
                  LIB3165-028-P1-K1-H1
Method
                  BLASTX
                  g115506
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
                  79
Match length
                  20
% identity
                  CALMODUEIN >gi 71688 pir MCKM calmodulin - Chlamydomonas
NCBI Description
                  reinhardtii >gi 167411 (M20729) calmodulin [Chlamydomonas
                  reinhardtii]
                  222324
Seq. No.
                  LIB3165-028-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  q266944
NCBI GI
                  488
BLAST score
                  3.0e-49
E value
                  97
Match length
                  93
% identity
                  60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
NCBI Description
                  >gi 71078 pir R5TOL8 ribosomal protein L8, cytosolic -
                   tomato >gi 19343 emb CAA45863 (X64562) ribosomal protein
                  L2 [Lycopersicon esculentum]
                  222325
Seq. No.
Seq. ID
                  LIB3165-028-P1-K1-H12
                   BLASTX
Method
NCBI GI
                   g2104949
                   361
BLAST score
                   2.0e-34
E value
                   102
Match length
                   70
% identity
                  (U96716) MAP kinase-like protein [Selaginella lepidophylla]
NCBI Description
                   222326
Seq. No.
Seq. ID
                   LIB3165-028-P1-K1-H3
                   BLASTX
Method
                   q4335773
NCBI GI
BLAST score
                   283
                   2.0e-25
E value
Match length
                   119
                   61
% identity
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                   222327
Seq. No.
                   LIB3165-028-P1-K1-H4
Seq. ID
Method
                   BLASTX
```

q487046

3.0e - 34

359

NCBI GI

E value

BLAST score



Match length 126 % identity 60

NCBI Description photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor

[Nicotiana sylvestris]

Seq. No. 222328

Seq. ID LIB3165-028-P1-K1-H7

Method BLASTX
NCBI GI g4519539
BLAST score 320
E value 1.0e-29
Match length 88
% identity 74

NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus

domestica]

Seq. No. 222329

Seq. ID LIB3165-028-P1-K1-H8

Method BLASTX
NCBI GI g399307
BLAST score 427
E value 3.0e-42
Match length 130
% identity 63

NCBI Description PRENYL TRANSFERASE >gi 99282 pir A40433 prephytoene

pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi 336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi 1016130 (U30821)

prenyl transferase [Cyanophora paradoxa]

Seq. No. 222330

Seq. ID LIB3165-028-P1-K1-H9

Method BLASTX
NCBI GI 94406530
BLAST score 293
E value 2.0e-26
Match length 104
% identity 62

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 222331

Seq. ID LIB3165-030-P1-K1-A11

Method BLASTX
NCBI GI g400890
BLAST score 199
E value 1.0e-15
Match length 104
% identity 53

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 222332

```
LIB3165-030-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  q402753
NCBI GI
BLAST score
                  553
                  5.0e-57
E value
                  119
Match length
                  93
% identity
                 (X71439) translation elongation factor EF-G [Glycine max]
NCBI Description
                  222333
Seq. No.
Seq. ID
                  LIB3165-030-P1-K1-A8
                  BLASTX
Method
                  q2738248
NCBI GI
                  237
BLAST score
                  5.0e-20
E value
                  92
Match length
                  76
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   222334
Seq. No.
                  LIB3165-030-P1-K1-B4
Seq. ID
                  BLASTX
Method
                   q402753
NCBI GI
                   307
BLAST score
                   2.0e-28
E value
                   98
Match length
% identity
                  (X71439) translation elongation factor EF-G [Glycine max]
NCBI Description
                   222335
Seq. No.
                   LIB3165-030-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   g3687237
NCBI GI
BLAST score
                   351
                   2.0e-33
E value
                   117
Match length
                   62
% identity
                  (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   222336
Seq. No.
                   LIB3165-030-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g115472
NCBI GI
                   350
 BLAST score
                   3.0e-33
 E value
                   86
Match length
                   77
 % identity
 NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                   DEHYDRATASE) >gi_99567_pir__A35163 carbonate dehydratase
                   (EC 4.2.1.1) precursor - spinach chloroplast >gi_170105
                   (J05403) carbonic anhydrase (EC 4.2.1.1) [Spinacia-
                   oleracea]
```

31463

222337

LIB3165-030-P1-K1-C5

Seq. No.

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g3776536
BLAST score
                  108
E value
                  5.0e-12
Match length
                  110
% identity
                  (AF095794) polyubiquitin [Schizosaccharomyces pombe]
NCBI Description
                  222338
Seq. No.
Seq. ID
                  LIB3165-030-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  345
                  1.0e-32
E value
                  106
Match length
% identity
                  65
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  222339
Seq. No.
                  LIB3165-030-P1-K1-D11
Seq. ID
Method
                  BLASTX
                  q20729
NCBI GI
BLAST score
                  242
                  1.0e-20
E value
                  90
Match length
                  62
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  222340
Seq. ID
                  LIB3165-030-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  374
E value
                  5.0e-36
Match length
                  95
                  77
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  222341
Seq. ID
                  LIB3165-030-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3193303
BLAST score
                  342
E value
                  2.0e-32
                  90
Match length
                  70
% identity
NCBI Description
                  (AF069298) similar to several proteins containing a tandem
                  repeat region such as Plasmodium falciparum GGM tandem
                  repeat protein (GB:U27807); partial CDS [Arabidopsis
                  thaliana]
                  222342
Seq. No.
```

Seq. ID LIB3165-030-P1-K1-E1

Method BLASTX NCBI GI g1352821 BLAST score 290

E value

Match length

% identity

111

53



```
E value
                   1.0e-26
Match length
                   61
                   97
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(EC \ 4.1.1.39)} small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222343
Seq. No.
Seq. ID
                   LIB3165-030-P1-K1-E10
                   BLASTX
Method
NCBI GI
                   g1200116
                   161
BLAST score
                   1.0e-11
E value
                   39
Match length
% identity
                   85
                   (X95752) c subunit of V-type ATPase [Nicotiana tabacum]
NCBI Description
                   222344
Seq. No.
                   LIB3165-030-P1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3882081
BLAST score
                   558
                   1.0e-57
E value
Match length
                   117
                   37
% identity
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
                   222345
Seq. No.
                   LIB3165-030-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g3158474
NCBI GI
BLAST score
                   457
                   8.0e-46
E value
                   109
Match length
                   83
% identity
NCBI Description
                   (AF067184) aquaporin 1 [Samanea saman]
                   222346
Seq. No.
                   LIB3165-030-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g3063392
NCBI GI
                   325
BLAST score
                   3.0e-30
E value
                   93
Match length
                   73
% identity
NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]
                   222347
Seq. No.
                   LIB3165-030-P1-K1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   a3687237
                   296
BLAST score
                   7.0e-27
```

```
(AC005169) putative Cys3His zinc-finger protein
NCBI Description
                  [Arabidopsis thaliana]
                  222348
Seq. No.
                  LIB3165-030-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  g3378650
NCBI GI
                  465
BLAST score
                  1.0e-46
E value
                  121
Match length
                  70
% identity
                 (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
                  222349
Seq. No.
Seq. ID
                  LIB3165-030-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  q4406530
BLAST score
                  240
                  2.0e-20
E value
Match length
                  91
                  62
% identity
                 (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  222350
Seq. No.
                  LIB3165-030-P1-K1-G1
Seq. ID
                  BLASTX
Method
                  g544437
NCBI GI
BLAST score
                  324
                  3.0e-30
E value
Match length
                  74
% identity
                  86
                  GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
NCBI Description
                  >gi 296358 emb_CAA47018 (X66377) CIT-SAP [Citrus sinensis]
Seq. No.
                   222351
                  LIB3165-030-P1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                  g3913651
BLAST score
                   424
E value
                  7.0e-42
Match length
                  109
% identity
                  73
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                   ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                   222352
                  LIB3165-030-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406530
                   300
BLAST score
                   2.0e-27
E value
                  83
Match length
                   75
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
```

31466

222353

Seq. No.

LIB3165-030-P1-K1-G9 Seg. ID BLASTX Method NCBI GI g3327394 BLAST score 163 3.0e-11 E value 50 Match length 56 % identity (AC004483) putative RNA helicase [Arabidopsis thaliana] NCBI Description 222354 Seq. No. Seq. ID LIB3165-030-P1-K1-H1 BLASTX Method g100616 NCBI GI BLAST score 261 8.0e-23 E value 58 Match length 86 % identity ribulose-bisphosphate carboxylase activase B precursor -NCBI Description barley >gi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] 222355 Seq. No. Seq. ID LIB3165-030-P1-K1-H10 BLASTX Method g2506443 NCBI GI 447 BLAST score 1.0e-44E value 107 Match length 83 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description CHLOROPLAST >gi 2117520 pir JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi 1402885 emb CAA66816 (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana] Seq. No. 222356 Seq. ID LIB3165-030-P1-K1-H12 BLASTX Method q231688 NCBI GI BLAST score 468 4.0e-47 E value 114 Match length 80 % identity

CATALASE ISOZYME 2 >gi_99599_pir_ S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton >gi 18488_emb_CAA39998_ (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

222357 Seq. No.

LIB3165-030-P1-K1-H2 Seq. ID

Method BLASTX NCBI GI g1130684

BLAST score

158

```
BLAST score
                  356
                  6.0e - 34
E value
                  85
Match length
                  84
% identity
NCBI Description (Z46960) acetohydroxyacid synthase [Gossypium hirsutum]
                  222358
Seq. No.
                  LIB3165-030-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g1130684
NCBI GI
                  154
BLAST score
                  2.0e-10
E value
                  63
Match length
                  56
% identity
NCBI Description (Z46960) acetohydroxyacid synthase [Gossypium hirsutum]
                  222359
Seq. No.
                  LIB3165-031-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g128194
NCBI GI
BLAST score
                  573
                  2.0e-59
E value
                  119
Match length
                  87
% identity
                  NITRATE REDUCTASE (NR) >gi 81572 pir A41667 nitrate
NCBI Description
                  reductase (NADH) (EC 1.6.6.1) - winter squash >gi 167499
                   (M33154) nitrate reductase [Cucurbita maxima]
                  222360
Seq. No.
Seq. ID
                  LIB3165-031-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  q1352821
                  682
BLAST score
                   4.0e-72
E value
                  127
Match length
                   97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   222361
Seq. ID
                   LIB3165-031-P1-K1-A11
                   BLASTX
Method
                   q3808101
NCBI GI
                   358
BLAST score
                   4.0e - 34
E value
                   110
Match length
% identity
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
                   222362
Seq. No.
                   LIB3165-031-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3746060
```

```
E value
                  1.0e-10
Match length
                  37
                  84
% identity
                  (AC005311) unknown protein [Arabidopsis thaliana]
NCBI Description
                  222363
Seq. No.
                  LIB3165-031-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707019
                  202
BLAST score
                  6.0e-16
E value
                  68
Match length
% identity
                  53
                  (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  222364
Seq. No.
Seq. ID
                  LIB3165-031-P1-K1-A5
                  BLASTX
Method
NCBI GI
                  q131397
                  258
BLAST score
                  2.0e-22
E value
                  116
Match length
                  52
% identity
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi 81480 pir S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi 755802 emb CAA29056 (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi 225597 prf 1307179B luminal protein 16kD
                   [Spinacia oleracea]
Seq. No.
                   222365
Seq. ID
                  LIB3165-031-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g68200
BLAST score
                   488
                   2.0e-49
E value
Match length
                  119
% identity
                   84
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   222366
Seq. No.
                   LIB3165-031-P1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g20729
BLAST score
                   355
                   8.0e-34
E value
                   102
Match length
                   72
% identity
```

Seq. No. 222367

NCBI Description

Seq. ID LIB3165-031-P1-K1-B12

Method BLASTX

(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.

Seq. ID

222372

LIB3165-031-P1-K1-C1

```
g2465008
NCBI GI
                  285
BLAST score
                  1.0e-25
E value
                  123
Match length
                  46
% identity
                  (AJ001445) ripening-induced protein [Fragaria vesca]
NCBI Description
                  222368
Seq. No.
Seq. ID
                  LIB3165-031-P1-K1-B3
                  BLASTX
Method
                  g625547
NCBI GI
BLAST score
                  444
                  3.0e-44
E value
                  119
Match length
                  71
% identity
                  chlorophyll a/b-binding protein type I - common tobacco
NCBI Description
                  >gi 493723 emb CAA45523 (X64198) photosystem I
                  light-harvesting chlorophyll a/b-binding protein [Nicotiana
                  tabacum]
                  222369
Seq. No.
                  LIB3165-031-P1-K1-B4
Seq. ID
                  BLASTX
Method
                  q4406530
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
                  103
Match length
                  62
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
Seq. No.
                  222370
                  LIB3165-031-P1-K1-B8
Seq. ID
                  BLASTX
Method
                  g3023752
NCBI GI
BLAST score
                  232
                  2.0e-19
E value
                   92
Match length
                   55
% identity
                  FERREDOXIN I PRECURSOR >qi 1418982 emb CAA99756 (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
                   222371
Seq. No.
Seq. ID
                  LIB3165-031-P1-K1-B9
Method
                   BLASTX
                   q1345698
NCBI GI
BLAST score
                   369
                   2.0e-35
E value
                   77
Match length
                   91
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
NCBI Description
                   (CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll
                   a/b-binding protein - upland cotton
                   >gi 452314 emb CAA38025_ (X54090) chlorophyll ab binding
                   protein [Gossypium hirsutum]
```

Method

BLASTX



```
Method
                  BLASTX
NCBI GI
                  g2342727
BLAST score
                  393
                  3.0e-38
E value
Match length
                  83
                  77
% identity
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  222373
Seq. No.
                  LIB3165-031-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  q4539292
NCBI GI
BLAST score
                   452
                   4.0e-45
E value
                   100
Match length
                   83
% identity
                   (ALO49480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   222374
Seq. No.
Seq. ID
                   LIB3165-031-P1-K1-C12
                   BLASTX
Method
                   q3643090
NCBI GI
BLAST score
                   164
                   2.0e-11
E value
                   93
Match length
                   46
% identity
                   (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                   crystallinum]
                   222375
Seq. No.
                   LIB3165-031-P1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1352821
BLAST score
                   525
                   1.0e-53
E value
                   101
Match length
                   97
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222376
Seq. No.
                   LIB3165-031-P1-K1-C4
Seq. ID
                   BLASTN
Method
                   g2924257
NCBI GI
BLAST score
                   70
                   5.0e-31
E value
Match length
                   182
                   94
% identity
NCBI Description Tobacco chloroplast genome DNA
                   222377
Seq. No.
                   LIB3165-031-P1-K1-C6
Seq. ID
```

```
q3334665
NCBI GI
                   256
BLAST score
                   4.0e-22
E value
                   108
Match length
                   45
% identity
                  (Y10492) putative cytochrome P450 [Glycine max]
NCBI Description
                   222378
Seq. No.
                   LIB3165-031-P1-K1-C8
Seq. ID
                   BLASTN
Method
                   q2623914
NCBI GI
                   322
BLAST score
                   0.0e+00
E value
                   365
Match length
                   96
% identity
                   Gossypium darwinii ATPase B subunit (atpB) and ribulose
NCBI Description
                   1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL)
                   genes, chloroplast genes encoding chloroplast proteins,
                   partial cds, and atpB-rbcL intergenic spacer
                   222379
Seq. No.
                   LIB3165-031-P1-K1-D10
Seq. ID
                   BLASTX
Method
                  `g3095075
NCBI GI
BLAST score
                   177
                   6.0e-13
E value
                   97
Match length
                   23
% identity
                   (AF031471) pollen allergen [Juniperus oxycedrus]
NCBI Description
                   222380
Seq. No.
Seq. ID
                   LIB3165-031-P1-K1-D11
                   BLASTX
Method
                   q115765
NCBI GI
BLAST score
                   404
                   2.0e-39
E value
                   94
Match length
                   78
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
NCBI Description
                   (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
                    (X14036) chlorophyll a/b-binding protein [Lycopersicon
                    esculentum] >gi_170431 (M20241) chlorophyll a/b-binding
                    protein [Lycopersicon esculentum] >gi_226546_prf__1601518A
                    chlorophyll a/b binding protein II [Lycopersicon
                    esculentum]
                    222381
Seq. No.
                    LIB3165-031-P1-K1-D12
Seq. ID
Method
                    BLASTX
                    g1354515
NCBI GI
```

207 BLAST score 2.0e-16 E value 84 Match length

56 % identity

(U55837) carbonic anhydrase [Populus tremula x Populus NCBI Description tremuloides]

```
222382
Seq. No.
Seq. ID
                  LIB3165-031-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  297
                  5.0e-27
E value
Match length
                  89
% identity
                  69
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  222383
                  LIB3165-031-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  616
                  2.0e-64
E value
Match length
                  118
% identity
                  97
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  222384
Seq. ID
                  LIB3165-031-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g228403
BLAST score
                  456
                  1.0e-45
E value
Match length
                  97
                  91
% identity
NCBI Description glycolate oxidase [Lens culinaris]
Seq. No.
                  222385
Seq. ID
                  LIB3165-031-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q3687676
BLAST score
                  560
E value
                  8.0e-58
Match length
                  111
% identity
                  95
NCBI Description (AF052424) rubisco activase precursor [Datisca glomerata]
Seq. No.
                  222386
Seq. ID
                  LIB3165-031-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  468
                  5.0e-47
E value
Match length
                  91
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

No. 222387

Seq. No.

```
Seq. ID
                  LIB3165-031-P1-K1-D8
                  BLASTN
Method
NCBI GI
                  q4096078
BLAST score
                  38
                  6.0e-12
E value
                  62
Match length
                  90
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  222388
Seq. No.
Seq. ID
                  LIB3165-031-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  585
                  9.0e-61
E value
Match length
                  110
                   98
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   222389
Seq. No.
                  LIB3165-031-P1-K1-E10
Seq. ID
Method
                  BLASTX
                   q100200
NCBI GI
BLAST score
                   415
                   8.0e-41
E value
                   111
Match length
                   73
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                   222390
Seq. No.
                   LIB3165-031-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1730512
BLAST score
                   592
E value
                   1.0e-61
Match length
                   125
% identity
                   97
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST
NCBI Description
                   >gi_2129669_pir__S71368 phosphoglycerate kinase -
                   Arabidopsis thaliana (fragment) >gi_1022805 (U37701)
                   phosphoglycerate kinase [Arabidopsis thaliana]
                   222391
Seq. No.
Seq. ID
                   LIB3165-031-P1-K1-E12
Method
                   BLASTX
                   q4406530
NCBI GI
                   335
BLAST score
E value
                   2.0e-31
                   90
Match length
                   77
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   222392
Seq. No.
Seq. ID
                   LIB3165-031-P1-K1-E2
                   BLASTX
Method
```

```
NCBI GI
                  g1213450
                  230
BLAST score
                   4.0e-19
E value
                  82
Match length
                   55
% identity
                  (U48963) isopentenyl pyrophosphate isomerase [Clarkia
NCBI Description
                  breweri]
                   222393
Seq. No.
                   LIB3165-031-P1-K1-E3
Seq. ID
                   BLASTX
Method
                   g2970654
NCBI GI
                   255
BLAST score
                   5.0e-22
E value
Match length
                   99
                   63
% identity
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                   unguiculata]
                   222394
Seq. No.
                   LIB3165-031-P1-K1-E4
Seq. ID
                   BLASTN
Method
                   g2687437
NCBI GI
                   60
BLAST score
                   6.0e-26
E value
                   72
Match length
                   96
% identity
                   Jepsonia parryi large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   222395
Seq. No.
                   LIB3165-031-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2924325
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
                   41
Match length
                   88
% identity
NCBI Description (Z93765) hypothetical protein [Malus domestica]
                   222396
Seq. No.
                   LIB3165-031-P1-K1-E6
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
                   330
BLAST score
                   9.0e-31
E value
                   88
Match length
```

78 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

222397 Seq. No.

LIB3165-031-P1-K1-E8 Seq. ID

BLASTX Method

E value

Match length

% identity

```
q4406530
NCBI GI
                  307
BLAST score
                  4.0e-28
E value
Match length
                  84
                  75
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  222398
Seq. No.
                  LIB3165-031-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049353
BLAST score
                  369
E value
                  2.0e-35
Match length
                  109
                  69
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                  222399
Seq. No.
                  LIB3165-031-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  g3687652
NCBI GI
BLAST score
                   611
                  8.0e-64
E value
                  117
Match length
                   98
% identity
                  (AF047352) rubisco activase precursor [Datisca glomerata]
NCBI Description
                  222400
Seq. No.
                  LIB3165-031-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g505482
                   397
BLAST score
                   8.0e-39
E value
                  106
Match length
                   80
% identity
NCBI Description
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
                   photosystem II [Nicotiana tabacum]
Seq. No.
                   222401
Seq. ID
                  LIB3165-031-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   8.0e-11
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   222402
                   LIB3165-031-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2754849
BLAST score
                   574
```

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

2.0e-59 122

BLAST score

Match length

% identity

E value

560

117

97

8.0e-58



[Fritillaria agrestis]

```
Seq. No.
                   222403
Seq. ID
                   LIB3165-031-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g2687434
BLAST score
                   306
E value
                   1.0e-172
Match length
                   378
% identity
                   96
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                   partial sequence
                   222404
Seq. No.
Seq. ID
                   LIB3165-031-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3925703
BLAST score
                   538
E value
                   3.0e-55
Match length
                   122
                   87
% identity
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                   222405
Seq. ID
                   LIB3165-031-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q1352821
BLAST score
                   502
E value
                   5.0e-51
Match length
                   95
% identity
                   100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222406
Seq. No.
Seq. ID
                   LIB3165-031-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g289920
                   584
BLAST score
E value
                   3.0e-61
Match length
                   116
% identity
                   99
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
Seq. No.
                   222407
Seq. ID
                   LIB3165-031-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g289920
```

31477

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

```
hirsutum]
                    222408
 Seq. No.
 Seq. ID
                    LIB3165-031-P1-K1-G3
 Method
                    BLASTX
 NCBI GI
                    q167367
 BLAST score
                    455
 E value
                    2.0e-45
 Match length
                    120
                    74
 % identity
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]
 Seq. No.
                    222409
 Seq. ID
                    LIB3165-031-P1-K1-G7
 Method
                    BLASTX
 NCBI GI
                    g1710780
 BLAST score
                    359
 E value
                    3.0e - 34
 Match length
                    101
 % identity
                    69
                    40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_
 NCBI Description
                     (X96613) cytoplasmic ribosomal protein S7 [Podospora
                    anserina]
 Seq. No.
                    222410
 Seq. ID
                    LIB3165-031-P1-K1-G8
 Method
                    BLASTX
 NCBI GI
                    q4406530
BLAST score
                    349
- E value
                    4.0e-33
Match length
                    93
 % identity
                    76
 NCBI Description (AF126870) rubisco activase [Vigna radiata]
 Seq. No.
                    222411
 Seq. ID
                    LIB3165-031-P1-K1-H10
 Method
                    BLASTX
NCBI GI
                    g231688
 BLAST score
                    453
 E value
                    2.0e-45
 Match length
                    102
                    85
 % identity
                    CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC
 NCBI Description
                    1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]
 Seq. No.
                    222412
 Seq. ID
                    LIB3165-031-P1-K1-H12
```

Method BLASTX
NCBI GI g2129511
BLAST score 142
E value 1.0e-13
Match length 49
% identity 71

NCBI Description glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, microbody - cucurbit >gi 1304042 dbj BAA08410 (D49432)

hydroxypyruvate reductase [Cucurbita sp.]

Seq. No. 222413 LIB3165-031-P1-K1-H2 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 522 3.0e-53E value 101

97

% identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222414

Match length

LIB3165-031-P1-K1-H3 Seq. ID

Method BLASTX NCBI GI g1620898 BLAST score 223 3.0e-18 E value

Match length 60 73 % identity

NCBI Description (D87957) protein involved in sexual development [Homo

sapiens]

Seq. No. 222415

LIB3165-031-P1-K1-H6 Seq. ID

Method BLASTX NCBI GI q118564 BLAST score 415 E value 5.0e-41Match length 90 88 % identity

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 222416

LIB3165-031-P1-K1-H7 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 455 E value 2.0e-45 Match length 91 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222417

```
Seq. ID
                  LIB3165-032-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                  247
E value
                   4.0e-21
Match length
                  124
                   48
% identity
                   (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                   222418
Seq. No.
                   LIB3165-032-P1-K1-A11
Seq. ID
Method
                   BLASTX
                   q2511590
NCBI GI
                   236
BLAST score
                   8.0e-20
E value
Match length
                   52
                   87
% identity
                  (Y13692) multicatalytic endopeptidase complex, proteasome
NCBI Description
                   component, beta subunit [Arabidopsis thaliana] >gi_3421111
                   (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis
                   thaliana]
Seq. No.
                   222419
                   LIB3165-032-P1-K1-A3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g706852
BLAST score
                   42
E value
                   2.0e-14
Match length
                   102
                   85
% identity
                  Lycopersicon esculentum photosystem II 22 kDa component
NCBI Description
                   (psbS) gene, complete cds
                   222420
Seq. No.
                   LIB3165-032-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g3036951
NCBI GI
BLAST score
                   431
                   1.0e-42
E value
                   81
Match length
                   100
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   222421
Seq. No.
                   LIB3165-032-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
BLAST score
                   465
                   1.0e-46
E value
```

100 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

88

Match length

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

Method

BLASTX



ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
Seq. No.
                  222422
                  LIB3165-032-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  g3289002
NCBI GI
                  199
BLAST score
                  2.0e-15
E value
Match length
                  66
                  22
% identity
NCBI Description (AF073522) CRP1 [Zea mays]
                  222423
Seq. No.
                  LIB3165-032-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
                  315
BLAST score
                  4.0e-29
E value
                  113
Match length
                  61
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  222424
Seq. No.
                  LIB3165-032-P1-K1-B11
Seq. ID
                  BLASTX
Method
                  g100200
NCBI GI
BLAST score
                  442
                  6.0e-44
E value
                  114
Match length
                  75
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  222425
Seq. No.
                  LIB3165-032-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  602
                  1.0e-62
E value
Match length
                  128
% identity
NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
                  222426
Seq. No.
                  LIB3165-032-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191152
BLAST score
                  223
E value
                  2.0e-18
Match length
                  107
% identity
                  63
                  (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  222427
Seq. No.
Seq. ID
                  LIB3165-032-P1-K1-B5
```

Seq. ID

Method

```
NCBI GI
                  q2738248
BLAST score
                  512
                  3.0e-52
E value
Match length
                  128
% identity
                  80
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  222428
                  LIB3165-032-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g4406530
NCBI GI
                  338
BLAST score
                  9.0e-32
E value
Match length
                  114
% identity
                  64
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  222429
Seq. No.
Seq. ID
                  LIB3165-032-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3913651
BLAST score
                  376
E value
                  3.0e-36
                  110
Match length
                  65
% identity
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
                  (FNR) >gi_2225993_emb_CAA74359_ (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                  222430
Seq. ID
                  LIB3165-032-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  573
E value
                  2.0e-59
Match length
                  128
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  222431
                  LIB3165-032-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  507
E value
                  1.0e-51
Match length
                  98
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222432
Seq. No.
```

31482

LIB3165-032-P1-K1-C2

BLASTX



```
NCBI GI
                  g1352821
                  574
BLAST score
E value
                  2.0e-59
Match length
                  119
% identity
                  95
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222433
Seq. No.
                  LIB3165-032-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
                  38
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  222434
Seq. No.
                  LIB3165-032-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2493144
BLAST score
                  422
E value
                  1.0e-41
Match length
                  99
                  58
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
                  16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                  (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana]
```

222435 Seq. No.

LIB3165-032-P1-K1-C7 Seq. ID BLASTX Method NCBI GI g4406530 BLAST score 346 9.0e-33 E value

93 Match length 76 % identity

NCBI Description (AF126870) rubisco activase [Vigna radiata]

222436 Seq. No.

LIB3165-032-P1-K1-C8 Seq. ID

Method BLASTX NCBI GI g2129538 BLAST score 220 2.0e-18 E value 45 Match length 93 % identity

NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)

AT103 [Arabidopsis thaliana]

```
222437
Seq. No.
Seq. ID
                  LIB3165-032-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3334113
BLAST score
                  333
                  3.0e-31
E value
                  89
Match length
                  74
% identity
NCBI Description
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  222438
                  LIB3165-032-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  330
                  8.0e-31
E value
Match length
                  112
% identity
                  63
NCBI Description
                 (AF126870) rubisco activase [Vigna radiata]
                  222439
Seq. No.
                  LIB3165-032-P1-K1-D11
Seq. ID
Method
                  BLASTX
                  q100616
NCBI GI
BLAST score
                  464
                  1.0e-46
E value
                  119
Match length
                  76
% identity
                  ribulose-bisphosphate carboxylase activase B precursor -
NCBI Description
                  barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
                  carboxylase activase [Hordeum vulgare] >gi 167095 (M55449)
                  ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                  vulgare]
Seq. No.
                  222440
                  LIB3165-032-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056568
BLAST score
                  298
E value
                   4.0e-27
Match length
                  122
                  17
% identity
NCBI Description (U90944) PDI-like protein [Zea mays]
Seq. No.
                   222441
                  LIB3165-032-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1350736
BLAST score
                  164
E value
                  2.0e-11
                  39
Match length
                  79
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37 >gi 629673 pir S44313 ribosomal
```

ribosomal protein L37 [Lycopersicon esculentum]

protein L37 - tomato >gi_483586_emb_CAA55674_ (X79074)

```
222442
Seq. No.
                  LIB3165-032-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g1332579
NCBI GI
BLAST score
                  516
                  1.0e-52
E value
                  106
Match length
                  10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                  222443
                  LIB3165-032-P1-K1-D5
Seq. ID
                  BLASTX
Method
                  g2924325
NCBI GI
                  307
BLAST score
                  4.0e-28
E value
                  70
Match length
                  80
% identity
                  (Z93765) hypothetical protein [Malus domestica]
NCBI Description
                  222444
Seq. No.
                  LIB3165-032-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850111
                  144
BLAST score
                  5.0e-09
E value
Match length
                  49
% identity
                  55
                  (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                  involvement in lipid metabolism [Schizosaccharomyces pombe]
                  222445
Seq. No.
                  LIB3165-032-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  500
E value
                  9.0e-51
                  97
Match length
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222446
Seq. ID
                  LIB3165-032-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g120661
BLAST score
                  554
E value
                   4.0e-57
Match length
                  121
% identity
                  88
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                   CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate
```

dehydrogenase A-subunit precursor [Nicotiana tabacum]



Seq. No. 222447

LIB3165-032-P1-K1-E1 Seq. ID

Method BLASTX q1352821 NCBI GI 510 BLAST score 6.0e-52 E value Match length 98 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222448

Seq. ID LIB3165-032-P1-K1-E11

Method BLASTN NCBI GI g2564049 BLAST score 40 4.0e-13 E value

Match length 224 79 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MLE2, complete sequence [Arabidopsis thaliana]

222449 Seq. No.

LIB3165-032-P1-K1-E12 Seq. ID

Method BLASTX NCBI GI g3024020 620 BLAST score 7.0e-65 E value 121 Match length 95 % identity

INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) NCBI Description

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 222450

LIB3165-032-P1-K1-E2 Seq. ID

BLASTX Method q2493694 NCBI GI BLAST score 248 E value 3.0e-21 119 Match length 45 % identity

PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII NCBI Description

6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein

of photosystem II [Spinacia oleracea]

222451 Seq. No.

LIB3165-032-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI q4220480 BLAST score 390 2.0e-38 E value Match length 124



% identity (AC006069) unknown protein [Arabidopsis thaliana] NCBI Description 222452 Seq. No. LIB3165-032-P1-K1-E6 Seq. ID Method BLASTX NCBI GI q3158476 BLAST score 535 E value 7.0e-55 117 Match length 86 % identity (AF067185) aquaporin 2 [Samanea saman] NCBI Description 222453 Seq. No. LIB3165-032-P1-K1-E9 Seq. ID Method BLASTX NCBI GI q1346155 BLAST score 553 5.0e-57 E value Match length 121 % identity 88 SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR NCBI Description (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine
hydroxymethyltransferase [Flaveria pringlei] 222454 Seq. No. Seq. ID LIB3165-032-P1-K1-F10 Method BLASTX NCBI GI g1632831 BLAST score 442 6.0e-44E value Match length 100 % identity 86 (Z49698) orf [Ricinus communis] NCBI Description 222455 Seq. No. LIB3165-032-P1-K1-F11 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 516 1.0e-52 E value 100 Match length % identity 99 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC $\overline{4.1.1.39}$) small chain ribulose bisphosphate carboxylase [Gossypium hirsutum]

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

222456

Seq. No. Seq. ID LIB3165-032-P1-K1-F12

BLASTX Method NCBI GI q1507699 BLAST score 271

```
6.0e-24 -
E value
Match length
                  66
                  77
% identity
NCBI Description
                  (L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)
                  COL2 [Arabidopsis thaliana]
                  222457
Seq. No.
                  LIB3165-032-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g100200
NCBI GI
BLAST score
                  390
                  8.0e-38
E value
Match length
                  105
                  72
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  222458
Seq. No.
                  LIB3165-032-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115833
BLAST score
                  467
E value
                  7.0e-47
Match length
                  119
                  76
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                  222459
Seq. No.
Seq. ID
                  LIB3165-032-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2765081
BLAST score
                  449
E value
                  8.0e-45
Match length
                  121
% identity
                  74
NCBI Description (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                   222460
Seq. ID
                  LIB3165-032-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2317910
BLAST score
                  349
E value
                   4.0e-33
Match length
                  122
% identity
NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]
                   222461
Seq. No.
Seq. ID
                  LIB3165-032-P1-K1-G11
                  BLASTX
Method
NCBI GI
                  g4406777
BLAST score
                  272
E value
                  5.0e-24
Match length
                  70
```

31488

73

% identity

% identity

97



```
(AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  222462
                  LIB3165-032-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                  66
E value
                  7.0e-29
Match length
                  182
% identity
                  84
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  222463
                  LIB3165-032-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1181615
BLAST score
                  601
E value
                  1.0e-62
Match length
                  128
                   90
% identity
                  (D83078) nitrilase [Nicotiana tabacum]
NCBI Description
                  222464
Seq. No.
Seq. ID
                  LIB3165-032-P1-K1-G5
                  BLASTX
Method
NCBI GI
                   q68200
BLAST score
                   305
                   5.0e-28
E value
Match length
                   93
                   70
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   222465
Seq. No.
                   LIB3165-032-P1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g68200
BLAST score
                   469
                   4.0e-47
E value
                   121
Match length
                   81
% identity
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   222466
Seq. No.
Seq. ID
                   LIB3165-032-P1-K1-G7
Method
                   BLASTN
                   g2687435
NCBI GI
BLAST score
                   265
                   1.0e-147
E value
Match length
                   305
```

31489

NCBI Description Hamamelis virginiana large subunit 26S ribosomal RNA gene,

Method

partial sequence

```
222467
Seq. No.
                   LIB3165-032-P1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4406530
                   346
BLAST score
                   9.0e-33
E value
                   93
Match length
                   76
% identity
                   (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                   222468
Seq. No.
                   LIB3165-032-P1-K1-H1
Seq. ID
                   BLASTX
Method
                   g228403
NCBI GI
                   195
BLAST score
                   5.0e-15
E value
                   43
Match length
                   84
% identity
                   glycolate oxidase [Lens culinaris]
NCBI Description
                   222469
Seq. No.
                   LIB3165-032-P1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2505874
                   182
BLAST score
                   2.0e-13
E value
                   57
Match length
                    63
% identity
                   (Y12776) putative kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    222470
                   LIB3165-032-P1-K1-H12
Seq. ID
                    BLASTX
Method
NCBI GI
                    q3269292
BLAST score
                    175
                    8.0e-13
E value
Match length
                    80
                    49
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                    222471
                    LIB3165-032-P1-K1-H2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g121902
BLAST score
                    158
E value
                    1.0e-10
Match length
                    35
                    91
% identity
                   HISTONE H1.1 >gi_1070594_pir__HSMU11 histone H1.1 -
Arabidopsis thaliana >gi_16317_emb_CAA44314_ (X62458)
NCBI Description
                    Histone H1 [Arabidopsis thaliana]
                    222472
Seq. No.
                    LIB3165-032-P1-K1-H3
Seq. ID
                    BLASTX
```

31490

```
q2832669
NCBI GI
                  162
BLAST score
                  4.0e-11
E value
Match length
                  102
% identity
                   43
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  222473
Seq. No.
                  LIB3165-032-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  q3281850
NCBI GI
BLAST score
                  145
                   4.0e-09
E value
                  83
Match length
                   43
% identity
                  (AL031004) monogalactosyldiacylglycerol synthase - like
NCBI Description
                  protein [Arabidopsis thaliana]
                   222474
Seq. No.
                  LIB3165-032-P1-K1-H7
Seq. ID
Method
                   BLASTX
                   g20729
NCBI GI
                   456
BLAST score
                   1.0e-45
E value
Match length
                   122
                   75
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   222475
Seq. No.
                   LIB3165-032-P1-K1-H8
Seq. ID
Method
                   BLASTX
                   q289920
NCBI GI
                   598
BLAST score
                   3.0e-62
E value
                   110
Match length
% identity
                   99
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   222476
Seq. No.
                   LIB3165-033-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3036946
BLAST score
                   315
E value
                   3.0e-29
Match length
                   60
% identity
                   100
                   (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   222477
Seq. No.
                   LIB3165-033-P1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115470
BLAST score
                   290
E value
                   3.0e-26
                   107
Match length
```

31491



% identity 58 CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE NCBI Description DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana] 222478 Seq. No. LIB3165-033-P1-K1-A12 Seq. ID BLASTN Method g2687434 NCBI GI 49 BLAST score 1.0e-18 E value 89 Match length 89 % identity NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence 222479 Seq. No. LIB3165-033-P1-K1-A2 Seq. ID BLASTN Method g3108248 NCBI GI 190 BLAST score 1.0e-102 E value 268 Match length 94 % identity NCBI Description Gossypium barbadense clone pXP027 repetitive DNA sequence 222480 Seq. No. LIB3165-033-P1-K1-A3 Seq. ID BLASTX Method g3687652 NCBI GI 355 BLAST score 6.0e-34 E value 102 Match length % identity NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata] 222481 Seq. No. LIB3165-033-P1-K1-A5 Seq. ID BLASTX Method NCBI GI g118564 565 BLAST score E value 2.0e-58 116 Match length % identity GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE NCBI Description REDUCTASE) (HPR) (GDH) >gi 65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi 18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi 18275 emb CAA32764 (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

222482 Seq. No.

LIB3165-033-P1-K1-A6 Seq. ID

BLASTX Method

```
NCBI GI
                   g289920
BLAST score
                   645
E value
                   9.0e-68
Match length
                   121
                   99
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   222483
                   LIB3165-033-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2980887
BLAST score
                   451
                   5.0e-45
E value
Match length
                   119
% identity
                   71
                   (AJ224961) Sucrose carrier [Ricinus communis]
NCBI Description
                   222484
Seq. No.
Seq. ID
                   LIB3165-033-P1-K1-A9
Method
                   BLASTX
                   q131397
NCBI GI
BLAST score
                   300
E value
                   2.0e-27
                   110
Match length
% identity
                   61
                   OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                   SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi_81480_pir__S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi 225597 prf 1307179B luminal protein 16kD
                    [Spinacia oleracea]
Seq. No.
                   222485
Seq. ID
                   LIB3165-033-P1-K1-B1
                   BLASTX
Method
NCBI GI
                   g1488043
BLAST score
                   192
                   1.0e-14
E value
                   63
Match length
% identity
NCBI Description (U63784) PAPS-reductase-like protein [Catharanthus roseus]
Seq. No.
                   222486
Seq. ID
                   LIB3165-033-P1-K1-B2
                   BLASTX
Method
NCBI GI
                   q68200
BLAST score
                   193
                   8.0e-15
E value
                   74
Match length
```

31493

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,

chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
fructose-bisphosphate aldolase [Spinacia oleracea]

64

% identity

NCBI Description

```
222487
Seq. No.
Seq. ID
                   LIB3165-033-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q3080418
BLAST score
                   260
                   1.0e-22
E value
Match length
                   114
% identity
                   44
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                   222488
Seq. ID
                   LIB3165-033-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g231610
BLAST score
                   324
E value
                   4.0e-30
Match length
                   111
% identity
                   64
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                   >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
                   (gamma subunit) [Nicotiana tabacum]
Seq. No.
                   222489
                   LIB3165-033-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4558563
BLAST score
                   201
E value
                   1.0e-15
Match length
                   96
% identity
                   46
                  (AC007138) putative NifU-like metallocluster assembly
NCBI Description
                   factor [Arabidopsis thaliana]
                   222490
Seq. No.
                   LIB3165-033-P1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g68200
BLAST score
                   458
                   7.0e-46
E value
Match length
                   112
                   83
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   222491
Seq. No.
Seq. ID
                   LIB3165-033-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g132168
BLAST score
                   530
E value
                   3.0e-54
Match length
                   126
% identity
                   77
```

PRECURSOR (RUBISCO ACTIVASE) >gi 81488 pir A31082

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

ribulose-bisphosphate carboxylase activase precursor - spinach >gi_170129 (J03610) rubisco activase precursor [Spinacia oleracea]

222492 Seq. No. LIB3165-033-P1-K1-C10 Seq. ID Method BLASTX NCBI GI q289920 BLAST score 457 E value 6.0e-46Match length 86 99 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 222493 Seq. No. Seq. ID LIB3165-033-P1-K1-C12 Method BLASTX NCBI GI q430947 BLAST score 409 E value 4.0e-40 Match length 101 % identity 81 (U01103) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana] Seq. No. 222494 LIB3165-033-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g100200 BLAST score 377 2.0e-36 E value 104 Match length % identity 71 NCBI Description chlorophyll a/b-binding protein type I precursor - tomato 222495 Seq. No. LIB3165-033-P1-K1-C4 Seq. ID BLASTX Method g3850111 NCBI GI BLAST score 149 E value 3.0e-10 Match length 49 % identity NCBI Description (AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe] 222496 Seq. No. Seq. ID LIB3165-033-P1-K1-C5 Method BLASTX NCBI GI g2129921 BLAST score 195 5.0e-15E value 51 Match length % identity 75

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

```
Seq. No. 222497
Seq. ID LIB3165-033-P1-K1-C6
Method BLASTX
NCBI GI g1352821
```

NCBI GI g135282 BLAST score 510 E value 6.0e-52 Match length 98 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222498

Seq. ID LIB3165-033-P1-K1-C7

Method BLASTX
NCBI GI g4262181
BLAST score 160
E value 6.0e-11
Match length 77
% identity 55

NCBI Description (AC005508) 37496 [Arabidopsis thaliana]

Seq. No. 222499

Seq. ID LIB3165-033-P1-K1-D10

Method BLASTX
NCBI GI 94468813
BLAST score 185
E value 7.0e-14
Match length 100
% identity 42

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 222500

Seq. ID LIB3165-033-P1-K1-D11

Method BLASTX
NCBI GI g2492514
BLAST score 580
E value 3.0e-60
Match length 118
% identity 94

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH

protease [Arabidopsis thaliana]

Seq. No. 222501

Seq. ID LIB3165-033-P1-K1-D12

Method BLASTX
NCBI GI g1352821
BLAST score 489
E value 2.0e-49
Match length 105
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222502 Seq. No. LIB3165-033-P1-K1-D4 Seq. ID BLASTN Method g450504 NCBI GI 47 BLAST score 2.0e-17 E value 51 Match length 98 % identity G.hirsutum rbcS gene for ribulose-1,5-bisphosphate NCBI Description carboxylase, small subunit Seq. No. 222503 LIB3165-033-P1-K1-D6 Seq. ID Method BLASTX q3451067 NCBI GI 349 BLAST score 4.0e-33 E value 92 Match length 76 % identity (AL031326) putative protein [Arabidopsis thaliana] NCBI Description

222504 Seq. No.

LIB3165-033-P1-K1-D7 Seq. ID

Method BLASTX g1352821 NCBI GI 488 BLAST score 2.0e-49 E value 95 Match length 97 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

222505 Seq. No.

LIB3165-033-P1-K1-D8 Seq. ID

BLASTX Method NCBI GI g1352821 BLAST score 506 2.0e-51 E value Match length 98 97 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222506

LIB3165-033-P1-K1-D9 Seq. ID

BLASTX Method NCBI GI q3298502



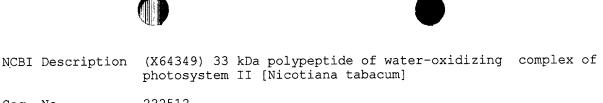
```
BLAST score
                  389
                  9.0e-38
E value
Match length
                  122
% identity
                  61
                  (AB015046) xylulokinase [Homo sapiens]
NCBI Description
                  222507
Seq. No.
                  LIB3165-033-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  g430947
NCBI GI
BLAST score
                  379
                  1.0e-36
E value
Match length
                  95
                  80
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  222508
                  LIB3165-033-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3355468
NCBI GI
BLAST score
                  522
E value
                  2.0e-53
Match length
                  123
% identity
                  88
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  222509
                  LIB3165-033-P1-K1-E12
Seq. ID
                  BLASTX
Method
                  g4115931
NCBI GI
                   337
BLAST score
                  1.0e-31
E value
                  124
Match length
                   59
% identity
                  (AF118223) contains similarity to Guillardia theta ABC
NCBI Description
                   transporter (GB:AF041468) [Arabidopsis thaliana]
                   222510
Seq. No.
                   LIB3165-033-P1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4406530
                   321
BLAST score
                   9.0e-30
E value
                   110
Match length
                   63
% identity
NCBI Description
                  (AF126870) rubisco activase [Vigna radiata]
                   222511
Seq. No.
                   LIB3165-033-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   a505482
BLAST score
                   406
```

9.0e-40

104 81

E value Match length

% identity



222512 Seq. No. LIB3165-033-P1-K1-E6 Seq. ID Method BLASTX NCBI GI q3914605 BLAST score 471 _E value 2.0e-47 Match length 128 70 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__\$39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

 Seq. No.
 222513

 Seq. ID
 LIB3165-033-P1-K1-F1

 Method
 BLASTX

 NCBI GI
 g3292814

 BLAST score
 153

 E value
 4.0e-10

 Match length
 96

44

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

 Seq. No.
 222514

 Seq. ID
 LIB3165-033-P1-K1-F10

 Method
 BLASTX

 NCBI GI
 g1418990

BLAST score 218
E value 1.0e-17
Match length 47
% identity 87

% identity

NCBI Description (Z75524) unknown [Lycopersicon esculentum]

Seq. No. 222515

Seq. ID LIB3165-033-P1-K1-F11

Method BLASTX
NCBI GI g1419090
BLAST score 337
E value 1.0e-31
Match length 96
% identity 70

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 222516

Seq. ID LIB3165-033-P1-K1-F2

Method BLASTX
NCBI GI g2245066
BLAST score 212
E value 4.0e-17
Match length 103
% identity 39

E value

Match length

4.0e-57

113



```
(Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
                   222517
Seq. No.
                   LIB3165-033-P1-K1-F3
Seq. ID
Method
                   BLASTX
                   g4056469
NCBI GI
                   650
BLAST score
                   2.0e-68
E value
                   124
Match length
                   98
% identity
                   (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                   factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                   gb AA712956, gb T46403, gb T46050, gb AI100391 and
                   gb_Z25043 come from t
                   222518
Seq. No.
                   LIB3165-033-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g3288821
NCBI GI
                   436
BLAST score
E value
                   3.0e-43
                   106
Match length
                   79
% identity
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
                   222519
Seq. No.
                   LIB3165-033-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   q100454
NCBI GI
BLAST score
                   532
                   2.0e-54
E value
                   129
Match length
                   84
% identity
                   photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                   >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein
                   of oxygen-evolving complex [Solanum tuberosum]
                   222520
Seq. No.
                   LIB3165-033-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829869
                   373
BLAST score
                   6.0e-36
E value
Match length
                   87
% identity
                   82
NCBI Description
                   (AC002396) pyruvate dehydrogenase E1 alpha subunit
                    [Arabidopsis thaliana]
                   222521
Seq. No.
                   LIB3165-033-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g70644
BLAST score
                   554
```

31500



19 % identity

NCBI Description ubiquitin precursor - common sunflower (fragment)

Seq. No.

222522

82

Seq. ID

LIB3165-033-P1-K1-G12

BLASTX Method g1168411 NCBI GI 514 BLAST score 2.0e-52 E value 128 Match length

% identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.

222523

Seq. ID

LIB3165-033-P1-K1-G4

Method BLASTX q2244844 NCBI GI BLAST score 152 6.0e-10 E value 118 Match length 40 % identity

(Z97337) hypothetical protein [Arabidopsis thaliana] NCBI Description

222524 Seq. No.

LIB3165-033-P1-K1-G6 Seq. ID

BLASTX Method g100203 NCBI GI BLAST score 185 2.0e-22 E value 99 Match length 58 % identity

cysteine proteinase (EC 3.4.22.-) precursor - tomato NCBI Description

>gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine

proteinase [Lycopersicon esculentum]

222525 Seq. No.

Seq. ID LIB3165-033-P1-K1-G9

Method BLASTX q3869088 NCBI GI 517 BLAST score 9.0e-53 E value Match length 100 % identity

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

222526 Seq. No.

Seq. ID LIB3165-033-P1-K1-H1

Method BLASTX NCBI GI q4106538 472 BLAST score 2.0e-47 E value 128 Match length % identity .

(AF104220) gamma-tocopherol methyltransferase [Arabidopsis NCBI Description

thaliana]

Seq. No. 222527



LIB3165-033-P1-K1-H6 Seq. ID BLASTX Method NCBI GI q1346155 BLAST score 584 1.0e-60 E value 127 Match length % identity 88 SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR NCBI Description (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi 481942 pir S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei] 222528 Seq. No. LIB3165-033-P1-K1-H7 Seq. ID Method BLASTX NCBI GI q121083 621 BLAST score 5.0e-65 E value Match length 123 92 % identity GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE NCBI Description DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi_282926_pir__A42109 glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) component P precursor garden pea >gi_20741_emb_CAA42443_ (X59773) component of aminomethyltransferase [Pisum sativum] 222529 Seq. No. LIB3165-033-P1-K1-H9 Seq. ID BLASTX Method g2098705 NCBI GI 228 BLAST score 6.0e-19 E value 98 Match length 48 % identity NCBI Description (U82973) pectinesterase [Citrus sinensis] 222530 Seq. No. LIB3165-034-P1-K1-A1 Seq. ID BLASTX Method NCBI GI q2879867 405 BLAST score 1.0e-39 E value Match length 110 70 % identity (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces NCBI Description pombe] 222531 Seq. No. LIB3165-034-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 546 4.0e-56 E value Match length 104



```
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222532
Seq. No.
                  LIB3165-034-P1-K1-A2
Seq. ID
                  BLASTX
```

Method NCBI GI q1350944 BLAST score 302 2.0e-27 E value Match length 78 79 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S17

222533 Seq. No. LIB3165-034-P1-K1-A3 Seq. ID BLASTX Method g1706261 NCBI GI 428 BLAST score 2.0e-42 E value

87 Match length 89 % identity

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598

cysteine proteinase 2 precursor - maize

>gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea

mays]

222534 Seq. No.

LIB3165-034-P1-K1-A4 Seq. ID

BLASTX Method q1168411 NCBI GI 501 BLAST score E value 6.0e-51Match length 126

81 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

222535 Seq. No.

LIB3165-034-P1-K1-A6 Seq. ID

Method BLASTX NCBI GI g169039 BLAST score 457 E value 1.0e-45 Match length 104 % identity 86

NCBI Description (M97477) aldolase [Pisum sativum]

222536 Seq. No.

LIB3165-034-P1-K1-A7 Seq. ID

Method BLASTX g1354515 NCBI GI BLAST score 238 4.0e-20 E value Match length 121



97

74

Match length

% identity

% identity (U55837) carbonic anhydrase [Populus tremula x Populus NCBI Description tremuloides] Seq. No. 222537 LIB3165-034-P1-K1-A8 Seq. ID BLASTX Method NCBI GI g100200 BLAST score 603 E value 7.0e-63 127 Match length 68 % identity chlorophyll a/b-binding protein type I precursor - tomato NCBI Description 222538 Seq. No. LIB3165-034-P1-K1-A9 Seq. ID Method BLASTX NCBI GI q3158474 BLAST score 182 E value 2.0e-13 Match length 53 70 % identity (AF067184) aquaporin 1 [Samanea saman] NCBI Description 222539 Seq. No. LIB3165-034-P1-K1-B1 Seq. ID Method BLASTX NCBI GI q121953 168 BLAST score E value 8.0e-12 Match length 41 83 % identity HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea NCBI Description >gi 20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum] Seq. No. 222540 Seq. ID LIB3165-034-P1-K1-B10 Method BLASTX NCBI GI q81857 BLAST score 215 E value 2.0e-17 Match length 42 90 % identity IgE-dependent histamine-releasing factor homolog - alfalfa NCBI Description $(fragment) > gi_19658_emb_CAA45349_ (X63872) translationally$ controlled tumor protein [Medicago sativa] Seq. No. 222541 LIB3165-034-P1-K1-B11 Seq. ID Method BLASTX NCBI GI g2653446 380 BLAST score 1.0e-36 E value

NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]



```
222542
Seq. No.
                  LIB3165-034-P1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914940
                  365
BLAST score
                  6.0e-35
E value
                  123
Match length
                  63
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                  [Spinacia oleracea]
                  222543
Seq. No.
                  LIB3165-034-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  q129867
NCBI GI
                  376
BLAST score
                  3.0e-39
E value
                  86
Match length
                  97
% identity
                  CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)
NCBI Description
                  >gi 2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex
                  subunit IV [Nicotiana tabacum]
Seq. No.
                  222544
                  LIB3165-034-P1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g228210
BLAST score
                  542
                  1.0e-55
E value
Match length
                  134
                  75
% identity
NCBI Description granule-bound starch synthase [Solanum tuberosum]
Seq. No.
                  222545
                  LIB3165-034-P1-K1-B8
Seq. ID
Method
                  BLASTX
                   a487046
NCBI GI
                   381
BLAST score
                   8.0e-37
E value
                   127
Match length
% identity
                  photosystem I chain II precursor - wood tobacco
NCBI Description
                   >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
Seq. No.
                   222546
                   LIB3165-034-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3738316
```

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

337

90 70

1.0e-31

BLAST score

Match length

% identity

E value



```
222547
Seq. No.
                  LIB3165-034-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  q2865623
NCBI GI
                  408
BLAST score
                  4.0e-40
E value
                  93
Match length
                  85
% identity
                  (AF045286)
NCBI Description
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                  222548
Seq. No.
                  LIB3165-034-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g20729
NCBI GI
                  178
BLAST score
                   4.0e-13
E value
                   67
Match length
                   57
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  222549
Seq. No.
                  LIB3165-034-P1-K1-C12
Seq. ID
                  BLASTX
Method
                   g1181599
NCBI GI
                   399
BLAST score
                   6.0e-39
E value
                   110
Match length
                   72
% identity
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                   222550
Seq. No.
                   LIB3165-034-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3269292
BLAST score
                   289
                   4.0e-26
E value
                   74
Match length
                   69
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   222551
Seq. No.
                   LIB3165-034-P1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q133867
BLAST score
                   477
E value
                   5.0e-48
                   109
Match length
                   83
% identity
                   40S RIBOSOMAL PROTEIN S11 >gi_82722 pir__S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                   ribosomal protein S11 [Zea mays].
```

31506

222552

LIB3165-034-P1-K1-C7

Seq. No. Seq. ID



BLASTX Method q498038 NCBI GI 465 BLAST score 1.0e-46 E value Match length 130 62 % identity

(L33792) lipid transfer protein [Senecio odorus] NCBI Description

Seq. No.

LIB3165-034-P1-K1-C9 Seq. ID

222553

BLASTX Method g1352821 NCBI GI 531 BLAST score 2.0e-54 E value Match length 102 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222554

Seq. No. LIB3165-034-P1-K1-D1 Seq. ID

BLASTX Method q4249385 NCBI GI 371 BLAST score E value 1.0e-35 Match length 104 67 % identity

(AC005966) T2K10.11 [Arabidopsis thaliana] NCBI Description

222555 Seq. No.

LIB3165-034-P1-K1-D11 Seq. ID

BLASTX Method q68200 NCBI GI BLAST score 503 4.0e-51 E value 124 Match length 83 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi 22633 emb CAA47293_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

222556 Seq. No.

LIB3165-034-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 677 2.0e-71 E value 130 Match length % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581_pir _RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

g430947

3.0e-44

444

108



```
222557
Seq. No.
                   LIB3165-034-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193285
BLAST score
                   217
E value
                   1.0e-17
Match length
                   56
                   70
% identity
                  (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   222558
                   LIB3165-034-P1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3121825
BLAST score
                   301
                   2.0e-27
E value
                   102
Match length
                   69
% identity
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                   ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                   bas1 protein [Spinacia oleracea]
                   222559
Seq. No.
                   LIB3165-034-P1-K1-D5
Seq. ID
Method
                   BLASTX
                   q1352821
NCBI GI
BLAST score
                   282
                   3.0e-25
E value
Match length
                   54
                   98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222560
Seq. No.
Seq. ID
                   LIB3165-034-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g1168408
BLAST score
                   169
E value
                   6.0e-12
                   38
Match length
                   89
% identity
NCBI Description
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
                   >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
                   222561
Seq. No.
                   LIB3165-034-P1-K1-D7
Seq. ID
```

31508



% identity (U01103) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana] 222562 Seq. No.

LIB3165-034-P1-K1-D9 Seq. ID BLASTX Method NCBI GI g1352821 BLAST score 710 2.0e-75 E value

Match length 133 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222563 LIB3165-034-P1-K1-E10 Seq. ID

Method BLASTX NCBI GI g100490 BLAST score 573 2.0e-59 E value Match length 115 28 % identity

polyubiquitin - garden snapdragon (fragment) NCBI Description

>gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum

majus]

222564 Seq. No.

LIB3165-034-P1-K1-E11 Seq. ID

BLASTX Method g68200 NCBI GI 323 BLAST score 5.0e-30 E value 87 Match length 78 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

222565 Seq. No.

LIB3165-034-P1-K1-E12 Seq. ID

BLASTX Method g228403 NCBI GI 529 BLAST score 4.0e-54E value 119 Match length % identity

NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 222566

LIB3165-034-P1-K1-E2 Seq. ID

Method BLASTX q1781348 NCBI GI 564 BLAST score



```
3.0e-58
E value
Match length
                  119
                  89
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
                  222567
Seq. No.
                  LIB3165-034-P1-K1-E3
Seq. ID
                  BLASTX
Method
                  g3914002
NCBI GI
                   607
BLAST score
                  3.0e-63
E value
                  128
Match length
                   91
% identity
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279
NCBI Description
                   (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                   222568
                   LIB3165-034-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2129921
NCBI GI
                   191
BLAST score
                   1.0e-14
E value
                   36
Match length
                   100
% identity
                   hypothetical protein 1 - Madagascar periwinkle >gi_758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
                   222569
Seq. No.
                   LIB3165-034-P1-K1-E6
Seq. ID
                   BLASTX
Method
                   g2739046
NCBI GI
                   167
BLAST score
                   1.0e-11
E value
                   90
Match length
                   38
% identity
                  (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                   [Glycine max]
                   222570
Seq. No.
                   LIB3165-034-P1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1483563
                   423
BLAST score
E value
                   1.0e-41
                   127
Match length
                   69
% identity
                  (X99825) leucine aminopeptidase [Petroselinum crispum]
NCBI Description
                   222571
Seq. No.
                   LIB3165-034-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4033838
BLAST score
                   298
```

4.0e-27

103 60

E value Match length

% identity

```
(Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                  222572
Seq. No.
                  LIB3165-034-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2499525
BLAST score
                  260
                  1.0e-22
E value
                  133
Match length
                  44
% identity
                  INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER
NCBI Description
                  (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153)
                  intestinal sodium/dicarboxylate cotransporter [Rattus
                  norvegicus]
                  222573
Seq. No.
                  LIB3165-034-P1-K1-F1
```

Seq. ID LIB3165-034-P1-K1-F1
Method BLASTX
NCBI GI g4455225
BLAST score 237
E value 4.0e-20
Match length 56

% identity 71

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

 Seq. No.
 222574

 Seq. ID
 LIB3165-034-P1-K1-F10

 Method
 BLASTX

NCBI GI g3603401
BLAST score 300
E value 3.0e-27
Match length 74
% identity 69

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 222575

Seq. ID LIB3165-034-P1-K1-F12

Method BLASTX
NCBI GI g430947
BLAST score 429
E value 2.0e-42
Match length 106
% identity 80

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 222576

Seq. ID LIB3165-034-P1-K1-F2

Method BLASTX
NCBI GI g3121825
BLAST score 339
E value 7.0e-32
Match length 127
% identity 64

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)

bas1 protein [Spinacia oleracea]



Seq. No. 222577

Seq. ID LIB3165-034-P1-K1-F3

Method BLASTX
NCBI GI g1352821
BLAST score 593
E value 1.0e-61
Match length 119
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222578

Seq. ID LIB3165-034-P1-K1-F5

Method BLASTX
NCBI GI g100616
BLAST score 236
E value 8.0e-20
Match length 54
% identity 85

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 222579

Seq. ID LIB3165-034-P1-K1-F6

Method BLASTX
NCBI GI g289920
BLAST score 604
E value 6.0e-63
Match length 123
% identity 93

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222580

Seq. ID LIB3165-034-P1-K1-F7

Method BLASTX
NCBI GI g289920
BLAST score 614
E value 4.0e-64
Match length 115
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222581

Seq. ID LIB3165-034-P1-K1-F8

Method BLASTN
NCBI GI g3108329
BLAST score 117
E value 2.0e-59



```
117
Match length
% identity
NCBI Description Gossypium barbadense clone pXP3-50 repetitive DNA sequence
                  222582
Seq. No.
                  LIB3165-034-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g430947
BLAST score
                  320
                  9.0e-30
E value
                  83
Match length
% identity
                  80
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  222583
                  LIB3165-034-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3747111
                  226
BLAST score
E value
                  1.0e-18
                  67
Match length
                   63
% identity
                 (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                  222584
Seq. No.
                  LIB3165-034-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2791423
                  197
BLAST score
E value
                   3.0e-15
Match length
                   64
% identity
                   56
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                  222585
Seq. ID
                  LIB3165-034-P1-K1-G3
Method
                  BLASTX
NCBI GI
                   q3420239
BLAST score
                   349
E value
                   4.0e-33
Match length
                   70
                   96
% identity
```

NCBI Description (AF059484) actin [Gossypium hirsutum]

222586 Seq. No.

Seq. ID LIB3165-034-P1-K1-G4

Method BLASTX NCBI GI g2979553 BLAST score 184 E value 1.0e-13 Match length 82 % identity

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

222587 Seq. No.

LIB3165-034-P1-K1-G7 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q3928543
BLAST score
                  465
E value
                  1.0e-46
Match length
                  114
                  71
% identity
                 (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  222588
Seq. No.
Seq. ID
                  LIB3165-034-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q2979553
BLAST score
                  183
E value
                  1.0e-13
Match length
                  82
                  43
% identity
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  222589
Seq. ID
                  LIB3165-034-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  128
E value
                  3.0e-14
Match length
                  67
                  63
% identity
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  222590
Seq. No.
                  LIB3165-034-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4324714
BLAST score
                  407
E value
                  4.0e-40
                  90
Match length
                  89
% identity
NCBI Description (AF110771) ammonium transporter [Arabidopsis thaliana]
Seq. No.
                  222591
Seq. ID
                  LIB3165-034-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  408
E value
                  5.0e-40
Match length
                  81
                  99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505 emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

Seq. No. 222592

Seq. ID LIB3165-034-P1-K1-H12



```
Method BLASTX
NCBI GI g1181599
BLAST score 356
E value 5.0e-34
Match length 99
% identity 71
```

NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]

Seq. No. 222593

Seq. ID LIB3165-034-P1-K1-H2

Method BLASTX
NCBI GI g4262250
BLAST score 286
E value 8.0e-26
Match length 91
% identity 70

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 222594

Seq. ID LIB3165-034-P1-K1-H3

Method BLASTX
NCBI GI g4406530
BLAST score 340
E value 6.0e-32
Match length 115
% identity 63

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 222595

Seq. ID LIB3165-034-P1-K1-H4

Method BLASTX
NCBI GI g289920
BLAST score 594
E value 9.0e-62
Match length 124
% identity 90

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222596

Seq. ID LIB3165-034-P1-K1-H8

Method BLASTX
NCBI GI g1352821
BLAST score 402
E value 2.0e-39
Match length 81
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir_ RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222597

Seq. ID LIB3165-034-P1-K2-A1

Method BLASTX NCBI GI g2879867



BLAST score 393 E value 3.0e-38 Match length 105 % identity 70

NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces

pombe]

Seq. No. 222598

Seq. ID LIB3165-034-P1-K2-A11

Method BLASTX
NCBI GI g1352821
BLAST score 324
E value 2.0e-30
Match length 63
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_(X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222599

Seq. ID LIB3165-034-P1-K2-A3

Method BLASTX
NCBI GI g1706261
BLAST score 418
E value 2.0e-41
Match length 84
% identity 88

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129 pir S59598

cysteine proteinase 2 precursor - maize

>gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea

mays]

Seq. No. 222600

Seq. ID LIB3165-034-P1-K2-A4

Method BLASTX
NCBI GI g1168411
BLAST score 525
E value 1.0e-53
Match length 137
% identity 80

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 222601

Seq. ID LIB3165-034-P1-K2-A6

Method BLASTX
NCBI GI g461501
BLAST score 347
E value 1.0e-60
Match length 131
% identity 90

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE 2, CHLOROPLAST

>gi_418803_pir__S29048 fructose-bisphosphate aldolase (EC

4.1.2.13) - garden pea (fragment)

Seq. No. 222602



LIB3165-034-P1-K2-A7 Seq. ID Method BLASTX NCBI GI g1354515 BLAST score 177 E value 2.0e-13 Match length 68 % identity 60 NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus tremuloides] 222603 Seq. No. LIB3165-034-P1-K2-A8 Seq. ID Method BLASTX NCBI GI g100200 594 BLAST score E value 8.0e-62 Match length 128 % identity 67 NCBI Description chlorophyll a/b-binding protein type I precursor - tomato Seq. No. 222604 LIB3165-034-P1-K2-A9 Seq. ID Method BLASTX NCBI GI g3158474 BLAST score 255 E value 5.0e-22 Match length 68 76 % identity NCBI Description (AF067184) aquaporin 1 [Samanea saman] Seq. No. 222605 LIB3165-034-P1-K2-B1 Seq. ID Method BLASTX NCBI GI g121953 BLAST score 172 E value 3.0e-12Match length 39 87 % identity NCBI Description HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123 (X05636) H1 histone (AA 1-263) [Pisum sativum] Seq. No. 222606 Seq. ID LIB3165-034-P1-K2-B10 Method BLASTX NCBI GI g81857 BLAST score 215 E value 2.0e-17 Match length 42 90 % identity NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa

Seq. No. 222607

Seq. ID LIB3165-034-P1-K2-B2

Method BLASTX

31517

controlled tumor protein [Medicago sativa]

(fragment) >gi_19658_emb_CAA45349_ (X63872) translationally



```
NCBI GI
                  q1168411
BLAST score
                  141
                  7.0e-09
E value
Match length
                  65
                  54
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  222608
Seq. No.
                  LIB3165-034-P1-K2-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914940
BLAST score
                  307
                  3.0e-28
E value
                  111
Match length
% identity
                  61
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                   [Spinacia oleracea]
                  222609
Seq. No.
                  LIB3165-034-P1-K2-B5
```

Seq. ID Method BLASTX NCBI GI g129867 BLAST score 360 8.0e-37 E value

Match length 78 % identity 88

NCBI Description CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)

>gi 2924273 emb CAA77425 (Z00044) cytochrome b/f complex

subunit IV [Nicotiana tabacum]

Seq. No. 222610

LIB3165-034-P1-K2-B6 Seq. ID

Method BLASTX NCBI GI g228210 BLAST score 572 E value 3.0e-59 Match length 130 % identity 81

NCBI Description granule-bound starch synthase [Solanum tuberosum]

Seq. No. 222611

LIB3165-034-P1-K2-B9 Seq. ID

Method BLASTX g3738316 NCBI GI BLAST score 330 E value 8.0e-31 Match length 88 % identity 70

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 222612

Seq. ID LIB3165-034-P1-K2-C10

Method BLASTX NCBI GI g2865623 BLAST score 387



1.0e-37 E value Match length 92 82 % identity (AF045286) NCBI Description GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana] Seq. No. 222613 LIB3165-034-P1-K2-C11 Seq. ID Method BLASTX NCBI GI g20729 270 BLAST score 7.0e-24E value Match length 87 % identity 66 NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum] Seq. No. 222614 Seq. ID LIB3165-034-P1-K2-C12 Method BLASTX NCBI GI g1363479 BLAST score 362 E value 1.0e-34 Match length 98 % identity 73 photosystem I protein psaL - cucumber NCBI Description >gi 801740 dbj BAA09047_ (D50456) PsaL [Cucumis sativus] Seq. No. 222615 LIB3165-034-P1-K2-C3 Seq. ID BLASTX Method NCBI GI g3269292 BLAST score 291 E value 2.0e-26 Match length 76 % identity 67 NCBI Description (AL030978) putative protein [Arabidopsis thaliana] Seq. No. 222616 LIB3165-034-P1-K2-C5 Seq. ID Method BLASTX NCBI GI g166867 BLAST score 258 E value 1.0e-22 Match length 82 % identity 63 NCBI Description (J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. ID LIB3165-034-P1-K2-C7

222617

BLASTX Method NCBI GI g498038 BLAST score 451 E value 5.0e-45 Match length 121 % identity 65

Seq. No.

31519



NCBI Description (L33792) lipid transfer protein [Senecio odorus]

222618 Seq. No.

LIB3165-034-P1-K2-C9 Seq. ID

Method BLASTX g1352821 NCBI GI BLAST score 548 2.0e-56 E value 115 Match length 95 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222619

LIB3165-034-P1-K2-D1 Seq. ID

Method BLASTX NCBI GI q4249385 385 BLAST score E value 3.0e - 37116 Match length 63 % identity

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

222620 Seq. No.

Seq. ID LIB3165-034-P1-K2-D11

Method BLASTX NCBI GI g1168411 BLAST score 442 4.0e-44 E value 109 Match length 83 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 222621

LIB3165-034-P1-K2-D12 Seq. ID

Method BLASTX q1352821 NCBI GI BLAST score 682 E value 5.0e-72139 Match length % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC $\overline{4.1.1.39}$) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222622 Seq. No.

Seq. ID LIB3165-034-P1-K2-D5

Method BLASTX NCBI GI g1352821 BLAST score 491 E value 9.0e-50 Match length 96

31520



% identity 96
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222623
Seq. ID 222623
LIB3165-034-P1-K2-D7

Seq. ID LIB3165-034
Method BLASTX
NCBI GI g430947
BLAST score 318
E value 1.0e-29
Match length 83
% identity 80

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

 Seq. No.
 222624

 Seq. ID
 LIB3165-034-P1-K2-D9

 Method
 BLASTX

 NCBT CT
 21352821

NCBI GI g1352821 BLAST score 709 E value 3.0e-75 Match length 139 % identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222625

Seq. ID LIB3165-034-P1-K2-E1

Method BLASTX
NCBI GI g4490332
BLAST score 162
E value 4.0e-11
Match length 67
% identity 54

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 222626

Seq. ID LIB3165-034-P1-K2-E10

Method BLASTX
NCBI GI g3335355
BLAST score 268
E value 6.0e-24
Match length 66
% identity 21

NCBI Description (AC004512) Match to polyubiquitin DNA gb_L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this

region. [Arabi

Seq. No. 222627



LIB3165-034-P1-K2-E11 Seq. ID Method BLASTX g1168411 NCBI GI BLAST score 271 E value 5.0e-24 76 Match length 75 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR Seq. No. 222628 Seq. ID LIB3165-034-P1-K2-E12 Method BLASTX NCBI GI g228403 BLAST score 522 3.0e-53 E value Match length 120 85 % identity NCBI Description glycolate oxidase [Lens culinaris] 222629 Seq. No. LIB3165-034-P1-K2-E2 Seq. ID Method BLASTX NCBI GI g2407279 BLAST score 451 3.0e-45E value Match length 101 % identity 84 NCBI Description (AF017362) aldolase [Oryza sativa] Seq. No. 222630 LIB3165-034-P1-K2-E3 Seq. ID Method BLASTX NCBI GI g3914002 BLAST score 646 E value 8.0e-68 Match length 137 % identity 91 NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279 (AF033862) Lon protease [Arabidopsis thaliana] Seq. No. 222631 Seq. ID LIB3165-034-P1-K2-E5 Method BLASTX NCBI GI g2129921 BLAST score 178 E value 6.0e-13 Match length 36 % identity NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi 758694 (U12573) putative [Catharanthus roseus] Seq. No. 222632

Seq. ID LIB3165-034-P1-K2-E6

Method BLASTX
NCBI GI g2739046
BLAST score 167
E value 1.0e-11

% identity



```
90
Match length
                   38
% identity
                   (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                   [Glycine max]
                  222633
Seq. No.
                  LIB3165-034-P1-K2-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1483563
BLAST score
                  328
                  9.0e-31
E value
                  97
Match length
                   70
% identity
                  (X99825) leucine aminopeptidase [Petroselinum crispum]
NCBI Description
Seq. No.
                  222634
                  LIB3165-034-P1-K2-E8
Seq. ID
Method
                  BLASTX
                  q4033838
NCBI GI
BLAST score
                   345
E value
                   1.0e-32
Match length
                  123
                   59
% identity
                  (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                   222635
Seq. No.
                  LIB3165-034-P1-K2-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2499525
BLAST score
                   246
E value
                   5.0e-21
Match length
                   122
                   46
% identity
                  INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER
NCBI Description
                   (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153)
                   intestinal sodium/dicarboxylate cotransporter [Rattus
                   norvegicus]
                   222636
Seq. No.
Seq. ID
                   LIB3165-034-P1-K2-F1
Method
                   BLASTX
                   g4455225
NCBI GI
BLAST score
                   399
                   7.0e - 39
E value
                   93
Match length
% identity
                   73
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   222637
Seq. No.
                   LIB3165-034-P1-K2-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3603401
BLAST score
                   300
E value
                   2.0e-27
Match length
                   74
```

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]



Seq. ID LIB3165-034-P1-K2-F12

Method BLASTX
NCBI GI g430947
BLAST score 413
E value 1.0e-40
Match length 103
% identity 81

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 222639

Seq. ID LIB3165-034-P1-K2-F2

Method BLASTX
NCBI GI g3121825
BLAST score 365
E value 7.0e-35
Match length 117
% identity 69

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 222640

Seq. ID LIB3165-034-P1-K2-F3

Method BLASTX
NCBI GI g1352821
BLAST score 543
E value 9.0e-56
Match length 105
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222641

Seq. ID LIB3165-034-P1-K2-F5

Method BLASTX
NCBI GI g100616
BLAST score 286
E value 1.0e-25
Match length 64
% identity 86

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 222642

Seq. ID LIB3165-034-P1-K2-F6

Method BLASTX NCBI GI g289920 BLAST score 605

% identity

43



```
E value
                  5.0e-63
Match length
                  124
                  92
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  222643
                  LIB3165-034-P1-K2-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g430947
BLAST score
                  320
                  9.0e-30
E value
Match length
                  83
                  80
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  222644
Seq. No.
                  LIB3165-034-P1-K2-G10
Seq. ID
                  BLASTX
Method
                  q1619602
NCBI GI
                  242
BLAST score
                  2.0e-20
E value
Match length
                  73
                  58
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  222645
                  LIB3165-034-P1-K2-G12
Seq. ID
Method
                  BLASTX
                  q2791423
NCBI GI
                  215
BLAST score
                  3.0e-17
E value
Match length
                  73
                  55
% identity
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
                  222646
Seq. No.
                  LIB3165-034-P1-K2-G3
Seq. ID
                  BLASTX
Method
                  g113217
NCBI GI
                  267
BLAST score
                   1.0e-23
E value
                  50
Match length
                  100
% identity
NCBI Description ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot
                   222647
Seq. No.
                  LIB3165-034-P1-K2-G4
Seq. ID
                  BLASTX
Method
                   g2979553
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
                   87
Match length
```

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. ID

222653

LIB3165-034-P1-K2-H2



```
222648
Seq. No.
                   LIB3165-034-P1-K2-G7
Seq. ID
Method
                   BLASTX
                   q3928543
NCBI GI
                   376
BLAST score
                   3.0e-36
E value
Match length
                   96
                   70
% identity
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   222649
Seq. No.
                   LIB3165-034-P1-K2-G8
Seq. ID
Method
                   BLASTX
                   g2979553
NCBI GI
BLAST score
                   194
                   7.0e-15
E value
Match length
                   88
                   42
% identity
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   222650
Seq. No.
                   LIB3165-034-P1-K2-H1
Seq. ID
                   BLASTX
Method
                   g4324714
NCBI GI
                   372
BLAST score
                   6.0e - 36
E value
Match length
                   89
                   83
% identity
                  (AF110771) ammonium transporter [Arabidopsis thaliana]
NCBI Description
                   222651
Seq. No.
                   LIB3165-034-P1-K2-H11
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
                   529
BLAST score
E value
                   4.0e-54
Match length
                   107
                   96
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   222652
Seq. No.
Seq. ID
                   LIB3165-034-P1-K2-H12
Method
                   BLASTX
NCBI GI
                   q1181599
                   397
BLAST score
                   7.0e - 39
E value
Match length
                   110
% identity
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
```



```
Method
                  BLASTX
NCBI GI
                  g4262250
                  434
BLAST score
                  5.0e-43
E value
Match length
                  124
                  75
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                  222654
Seq. No.
                  LIB3165-034-P1-K2-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4406530
                  241
BLAST score
                  5.0e-23
E value
Match length
                  104
% identity
                  62
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  222655
Seq. No.
                  LIB3165-034-P1-K2-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g289920
                  405
BLAST score
                  1.0e-39
E value
Match length
                  89
                  84
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  222656
Seq. No.
                  LIB3165-034-P1-K2-H6
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
                   355
BLAST score
                  5.0e-34
E value
                  68
Match length
% identity
                  99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   222657
                  LIB3165-034-P1-K2-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                   402
                   2.0e-39
                  81
                   95
% identity
```

E value Match length

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



Seq. No. 222658 Seq. ID LIB3165-034-P1-K3-A1 Method BLASTX NCBI GI q1350944 BLAST score 391 6.0e-38 E value 80 Match length % identity 96 NCBI Description 40S RIBOSOMAL PROTEIN S17 222659 Seq. No. LIB3165-034-P1-K3-A11 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 657 4.0e-69 E value Match length 122 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 222660 Seq. No. Seq. ID LIB3165-034-P1-K3-A3 BLASTX Method NCBI GI q1706261 BLAST score 438 E value 2.0e-43 Match length 87 90 % identity NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129 pir S59598 cysteine proteinase 2 precursor - maize >gi 644490 dbj BAA08245 (D45403) cysteine proteinase [Zea mays] 222661 Seq. No. Seq. ID LIB3165-034-P1-K3-A4 Method BLASTX NCBI GI g68200 BLAST score 607 3.0e-63 E value Match length 146 84 % identity NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea] 222662 Seq. No. LIB3165-034-P1-K3-A6 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g1781348
BLAST score 738
E value 1.0e-78
Match length 151
% identity 92



```
NCBI Description
                  (Y10380) homologous to plastidic aldolases [Solanum
                  tuberosum]
Seq. No.
                  222663
                  LIB3165-034-P1-K3-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1354515
BLAST score
                  243
                  1.0e-20
E value
Match length
                  122
% identity
                  48
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
Seq. No.
                  222664
Seq. ID
                  LIB3165-034-P1-K3-A8
Method
                  BLASTX
NCBI GI
                  q100200
                  290
BLAST score
                  9.0e-54
E value
                  175
Match length
                  55
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  222665
                  LIB3165-034-P1-K3-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q121953
BLAST score
                  181
                  3.0e-13
E value
Match length
                   42
                  86
% identity
                  HISTONE H1 >gi 81905_pir__S00033 histone H1.b - garden pea
NCBI Description
                  >gi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263)
                   [Pisum sativum]
                   222666
Seq. No.
                  LIB3165-034-P1-K3-B10
Seq. ID
Method
                  BLASTX
                  g81857
NCBI GI
BLAST score
                   215
                   2.0e-17
E value
Match length
                   42
% identity
                   90
NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa
                   (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally
                   controlled tumor protein [Medicago sativa]
                   222667
Seq. No.
                   LIB3165-034-P1-K3-B11
Seq. ID
Method
                   BLASTX
                   q1076627
NCBI GI
BLAST score
                   514
E value
                   3.0e-52
Match length
                   132
```

NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco

77

% identity



>gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
[Nicotiana tabacum]

 Seq. No.
 222668

 Seq. ID
 LIB3165-034-P1-K3-B3

 Method
 BLASTX

 NCBI GI
 g1173345

 BLAST score
 228

E value 5.0e-19
Match length 82
% identity 59

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED (1,7) P2ASE)

>gi_1076403_pir__S51838_sedoheptulose-1,7-biphosphatase - Arabidopsis_thaliana >gi_786466_bbs_159034_(S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis_thaliana, C24, Peptide Chloroplast, 393_aa]

[Arabidopsis thaliana]

Seq. No. 222669

Seq. ID LIB3165-034-P1-K3-B5

Method BLASTX
NCBI GI g129867
BLAST score 582
E value 3.0e-60
Match length 110
% identity 100

NCBI Description CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)

>gi_2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex

subunit IV [Nicotiana tabacum]

Seq. No. 222670

Seq. ID LIB3165-034-P1-K3-B6

Method BLASTX
NCBI GI g2833388
BLAST score 637
E value 1.0e-66
Match length 150
% identity 79

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi 629660 pir S43341 ADPglucose--starch

glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial

glycogen) synthase [Manihot esculenta]

Seq. No. 222671

Seq. ID LIB3165-034-P1-K3-B8

Method BLASTX
NCBI GI g131167
BLAST score 192
E value 6.0e-15
Match length 87
% identity 54

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi 100292 pir S18348 photosystem I chain II precursor - wood tobacco >gi 19748 emb CAA42623 (X60008) PSI-D2

222677



[Nicotiana sylvestris]

```
222672
Seq. No.
                  LIB3165-034-P1-K3-C10
Seq. ID
Method
                  BLASTX
                  g2865623
NCBI GI
                  581
BLAST score
                  4.0e-60
E value
                  132
Match length
                  84
% identity
                  (AF045286)
NCBI Description
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                  222673
Seq. No.
                  LIB3165-034-P1-K3-C11
Seq. ID
                  BLASTX
Method
                  q20729
NCBI GI
                  443
BLAST score
                  5.0e-44
E value
Match length
                  118
% identity
                  76
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   222674
Seq. No.
                  LIB3165-034-P1-K3-C12
Seq. ID
Method
                   BLASTX
                   q1181599
NCBI GI
                   454
BLAST score
                   3.0e-45
E value
Match length
                   119
% identity
                   75
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
                   222675
Seq. No.
                   LIB3165-034-P1-K3-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3269292
BLAST score
                   289
                   5.0e-26
E value
Match length
                   74
% identity
                   69
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   222676
Seq. No.
                   LIB3165-034-P1-K3-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q133867
BLAST score
                   584
                   2.0e-60
E value
Match length
                   128
                   87
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi_22470_emb_CAA39438 (X55967)
                   ribosomal protein S11 [Zea mays]
```

31531



Seq. ID LIB3165-034-P1-K3-C9
Method BLASTX
NCBI GI g1352821
BLAST score 599
E value 3.0e-62
Match length 118
% identity 93
NCBI Description BIBULOSE BISPHOSPHAT

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222678

Seq. ID LIB3165-034-P1-K3-D1

Method BLASTX
NCBI GI 94249385
BLAST score 407
E value 9.0e-40
Match length 125
% identity 62

Seq. No.

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 222679

Seq. ID LIB3165-034-P1-K3-D11

Method BLASTX
NCBI GI g1168411
BLAST score 577
E value 1.0e-59
Match length 141
% identity 83

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 222680

Seq. ID LIB3165-034-P1-K3-D12

Method BLASTX
NCBI GI g1352821
BLAST score 746
E value 2.0e-79
Match length 147
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222681

Seq. ID LIB3165-034-P1-K3-D2

Method BLASTX
NCBI GI g3193285
BLAST score 356
E value 9.0e-34
Match length 97
% identity 67

NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]



Seq. ID LIB3165-034-P1-K3-D4

Method BLASTX
NCBI GI g3121825
BLAST score 378
E value 2.0e-36
Match length 117
% identity 72

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 222683

Seq. ID LIB3165-034-P1-K3-D5

Method BLASTX
NCBI GI g1352821
BLAST score 667
E value 3.0e-70
Match length 122
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222684

Seq. ID LIB3165-034-P1-K3-D6

Method BLASTX
NCBI GI g1168408
BLAST score 251
E value 2.0e-21
Match length 56
% identity 91

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 222685

Seq. ID LIB3165-034-P1-K3-D7

Method BLASTX
NCBI GI g430947
BLAST score 486
E value 5.0e-49
Match length 120
% identity 81

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 222686

Seq. ID LIB3165-034-P1-K3-D9

Method BLASTX
NCBI GI g1352821
BLAST score 738
E value 1.0e-78
Match length 139

BLAST score

% identity

E value Match length 545 5.0e-56

119 87



```
% identity
                  96
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222687
Seq. ID
                  LIB3165-034-P1-K3-E1
Method
                  BLASTX
NCBI GI
                  g4490332
BLAST score
                  198
E value
                  3.0e-15
Match length
                  78
                  55
% identity
NCBI Description
                 (AL035656) putative protein [Arabidopsis thaliana]
                  222688
Seq. No.
Seq. ID
                  LIB3165-034-P1-K3-E10
Method
                  BLASTX
NCBI GI
                  q1800281
BLAST score
                  680
                  9.0e-72
E value
Match length
                  136
                  22
% identity
NCBI Description
                 (U82086) polyubiquitin [Fragaria x ananassa]
Seq. No.
                  222689
Seq. ID
                  LIB3165-034-P1-K3-E11
Method
                  BLASTX
NCBI GI
                  g68200
BLAST score
                  421
E value
                  2.0e-41
Match length
                  108
                  80
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
                  222690
Seq. No.
                  LIB3165-034-P1-K3-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g228403
BLAST score
                  618
E value
                  2.0e-64
Match length
                  135
                  88
% identity
NCBI Description glycolate oxidase [Lens culinaris]
                  222691
Seq. No.
                  LIB3165-034-P1-K3-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1781348
```

31534



NCBI Description (Y10380) homologous to plastidic aldolases [Solanum tuberosum] 222692 Seq. No. LIB3165-034-P1-K3-E3 Seq. ID Method BLASTX NCBI GI q3914002 BLAST score 695 2.0e-73 E value 147 Match length 91 % identity NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279 (AF033862) Lon protease [Arabidopsis thaliana] 222693 Seq. No. Seq. ID LIB3165-034-P1-K3-E5 Method BLASTX NCBI GI q2129921 BLAST score 191 E value 2.0e-14 Match length 36 100 % identity NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi 758694 (U12573) putative [Catharanthus roseus] Seq. No. 222694 LIB3165-034-P1-K3-E6 Seq. ID Method BLASTX NCBI GI g2739046 BLAST score 195 7.0e-15 E value Match length 102 38 % identity (AF024652) polyphosphoinositide binding protein Ssh2p NCBI Description [Glycine max] 222695 Seq. No. Seq. ID LIB3165-034-P1-K3-E7 Method BLASTX NCBI GI g1483563 BLAST score 563 E value 5.0e-58 Match length 146 % identity 77 (X99825) leucine aminopeptidase [Petroselinum crispum] NCBI Description 222696 Seq. No. Seq. ID LIB3165-034-P1-K3-E8

Method BLASTX g4033838 NCBI GI BLAST score 386 E value 3.0e - 37Match length 134 % identity

(Y18550) sigma-like factor [Arabidopsis thaliana] NCBI Description

222697 Seq. No.

31535



```
LIB3165-034-P1-K3-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2499525
BLAST score
                  287
                  1.0e-25
E value
Match length
                  147
                  44
% identity
                  INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER
NCBI Description
                  (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi 1663535 (U51153)
                  intestinal sodium/dicarboxylate cotransporter [Rattus
                  norvegicus]
                  222698
Seq. No.
                  LIB3165-034-P1-K3-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455225
BLAST score
                  358
E value
                  5.0e - 34
Match length
                  88
% identity
                  70
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  222699
                  LIB3165-034-P1-K3-F10
Seq. ID
Method
                  BLASTX
                  g3603401
NCBI GI
BLAST score
                  141
E value
                  4.0e-17
Match length
                  66
                  61
% identity
                 (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
NCBI Description
                  222700
Seq. No.
                  LIB3165-034-P1-K3-F12
Seq. ID
                  BLASTX
Method
                   q430947
NCBI GI
BLAST score
                   458
E value
                   9.0e-46
                  114
Match length
                   81
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   222701
Seq. No.
                  LIB3165-034-P1-K3-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3121825
BLAST score
                   360
E value
                   3.0e - 34
Match length
                   114
                   71
% identity
```

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 222702

Seq. ID LIB3165-034-P1-K3-F3



Method BLASTX
NCBI GI g1352821
BLAST score 655
E value 8.0e-69
Match length 122
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222703

Seq. ID LIB3165-034-P1-K3-F5

Method BLASTX
NCBI GI g100616
BLAST score 270
E value 1.0e-23
Match length 60
% identity 87

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 222704

Seq. ID LIB3165-034-P1-K3-F6

Method BLASTX
NCBI GI g289920
BLAST score 540
E value 5.0e-69
Match length 139
% identity 90

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222705

Seq. ID LIB3165-034-P1-K3-F7

Method BLASTX
NCBI GI g289920
BLAST score 718
E value 3.0e-76
Match length 138
% identity 96

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222706

Seq. ID LIB3165-034-P1-K3-G1

Method BLASTX
NCBI GI g430947
BLAST score 455
E value 2.0e-45
Match length 113
% identity 81

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

% identity

NCBI Description



[Arabidopsis thaliana]

```
222707
Seq. No.
                  LIB3165-034-P1-K3-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  257
                  3.0e-22
E value
                  78
Match length
% identity
                  56
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                  222708
Seq. No.
                  LIB3165-034-P1-K3-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2791423
BLAST score
                  227
E value
                  1.0e-18
Match length
                  81
                  53
% identity
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
                  222709
Seq. No.
                  LIB3165-034-P1-K3-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703108
BLAST score
                  554
E value
                  5.0e-57
                  103
Match length
                  99
% identity
NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
                  thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
                  thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
Seq. No.
                  222710
                  LIB3165-034-P1-K3-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2979553
BLAST score
                  201
E value
                  1.0e-15
Match length
                  90
% identity
                  43
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  222711
Seq. ID
                  LIB3165-034-P1-K3-G7
Method
                  BLASTX
NCBI GI
                  q3928543
BLAST score
                  573
E value
                  3.0e-59
Match length
                  136
```

thaliana]

(AB016819) UDP-glucose glucosyltransferase [Arabidopsis



LIB3165-034-P1-K3-G8 Seq. ID

Method BLASTX q2979553 NCBI GI BLAST score 223 E value 3.0e-18 Match length 110 % identity 41

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 222713

Seq. ID LIB3165-034-P1-K3-G9

Method BLASTX NCBI GI g131384 BLAST score 224 E value 1.0e-18 Match length 68 % identity 69

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi 344004 dbj BAA02554 (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi 226937 prf 1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 222714

LIB3165-034-P1-K3-H1 Seq. ID

Method BLASTX NCBI GI q4324714 BLAST score 437 2.0e-43 E value 96 Match length 89 % identity

NCBI Description (AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No. 222715

LIB3165-034-P1-K3-H11 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 569 9.0e-59 E value Match length 109 99 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222716

LIB3165-034-P1-K3-H2 Seq. ID

Method BLASTX NCBI GI g4262250 BLAST score 445



E value 3.0e-44 Match length 126 % identity 75

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 222717

Seq. ID LIB3165-034-P1-K3-H3

Method BLASTX
NCBI GI g3914605
BLAST score 392
E value 5.0e-38
Match length 130
% identity 62

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 541930_pir__S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi 415852 emb CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 222718

Seq. ID LIB3165-034-P1-K3-H4

Method BLASTX
NCBI GI g289920
BLAST score 184
E value 2.0e-21
Match length 73
% identity 66

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222719

Seq. ID LIB3165-034-P1-K3-H6

Method BLASTX
NCBI GI g1352821
BLAST score 670
E value 1.0e-70
Match length 130
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222720

Seq. ID LIB3165-034-P1-K3-H8

Method BLASTX
NCBI GI g1352821
BLAST score 403
E value 3.0e-39
Match length 118
% identity 78

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

NCBI GI

BLAST score

q169039

617



ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
Seq. No.
                  222721
                  LIB3165-034-P1-K4-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133825
BLAST score
                  400
                  5.0e-39
E value
Match length
                  108
% identity
                  71
NCBI Description
                  40S RIBOSOMAL PROTEIN S17 >gi 71199 pir R4HU17 ribosomal
                  protein S17 - human >gi 337501 (M13932) ribosomal protein
                  S17 [Homo sapiens] >gi 337503 (M18000) S17 ribosomal
                  protein [Homo sapiens] >gi_4506693_ref_NP_001012.1_pRPS17_
                  ribosomal protein S17
Seq. No.
                  222722
Seq. ID
                  LIB3165-034-P1-K4-A11
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  503
E value
                  4.0e-51
Match length
                  97
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222723
                  LIB3165-034-P1-K4-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g67656
BLAST score
                  191
                  5.0e-16
E value
Match length
                  52
% identity
                  70
NCBI Description aleurain (EC 3.4.22.-) precursor - barley
Seq. No.
                  222724
Seq. ID
                  LIB3165-034-P1-K4-A4
Method
                  BLASTX
NCBI GI
                  g68200
BLAST score
                  510
E value
                  5.0e-52
Match length
                  124
% identity
                  84
NCBI Description
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                  chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
                  222725
Seq. No.
Seq. ID
                  LIB3165-034-P1-K4-A6
Method
                  BLASTX
```



```
E value
                  2.0e-64
Match length
                  126
% identity
                   92
                  (M97477) aldolase [Pisum sativum]
NCBI Description
                  222726
Seq. No.
                  LIB3165-034-P1-K4-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                   255
                  5.0e-22
E value
Match length
                  125
% identity
                   49
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                   222727
Seq. No.
Seq. ID
                  LIB3165-034-P1-K4-A8
Method
                  BLASTX
NCBI GI
                  q100200
BLAST score
                   603
E value
                   7.0e-63
Match length
                   127
% identity
                   68
                 chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
                   222728
Seq. No.
Seq. ID
                  LIB3165-034-P1-K4-A9
Method
                  BLASTX
                   q3158474
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
Match length
                   53
                   70
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                   222729
Seq. No.
Seq. ID
                   LIB3165-034-P1-K4-B1
Method
                   BLASTX
NCBI GI
                   q16314
BLAST score
                   147
                   2.0e-09
E value
Match length
                   32
% identity
NCBI Description (X62456) histone H1-1 [Arabidopsis thaliana]
                   222730
Seq. No.
Seq. ID
                   LIB3165-034-P1-K4-B10
Method
                   BLASTX
                   g81857
NCBI GI
                   215
```

BLAST score E value 2.0e-17 Match length 42 % identity 90

IgE-dependent histamine-releasing factor homolog - alfalfa NCBI Description (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally

controlled tumor protein [Medicago sativa]

E value

Match length

% identity

4.0e-58

126 81



```
222731
Seq. No.
Seq. ID
                  LIB3165-034-P1-K4-B11
Method
                  BLASTX
NCBI GI
                  q2653446
BLAST score
                  380
E value
                  1.0e-36
Match length
                  97
% identity
NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]
Seq. No.
                  222732
Seq. ID
                  LIB3165-034-P1-K4-B2
Method
                  BLASTX
NCBI GI
                  q68200
BLAST score
                  248
                  3.0e-21
E value
Match length
                  88
                  64
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                  222733
Seq. No.
                  LIB3165-034-P1-K4-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914940
BLAST score
                  335
                  2.0e-31
E value
Match length
                  116
% identity
                  63
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                   >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                   [Spinacia oleracea]
Seq. No.
                   222734
Seq. ID
                  LIB3165-034-P1-K4-B5
Method
                  BLASTX
NCBI GI
                  q82437
BLAST score
                  477
E value
                   4.0e-48
Match length
                  88
% identity
                   100
NCBI Description
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K
                  protein short form - barley chloroplast (fragment)
                  >gi 1617032 emb CAA32269 (X14107) petD [Hordeum vulgare]
Seq. No.
                   222735
Seq. ID
                  LIB3165-034-P1-K4-B6
                  BLASTX
Method
NCBI GI
                  g228210
BLAST score
                  563
```

NCBI Description granule-bound starch synthase [Solanum tuberosum]



72

% identity

```
222736
Seq. No.
                   LIB3165-034-P1-K4-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g131167
                   374
BLAST score
                   5.0e-36
E value
                   124
Match length
                   66
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_100292_pir__S18348 photosystem I chain II precursor -
                   wood tobacco >gi 19748 emb CAA42623 (X60008) PSI-D2
                   [Nicotiana sylvestris]
                   222737
Seq. No.
                   LIB3165-034-P1-K4-B9
Seq. ID
Method
                   BLASTX
                   q3738316
NCBI GI
BLAST score
                   319
                   1.0e-29
E value
Match length
                   82
                   73
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                   222738
Seq. No.
                   LIB3165-034-P1-K4-C10
Seq. ID
Method
                   BLASTX
                   q2865623
NCBI GI
BLAST score
                   461
                   3.0e-46
E value
Match length
                   106
                   84
 % identity
                   (AF045286)
NCBI Description
                   GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                   222739
 Seq. No.
 Seq. ID
                   LIB3165-034-P1-K4-C11
Method
                   BLASTX
                   q20729
 NCBI GI
 BLAST score
                   323
                   5.0e-30
 E value
 Match length
                   94
 % identity
                   70
 NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
 Seq. No.
                   222740
 Seq. ID
                   LIB3165-034-P1-K4-C12
                   BLASTX
 Method
 NCBI GI
                   q1181599
 BLAST score
                   374
 E value
                   5.0e-36
. Match length
                   103
```

NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]



Seq. No. 222741 LIB3165-034-P1-K4-C3 Seq. ID Method BLASTX g3269292 NCBI GI BLAST score 289 5.0e-26 E value Match length 74 % identity 69 (AL030978) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 222742 LIB3165-034-P1-K4-C5 Seq. ID Method BLASTX NCBI GI q133867 BLAST score 451 5.0e-45 E value 104 Match length % identity 84 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal NCBI Description protein S11 - maize >gi 22470 emb CAA39438 (X55967) ribosomal protein S11 [Zea mays] Seq. No. 222743 LIB3165-034-P1-K4-C7 Seq. ID Method BLASTX NCBI GI q498038 BLAST score 454 E value 2.0e-45 Match length 121 % identity 65 NCBI Description (L33792) lipid transfer protein [Senecio odorus] 222744 Seq. No. LIB3165-034-P1-K4-C9 Seq. ID Method BLASTX g1352821 NCBI GI 495 BLAST score E value 3.0e-5096 Match length 97 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222745 Seq. No.

Seq. ID LIB3165-034-P1-K4-D1

BLASTX Method g4249385 NCBI GI BLAST score 367 E value 3.0e - 35Match length 102 % identity

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

222746 Seq. No.

31545



Seq. ID LIB3165-034-P1-K4-D10

BLASTX Method NCBI GI q1781348 BLAST score 139 E value 5.0e-09 35 Match length 77 % identity

(Y10380) homologous to plastidic aldolases [Solanum NCBI Description

tuberosum]

222747 Seq. No.

LIB3165-034-P1-K4-D11 Seq. ID

Method BLASTX NCBI GI q68200 476 BLAST score 5.0e-48 E value 117 Match length 84 % identity

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,

chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

222748 Seq. No.

LIB3165-034-P1-K4-D12 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 640 3.0e-67 E value 125 Match length 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222749

LIB3165-034-P1-K4-D2 Seq. ID

Method BLASTX NCBI GI q3193285 BLAST score 266 E value 3.0e-23 Match length 74 % identity 65

NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No. 222750

Seq. ID LIB3165-034-P1-K4-D4

Method BLASTX NCBI GI g3121825 BLAST score 262 E value 7.0e-23 Match length 94 % identity 66

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)

bas1 protein [Spinacia oleracea]

Method

NCBI GI

BLASTX

g100490

```
Seq. No.
                  222751
                  LIB3165-034-P1-K4-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  523
E value
                  2.0e-53
Match length
                  99
                  100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222752
Seq. ID
                  LIB3165-034-P1-K4-D6
Method
                  BLASTX
NCBI GI
                  q1168408
BLAST score
                  145
E value
                  4.0e-09
Match length
                  31
% identity
                  94
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
                  >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                  222753
                  LIB3165-034-P1-K4-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g430947
BLAST score
                  411
E value
                  2.0e-40
Match length
                  101
% identity
                  81
NCBI Description
                  (U01103) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
                  222754
Seq. No.
Seq. ID
                  LIB3165-034-P1-K4-D9
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  674
E value
                  3.0e-71
Match length
                  126
% identity
                  97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222755
Seq. ID
                  LIB3165-034-P1-K4-E10
```

31547



BLAST score 573 2.0e-59 E value Match length 115 28 % identity NCBI Description

polyubiquitin - garden snapdragon (fragment)

>gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum

majus]

222756 Seq. No.

LIB3165-034-P1-K4-E11 Seq. ID

Method BLASTX NCBI GI g68200 BLAST score 318 2.0e-29 E value Match length 86 78 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi 22633 emb CAA47293 (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 222757

Seq. ID LIB3165-034-P1-K4-E12

Method BLASTX NCBI GI g228403 BLAST score 498 E value 1.0e-50 Match length 112 % identity 86

NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 222758

Seq. ID LIB3165-034-P1-K4-E2

Method BLASTX g1781348 NCBI GI BLAST score 564 E value 3.0e-58Match length 119 % identity 89

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 222759

LIB3165-034-P1-K4-E3 Seq. ID

Method BLASTX NCBI GI q3914002 BLAST score 594 E value 8.0e-62 Match length 123 % identity 92

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >qi 2935279

(AF033862) Lon protease [Arabidopsis thaliana]

Seq. No. 222760

Seq. ID LIB3165-034-P1-K4-E6

Method BLASTX NCBI GI g2739046 BLAST score 150



E value 9.0e-10 Match length 82 % identity 38

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 222761

Seq. ID LIB3165-034-P1-K4-E7

Method BLASTX NCBI GI g1483563 BLAST score 406 E value 1.0e-41 Match length 116 % identity 78

NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No. 222762

LIB3165-034-P1-K4-E8 Seq. ID

BLASTX Method NCBI GI g4033838 BLAST score 337 E value 1.0e-31 Match length 111

63 % identity

NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No. 222763

LIB3165-034-P1-K4-E9 Seq. ID

Method BLASTX NCBI GI g2499525 BLAST score 246 E value 5.0e-21Match length 122 % identity 46

NCBI Description INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER

(NA(+)/DICARBOXYLATE COTRANSPORTER) >gi 1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus

norvegicus]

Seq. No. 222764

Seq. ID LIB3165-034-P1-K4-F1

Method BLASTX NCBI GI q4455225 BLAST score 346 E value 1.0e-32 Match length 83 % identity 73

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 222765

Seq. ID LIB3165-034-P1-K4-F10

Method BLASTX NCBI GI q3603401 BLAST score 300 E value 2.0e-27 Match length 74 % identity 69

```
NCBI Description
                  (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                  222766
Seq. ID
                  LIB3165-034-P1-K4-F12
Method
                  BLASTX
NCBI GI
                  g430947
BLAST score
                  401
                  4.0e-39
E value
                  99
Match length
% identity
                  81
NCBI Description
                  (U01103) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  222767
Seq. ID
                  LIB3165-034-P1-K4-F2
Method
                  BLASTX
NCBI GI
                  g3121825
BLAST score
                  306
                  5.0e-28
E value
Match length
                  101
                  69
% identity
NCBI Description
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
                  ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)
                  bas1 protein [Spinacia oleracea]
Seq. No.
                  222768
                  LIB3165-034-P1-K4-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  557
                  2.0e-57
E value
Match length
                  111
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

Seq. ID LIB3165-034-P1-K4-F5

Method BLASTX
NCBI GI g100616
BLAST score 222
E value 4.0e-18
Match length 50
% identity 88

NCBI Description ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 222770

Seq. ID LIB3165-034-P1-K4-F6

Method BLASTX NCBI GI g289920

```
BLAST score
                  566
E value
                  2.0e-58
Match length
                  115
                  92
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  222771
Seq. No.
                  LIB3165-034-P1-K4-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  619
                  9.0e-65
E value
                  115
Match length
% identity
                  99
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  222772
Seq. No.
                  LIB3165-034-P1-K4-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g430947
BLAST score
                  403
                  2.0e-39
E value
                  99
Match length
                  81
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  222773
                  LIB3165-034-P1-K4-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  207
                  2.0e-16
E value
Match length
                  60
% identity
                  62
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                  222774
Seq. No.
                  LIB3165-034-P1-K4-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791423
BLAST score
                  189
E value
                  2.0e-14
Match length
                  60
                  57
% identity
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                  222775
                  LIB3165-034-P1-K4-G3
Seq. ID
Method
                  BLASTX
```

NCBI GI q4139264 BLAST score 432 8.0e-43 E value Match length 81 % identity 100



```
NCBI Description
                  (AF111812) actin [Brassica napus]
                  222776
Seq. No.
                  LIB3165-034-P1-K4-G4
Seq. ID
Method
                  BLASTX
                  g2979553
NCBI GI
BLAST score
                  173
                  2.0e-12
E value
Match length
                  76
                  45
% identity
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  222777
                  LIB3165-034-P1-K4-G7
Seq. ID
                  BLASTX
Method
                  q3928543
NCBI GI
BLAST score
                  459
                  6.0e-46
E value
Match length
                  114
% identity
                  71
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  222778
                  LIB3165-034-P1-K4-G8
Seq. ID
                  BLASTX
Method
                  g2979553
NCBI GI
BLAST score
                  186
E value
                  6.0e-14
Match length
                  82
                  44
% identity
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  222779
                  LIB3165-034-P1-K4-H1
Seq. ID
                  BLASTX
Method
                  g4324714
NCBI GI
                  499
BLAST score
E value
                  1.0e-50
Match length
                  117
                  84
% identity
                  (AF110771) ammonium transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   222780
                  LIB3165-034-P1-K4-H11
Seq. ID
                  BLASTX
Method
                   q1352821
NCBI GI
BLAST score
                   468
                   5.0e-47
E value
Match length
                   91
                   99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
```

ribulose bisphosphate carboxylase [Gossypium hirsutum]



Seq. No. 222781 LIB3165-034-P1-K4-H12 Seq. ID BLASTX Method

NCBI GI g1181599 490 BLAST score 1.0e-49 E value 126 Match length 76 % identity

(D83007) subunit of photosystem I [Cucumis sativus] NCBI Description

222782 Seq. No.

LIB3165-034-P1-K4-H2 Seq. ID

Method BLASTX NCBI GI g4262250 BLAST score 381 8.0e-37 E value Match length 111 % identity 74

(AC006200) putative aldolase [Arabidopsis thaliana] NCBI Description

222783 Seq. No.

LIB3165-034-P1-K4-H3 Seq. ID

Method BLASTX g4406530 NCBI GI 310 BLAST score 2.0e-28 E value Match length 108 % identity 62

NCBI Description (AF126870) rubisco activase [Vigna radiata]

222784 Seq. No.

LIB3165-034-P1-K4-H6 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 500 E value 9.0e-51 Match length 95 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222785 Seq. No.

LIB3165-034-P1-K4-H8 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 402 E value 3.0e-39 Match length 96 84 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
Seq. No.
                  222786
Seq. ID
                  LIB3165-034-P1-K5-A1
Method
                  BLASTX
NCBI GI
                  q1350944
BLAST score
                  329
                  5.0e-31
E value
Match length
                  69
                  93
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S17
                  222787
Seq. No.
Seq. ID
                  LIB3165-034-P1-K5-A11
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                  522
E value
                  2.0e-53
Match length
                  100
% identity
                  98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >qi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222788
Seq. No.
                  LIB3165-034-P1-K5-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168411
BLAST score
                  504
E value
                  3.0e-51
Match length
                  122
% identity
                  84
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  222789
                  LIB3165-034-P1-K5-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q169039
BLAST score
                  614
E value
                  4.0e-64
Match length
                  130
                  90
% identity
NCBI Description (M97477) aldolase [Pisum sativum]
                  222790
Seq. No.
                  LIB3165-034-P1-K5-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
                  238
BLAST score
```

E value 4.0e-20 Match length 122 48 % identity

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

222791 Seq. No.

31554

Seq. ID

222796

LIB3165-034-P1-K5-B3



```
LIB3165-034-P1-K5-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  a100200
BLAST score
                  474
E value
                  5.0e-48
                  91
Match length
                  68
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  222792
Seq. No.
                  LIB3165-034-P1-K5-A9
Seq. ID
Method
                  BLASTX
                  g3158474
NCBI GI
BLAST score
                  192
E value
                  1.0e-14
Match length
                  58
                   67
% identity
                 (AF067184) aquaporin 1 [Samanea saman]
NCBI Description
                  222793
Seq. No.
                  LIB3165-034-P1-K5-B10
Seq. ID
                                                            ٠×-
                  BLASTX
Method
NCBI GI
                  q81857
BLAST score
                   211
E value
                   6.0e-17
                  42
Match length
% identity
                   88
                  IgE-dependent histamine-releasing factor homolog - alfalfa
NCBI Description
                   (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally
                  controlled tumor protein [Medicago sativa]
Seq. No.
                   222794
                  LIB3165-034-P1-K5-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2827755
BLAST score
                   370
E value
                   2.0e-35
Match length
                   97
% identity
                   73
                  INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE
NCBI Description
                   PHOSPHOHYDROLASE) (PPASE) >gi 951323 (U31467)
                  pyrophosphatase [Vigna radiata]
                   222795
Seq. No.
Seq. ID
                  LIB3165-034-P1-K5-B2
Method
                  BLASTX
NCBI GI
                   g68200
BLAST score
                   198
E value
                   2.0e-15
Match length
                   75
                   59
% identity
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
```



72

% identity

```
BLASTX
Method
                  g3914940
NCBI GI
                  335
BLAST score
                  2.0e-31
E value
                  116
Match length
                  63
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                  [Spinacia oleracea]
                  222797
Seq. No.
                  LIB3165-034-P1-K5-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82437
BLAST score
                  482
                  1.0e-48
E value
Match length
                  89
                  100
% identity
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K
NCBI Description
                  protein short form - barley chloroplast (fragment)
                  >gi 1617032_emb_CAA32269_ (X14107) petD [Hordeum vulgare]
                  222798
Seq. No.
                  LIB3165-034-P1-K5-B6
Seq. ID
Method
                  BLASTX
                  q228210
NCBI GI
BLAST score
                  572
                  3.0e-59
E value
                  130
Match length
                  81
% identity
NCBI Description granule-bound starch synthase [Solanum tuberosum]
                  222799
Seq. No.
                  LIB3165-034-P1-K5-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131167
BLAST score
                   224
E value
                  2.0e-18
Match length
                  112
                   52
% identity
                 PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_100292_pir__S18348 photosystem I chain II precursor -
                   wood tobacco >gi 19748 emb CAA42623 (X60008) PSI-D2
                   [Nicotiana sylvestris]
Seq. No.
                   222800
                  LIB3165-034-P1-K5-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3738316
BLAST score
                  141
E value
                   5.0e-09
Match length
                   39
```

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. ID

```
Seq. No.
                  222801
Seq. ID
                  LIB3165-034-P1-K5-C10
Method
                  BLASTX
NCBI GI
                  g2865623
BLAST score
                  385
                  2.0e-37
E value
                  90
Match length
                  82
% identity
                  (AF045286)
NCBI Description
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                  222802
Seq. No.
Seq. ID
                  LIB3165-034-P1-K5-C11
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  332
E value
                  4.0e-31
                  99
Match length
                  70
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  222803
Seq. No.
                  LIB3165-034-P1-K5-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363479
BLAST score
                  366
E value
                  5.0e-35
Match length
                  99
                  74
% identity
NCBI Description
                  photosystem I protein psaL - cucumber
                  >gi 801740 dbj BAA09047 (D50456) PsaL [Cucumis sativus]
                  222804
Seq. No.
                  LIB3165-034-P1-K5-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3269292
BLAST score
                  271
                  6.0e-24
E value
Match length
                  72
% identity
                  68
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                  222805
Seq. No.
                  LIB3165-034-P1-K5-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133867
BLAST score
                  469
E value
                  4.0e-47
Match length
                  107
% identity
                  84
NCBI Description
                 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
                  protein S11 - maize >gi_22470_emb_CAA39438 (X55967)
```

31557

ribosomal protein S11 [Zea mays]

LIB3165-034-P1-K5-C7

222806

```
Method
                  BLASTX
NCBI GI
                  g498038
                  356
BLAST score
                  4.0e-34
E value
                  96
Match length
                  64
% identity
NCBI Description (L33792) lipid transfer protein [Senecio odorus]
Seq. No.
                  222807
                  LIB3165-034-P1-K5-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
                  339
BLAST score
                  5.0e-32
E value
Match length
                  94
% identity
                  80
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  222808
                  LIB3165-034-P1-K5-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249385
BLAST score
                  360
E value
                  2.0e-34
                  104
Match length
% identity
                  65
NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.
                  222809
                  LIB3165-034-P1-K5-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1781348
BLAST score
                  141
E value
                  3.0e-09
Match length
                  35
                  83
% identity
NCBI Description (Y10380) homologous to plastidic aldolases [Solanum
                  tuberosum]
                  222810
Seq. No.
Seq. ID
                  LIB3165-034-P1-K5-D11
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  502
E value
                  5.0e-51
Match length
                  124
                  83
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
```

Seq. ID LIB3165-034-P1-K5-D12

Method BLASTX NCBI GI q1352821



BLAST score E value 4.0e-71 Match length 130 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222812

Seq. ID LIB3165-034-P1-K5-D2

Method BLASTX NCBI GI q3193285 BLAST score 270 E value 8.0e-24 Match length 76 % identity 64

NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No. 222813

Seq. ID LIB3165-034-P1-K5-D4

Method BLASTX NCBI GI g3121825 BLAST score 311 E value 1.0e-28 Match length 121 % identity 64

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 222814

Seq. ID LIB3165-034-P1-K5-D5

Method BLASTX NCBI GI g1352821 BLAST score 605 E value 5.0e-63 Match length 118 99 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222815

Seq. ID LIB3165-034-P1-K5-D6

Method BLASTX NCBI GI g1168408 BLAST score 175 E value 1.0e-12 38 Match length 92 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

% identity

86

NCBI Description glycolate oxidase [Lens culinaris]

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 222816 Seq. ID LIB3165-034-P1-K5-D7 Method BLASTX NCBI GI q430947 BLAST score 423 9.0e-42 E value Match length 103 % identity 82 NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana] Seq. No. 222817 Seq. ID LIB3165-034-P1-K5-D9 Method BLASTX NCBI GI g1352821 BLAST score 688 E value 8.0e-73 Match length 128 % identity 97 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 222818 LIB3165-034-P1-K5-E10 Seq. ID Method BLASTX NCBI GI q3603456 BLAST score 538 E value 3.0e-55 Match length 109 30 % identity NCBI Description (AF088848) polyubiquitin [Capsicum chinense] Seq. No. 222819 Seq. ID LIB3165-034-P1-K5-E11 Method BLASTX NCBI GI g1168411 BLAST score 332 E value 4.0e-31 Match length 89 79 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR Seq. No. 222820 LIB3165-034-P1-K5-E12 Seq. ID Method BLASTX NCBI GI q228403 BLAST score 512 E value 4.0e-52 Match length 115

31560



Seq. ID LIB3165-034-P1-K5-E2

Method BLASTX
NCBI GI g1781348
BLAST score 544
E value 6.0e-56
Match length 119
% identity 87

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 222822

Seq. ID LIB3165-034-P1-K5-E3

Method BLASTX
NCBI GI g3914002
BLAST score 571
E value 4.0e-59
Match length 120
% identity 91

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279

(AF033862) Lon protease [Arabidopsis thaliana]

Seq. No. 222823

Seq. ID LIB3165-034-P1-K5-E5

Method BLASTX
NCBI GI g2129921
BLAST score 184
E value 1.0e-13
Match length 36
% identity 97

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi 758694

(U12573) putative [Catharanthus roseus]

Seq. No. 222824

Seq. ID LIB3165-034-P1-K5-E6

Method BLASTX
NCBI GI g2739046
BLAST score 162
E value 4.0e-11
Match length 89
% identity 37

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 222825

Seq. ID LIB3165-034-P1-K5-E7

Method BLASTX
NCBI GI g231536
BLAST score 383
E value 1.0e-37
Match length 115
% identity 73

NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)

(LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase

(EC 3.4.11.1) - Arabidopsis thaliana

>gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase

```
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative
                   leucine aminopeptidase [Arabidopsis thaliana]
Seq. No.
                   222826
                  LIB3165-034-P1-K5-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4033838
BLAST score
                   325
                  3.0e-30
E value
Match length
                  117
% identity
                   60
NCBI Description
                 (Y18550) sigma-like factor [Arabidopsis thaliana]
                  222827
Seq. No.
                  LIB3165-034-P1-K5-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499525
BLAST score
                  242
E value
                  2.0e-20
Match length
                  122
% identity
                   47
NCBI Description
                  INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER
                   (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi 1663535 (U51153)
                   intestinal sodium/dicarboxylate cotransporter [Rattus
                  norvegicus]
Seq. No.
                   222828
Seq. ID
                  LIB3165-034-P1-K5-F1
Method
                  BLASTX
NCBI GI
                  g4455225
BLAST score
                  350
E value
                  3.0e - 33
                  84
Match length
                  74
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  222829
Seq. ID
                  LIB3165-034-P1-K5-F10
Method
                  BLASTX
NCBI GI
                  q3603401
BLAST score
                  300
E value
                   2.0e-27
Match length
                  74
% identity
                  69
NCBI Description
                 (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                  222830
Seq. ID
                  LIB3165-034-P1-K5-F12
Method
                  BLASTX
NCBI GI
                  g430947
```

BLAST score 196 E value 3.0e - 30Match length 101 % identity 75

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]



Seq. ID LIB3165-034-P1-K5-F2

Method BLASTX
NCBI GI g3121825
BLAST score 282
E value 3.0e-25
Match length 116
% identity 63

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 222832

Seq. ID LIB3165-034-P1-K5-F3

Method BLASTX
NCBI GI g1352821
BLAST score 532
E value 2.0e-54
Match length 107
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222833

Seq. ID LIB3165-034-P1-K5-F5

Method BLASTX
NCBI GI g100616
BLAST score 243
E value 1.0e-20
Match length 55
% identity 85

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 222834

Seq. ID LIB3165-034-P1-K5-F6

Method BLASTX
NCBI GI g289920
BLAST score 600
E value 2.0e-62
Match length 122
% identity 93

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222835

Seq. ID LIB3165-034-P1-K5-G1

Method BLASTX
NCBI GI g430947
BLAST score 423
E value 1.0e-41



```
Match length
                   103
% identity
                   82
NCBI Description
                   (U01103) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  222836
Seq. ID
                  LIB3165-034-P1-K5-G10
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  217
E value
                  1.0e-17
Match length
                  63
% identity
                  62
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  222837
Seq. ID
                  LIB3165-034-P1-K5-G12
Method
                  BLASTX
NCBI GI
                  q2791423
BLAST score
                  200
E value
                  1.0e-15
Match length
                  67
% identity
                  55
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                  222838
Seq. ID
                  LIB3165-034-P1-K5-G3
Method
                  BLASTX
NCBI GI
                  q4139264
BLAST score
                  449
E value
                  9.0e-45
Match length
                  84
% identity
                  100
NCBI Description (AF111812) actin [Brassica napus]
Seq. No.
                  222839
                  LIB3165-034-P1-K5-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979553
BLAST score
                  171
E value
                  3.0e-12
Match length
                  75
% identity
                  45
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  222840
                  LIB3165-034-P1-K5-G7
Seq. ID
```

Method BLASTX NCBI GI g3928543 BLAST score 426 E value 4.0e-42 110 Match length % identity 68

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 222841



```
Seq. ID
                  LIB3165-034-P1-K5-G8
Method.
                  BLASTX
NCBI GI
                  q2979553
BLAST score
                  191
E value
                  1.0e-14
Match length
                  98
% identity
                  40
NCBI Description
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  222842
                  LIB3165-034-P1-K5-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131384
BLAST score
                  115
E value
                  1.0e-08
Match length
                  58
                  69
% identity
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >qi 81934 pir S04132
                  photosystem II oxygen-evolving complex protein 1 precursor
                  - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA
                  -81 to 248) [Pisum sativum] >gi 344004 dbj BAA02554
                  (D13297) precursor for 33-kDa protein of photosystem II
                  [Pisum sativum] >gi_226937_prf__1611461A 02 evolving
                  complex 33kD protein [Arachis hypogaea]
Seq. No.
                  222843
Seq. ID
                  LIB3165-034-P1-K5-H1
Method
                  BLASTX
NCBI GI
                  q4324714
BLAST score
                  435
E value
                  2.0e-43
Match length
                  92
                  91
% identity
NCBI Description (AF110771) ammonium transporter [Arabidopsis thaliana]
Seq. No.
                  222844
                  LIB3165-034-P1-K5-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687224
BLAST score
                  141
E value
                  1.0e-08
Match length
                  87
                  46
% identity
NCBI Description
                 (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
                  reductase [Arabidopsis thaliana]
Seq. No.
                  222845
Seq. ID
                  LIB3165-034-P1-K5-H11
Method
                  BLASTX
NCBI GI
```

Method BLASTX
NCBI GI g1352821
BLAST score 537
E value 4.0e-55
Match length 109
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222846

Seq. ID LIB3165-034-P1-K5-H12

Method BLASTX
NCBI GI g1181599
BLAST score 502
E value 5.0e-51
Match length 130
% identity 76

NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]

Seq. No. 222847

Seq. ID LIB3165-034-P1-K5-H2

Method BLASTX
NCBI GI g4262250
BLAST score 400
E value 5.0e-39
Match length 115
% identity 75

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 222848

Seq. ID LIB3165-034-P1-K5-H3

Method BLASTX
NCBI GI 94406530
BLAST score 237
E value 5.0e-20
Match length 92
% identity 58

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 222849

Seq. ID LIB3165-034-P1-K5-H4

Method BLASTX
NCBI GI g289920
BLAST score 587
E value 6.0e-61
Match length 121
% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 222850

Seq. ID . LIB3165-034-P1-K5-H6

Method BLASTX
NCBI GI g1352821
BLAST score 535
E value 8.0e-55
Match length 109
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain



precursor - upland cotton >gi_450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222851 Seq. No. Seq. ID

LIB3165-034-P1-K5-H8

Method BLASTX g1352821 NCBI GI BLAST score 406 E value 8.0e-40 Match length 88 89 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase $(EC \overline{4.1.1.39})$ small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222852 Seq. No.

LIB3165-034-P1-K6-A1 Seq. ID

Method BLASTX NCBI GI g2879867 BLAST score 400 E value 5.0e-39 Match length 110 % identity 69

NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces

pombe]

222853 Seq. No.

LIB3165-034-P1-K6-A2 Seq. ID

Method BLASTX g2879867 NCBI GI BLAST score 390 E value 8.0e-38 Match length 113 65 % identity

NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces

pombe]

222854 Seq. No.

Seq. ID LIB3165-034-P1-K6-A3

Method BLASTX NCBI GI g1706261 BLAST score 438 E value 2.0e-43Match length 87 % identity 90

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129 pir S59598

cysteine proteinase 2 precursor - maize

>gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea

mays]

Seq. No. 222855

Seq. ID LIB3165-034-P1-K6-A4

Method BLASTX NCBI GI g68200 BLAST score 533

```
E value
                  1.0e-54
Match length
                  130
                  83
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
                   222856
Seq. No.
                  LIB3165-034-P1-K6-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g169039
BLAST score
                  592
E value
                  1.0e-61
Match length
                  121
                  92
% identity
                 (M97477) aldolase [Pisum sativum]
NCBI Description
                  222857
Seq. No.
                  LIB3165-034-P1-K6-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                   287
E value
                  9.0e-26
                  135
Match length
                   50
% identity
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
                  222858
Seq. No.
                  LIB3165-034-P1-K6-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  591
E value
                   2.0e-61
Match length
                  128
% identity
                   67
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  222859
                  LIB3165-034-P1-K6-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  242
                   2.0e-20
E value
Match length
                   64
                   77
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  222860
Seq. ID
                  LIB3165-034-P1-K6-B1
Method
                  BLASTX
NCBI GI
                  q121953
BLAST score
                  181
E value
                  2.0e-13
Match length
                  41
% identity
```

NCBI Description HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea



>gi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263) [Pisum sativum]

222861 Seq. No.

LIB3165-034-P1-K6-B10 Seq. ID

Method BLASTX NCBI GI q81857 BLAST score 215 E value 2.0e-17 Match length 42 90 % identity

NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa

(fragment) >gi 19658 emb CAA45349 (X63872) translationally

controlled tumor protein [Medicago sativa]

Seq. No. 222862

LIB3165-034-P1-K6-B11 Seq. ID

Method BLASTX NCBI GI g2827755 BLAST score 425 E value 5.0e-42

Match length 107 % identity 76

NCBI Description INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE

PHOSPHOHYDROLASE) (PPASE) >qi 951323 (U31467)

pyrophosphatase [Vigna radiata]

Seq. No. 222863

Seq. ID LIB3165-034-P1-K6-B12

Method BLASTX NCBI GI q730850 BLAST score 145 E value 4.0e-09 Match length 126 29 % identity

SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2) NCBI Description

>gi_626942_pir S48533 SUR2 protein - yeast (Saccharomyces

cerevisiae) >gi 458718 (U07171) Sur2p [Saccharomyces cerevisiae] >gi 849215 (U28374) Sur2p: syringomycin response protein 2 [Saccharomyces cerevisiae] >qi 1786173

(U10427) Syr2p [Saccharomyces cerevisiae]

Seq. No. 222864

Seq. ID LIB3165-034-P1-K6-B2

Method BLASTX NCBI GI g68200 BLAST score 230 E value 4.0e-19 89 Match length % identity 60

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

222865 Seq. No.

LIB3165-034-P1-K6-B3 Seq. ID

Method BLASTX



```
NCBI GI
                  g3914940
                  340
BLAST score
E value
                  5.0e-32
Match length
                  115
% identity
                  63
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                  [Spinacia oleracea]
                  222866
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-B5
Method
                  BLASTX
NCBI GI
                  q129867
BLAST score
                  480
                  2.0e-48
E value
Match length
                  93
                  97
% identity
NCBI Description
                  CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)
                  >qi 2924273 emb CAA77425 (Z00044) cytochrome b/f complex
                  subunit IV [Nicotiana tabacum]
Seq. No.
                  222867
                  LIB3165-034-P1-K6-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g228210
BLAST score
                  578
E value
                  7.0e-60
Match length
                  133
% identity
                  80
NCBI Description granule-bound starch synthase [Solanum tuberosum]
                  222868
Seq. No.
                  LIB3165-034-P1-K6-B8
Seq. ID
Method
                  BLASTX
                  g4263525
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
Match length
                  92
% identity
                  67
                  (AC004044) putative photosystem I reaction center subunit
NCBI Description
                  II precursor [Arabidopsis thaliana]
Seq. No.
                  222869
                  LIB3165-034-P1-K6-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738316
BLAST score
                  332
                  5.0e-31
E value
Match length
                  89
                  70
% identity
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3165-034-P1-K6-C10

Method BLASTX NCBI GI g2865623

31570



```
502
BLAST score
E value
                  6.0e-51
Match length
                  117
                  83
% identity
NCBI Description
                  (AF045286)
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                  [Arabidopsis thaliana]
                  222871
Seq. No.
                  LIB3165-034-P1-K6-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  346
                  1.0e-32
E value
Match length
                  102
% identity
                  71
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  222872
Seq. No.
                  LIB3165-034-P1-K6-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1181599
BLAST score
                  303
                  9.0e-28
E value
Match length
                  88
% identity
                  68
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                  222873
                  LIB3165-034-P1-K6-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3269292
BLAST score
                  289
                  5.0e-26
E value
                  74
Match length
                  69
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                  222874
Seq. No.
                  LIB3165-034-P1-K6-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  339
E value
                  7.0e-32
Match length
                  112
                  62
% identity
NCBI Description
                 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                  protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
```

Seq. ID LIB3165-034-P1-K6-C7

Method BLASTX NCBI GI q498038 BLAST score 416 E value 4.0e-42 Match length 128



% identity 64

NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No. 222876

Seq. ID LIB3165-034-P1-K6-C9

Method BLASTX
NCBI GI g1352821
BLAST score 531
E value 2.0e-54
Match length 102
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222877

Seq. ID LIB3165-034-P1-K6-D1

Method BLASTX
NCBI GI g4249385
BLAST score 402
E value 3.0e-39
Match length 112
% identity 66

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 222878

Seq. ID LIB3165-034-P1-K6-D11

Method BLASTX
NCBI GI g1168411
BLAST score 519
E value 5.0e-53
Match length 128
% identity 83

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 222879

Seq. ID LIB3165-034-P1-K6-D12

Method BLASTX
NCBI GI g1352821
BLAST score 671
E value 8.0e-71
Match length 133
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222880

Seq. ID LIB3165-034-P1-K6-D2

Method BLASTX
NCBI GI g3193285
BLAST score 226
E value 1.0e-18



Match length 69 % identity 61

NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No. 222881

Seq. ID LIB3165-034-P1-K6-D3

Method BLASTX
NCBI GI g4249385
BLAST score 164
E value 2.0e-11
Match length 68
% identity 51

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 222882

Seq. ID LIB3165-034-P1-K6-D4

Method BLASTX
NCBI GI g3121825
BLAST score 319
E value 2.0e-29
Match length 104
% identity 70

NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC

ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 222883

Seq. ID LIB3165-034-P1-K6-D5

Method BLASTX
NCBI GI g1352821
BLAST score 579
E value 5.0e-60
Match length 112
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222884

Seq. ID LIB3165-034-P1-K6-D6

Method BLASTX
NCBI GI g1168408
BLAST score 173
E value 2.0e-12
Match length 37
% identity 95

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 222885

Seq. ID LIB3165-034-P1-K6-D7

Method BLASTX NCBI GI g430947

```
BLAST score
                   450
                   7.0e-45
E value
Match length
                   109
% identity
                   82
```

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 222886

Seq. ID LIB3165-034-P1-K6-D9

Method BLASTX NCBI GI g1352821 BLAST score 690 E value 5.0e-73Match length 131 95 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >qi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222887

Seq. ID LIB3165-034-P1-K6-E1

Method BLASTX NCBI GI g4490332 BLAST score 142 E value 9.0e-09 Match length 61 % identity 54

(AL035656) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 222888

LIB3165-034-P1-K6-E10 Seq. ID

Method BLASTX NCBI GI g82426 585 BLAST score E value 1.0e-60 Match length 121 % identity 46

NCBI Description ubiquitin precursor - barley (fragment)

>gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor

(171 aa) [Hordeum vulgare]

222889 Seq. No.

LIB3165-034-P1-K6-E11 Seq. ID

Method BLASTX NCBI GI g68200 BLAST score 328 E value 1.0e-30 Match length 88 % identity 78

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,

chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 222890

Seq. ID LIB3165-034-P1-K6-E12



```
BLASTX
Method
                  q228403
NCBI GI
                  490
BLAST score
                  1.0e-49
E value
                  113
Match length
% identity
                  glycolate oxidase [Lens culinaris]
NCBI Description
                  222891
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-E2
                  BLASTX
Method
                  g1781348
NCBI GI
BLAST score
                  546
                   4.0e-56
E value
                  119
Match length
                   87
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   222892
                  LIB3165-034-P1-K6-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3914002
BLAST score
                   624
                   3.0e-65
E value
                  131
Match length
                   91
% identity
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279
                   (AF033862) Lon protease [Arabidopsis thaliana]
                   222893
Seq. No.
                   LIB3165-034-P1-K6-E5
Seq. ID
                   BLASTX
Method
                   g2129921
NCBI GI
BLAST score
                   191
                   1.0e-14
E value
                   36
Match length
                   100
% identity
NCBI Description
                 hypothetical protein 1 - Madagascar periwinkle >gi_758694
                   (U12573) putative [Catharanthus roseus]
Seq. No.
                   222894
                   LIB3165-034-P1-K6-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2739046
                   163
BLAST score
                   3.0e-11
E value
                   89
Match length
% identity
                   37
                  (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                   [Glycine max]
                   222895
Seq. No.
                   LIB3165-034-P1-K6-E7
Seq. ID
```

BLASTX Method g1483563 NCBI GI 365 BLAST score



```
6.0e-47
E value
Match length
                  129
                  80
% identity
                  (X99825) leucine aminopeptidase [Petroselinum crispum]
NCBI Description
                  222896
Seq. No.
                  LIB3165-034-P1-K6-E8
Seq. ID
                  BLASTX
Method
                  q4033838
NCBI GI
                  330
BLAST score
                  8.0e-31
E value
                  114
Match length
                  61
% identity
                  (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                  222897
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-E9
                  BLASTX
Method
NCBI GI
                  g2499525
BLAST score
                  260
                  1.0e-22
E value
                  133
Match length
                  44
% identity
                  INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER
NCBI Description
                   (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi 1663535 (U51153)
                  intestinal sodium/dicarboxylate cotransporter [Rattus
                  norvegicus]
                  222898
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-F1
                  BLASTX
Method
                  q4455225
NCBI GI
BLAST score
                   392
                   4.0e-38
E value
Match length
                  91
                  74
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   222899
Seq. No.
                  LIB3165-034-P1-K6-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1168728
BLAST score
                   300
                   3.0e-27
E value
Match length
                   112
% identity
                   50
                  CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)
NCBI Description
                   cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   222900
                   LIB3165-034-P1-K6-F12
Seq. ID
```

Method BLASTX

NCBI GI q430947 445 BLAST score 3.0e-44E value 110 Match length % identity 80



```
(U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  222901
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-F2
                  BLASTX
Method
                  g3121825
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
                  103
Match length
                  69
% identity
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi 1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
                  222902
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-F3
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                  605
                  5.0e-63
E value
                  120
Match length
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   222903
Seq. ID
                  LIB3165-034-P1-K6-F5
                   BLASTX
Method
NCBI GI
                   q100616
                   236
BLAST score
                   8.0e-20
E value
                   54
Match length
                   85
% identity
NCBI Description ribulose-bisphosphate carboxylase activase B precursor -
                   barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                   carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
                   ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                   vulgare]
                   222904
Seq. No.
                   LIB3165-034-P1-K6-F6
Seq. ID
Method
                   BLASTX
                   g289920
NCBI GI
                   575
BLAST score
                   2.0e-59
E value
Match length
                   124
% identity
                   88
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
```

222905

BLASTX

LIB3165-034-P1-K6-F7

Seq. No.

Seq. ID

Method



```
NCBI GI
                   g289920
BLAST score
                   663
                   7.0e-70
E value
Match length
                   124
                   99
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   222906
Seq. No.
                   LIB3165-034-P1-K6-G1
Seq. ID
                   BLASTX
Method
                   q430947
NCBI GI
BLAST score
                   440
                   1.0e-43
E value
                   107
Match length
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   222907
Seq. No.
                   LIB3165-034-P1-K6-G10
Seq. ID
Method
                   BLASTX
                   g3747111
NCBI GI
BLAST score
                   229
                   6.0e-19
E value
                   69
Match length
                   61
% identity
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
Seq. No.
                   222908
                   LIB3165-034-P1-K6-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2791423
BLAST score
                   217
E value
                   1.0e-17
                   71
Match length
                   56
% identity
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
                   222909
Seq. No.
                   LIB3165-034-P1-K6-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703115
BLAST score
                   420
                   2.0e-41
E value
                   84
Match length
                   93
% identity
                   ACTIN 3 >gi 2129526_pir__$68112 actin 3 - Arabidopsis
NCBI Description
                   thaliana >gi_114569\overline{5} (U\overline{39}480) actin [Arabidopsis thaliana]
                   >gi 3236244 (AC004684) actin 3 protein [Arabidopsis
                   thaliana]
```

Seq. ID LIB3165-034-P1-K6-G4

Method BLASTX NCBI GI g2979553 BLAST score 184



```
1.0e-13
E value
Match length
                  82
                  44
% identity
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  222911
Seq. No.
                  LIB3165-034-P1-K6-G7
Seq. ID
Method
                  BLASTX
                  g3928543
NCBI GI
BLAST score
                  453
                  6.0e-46
E value
Match length
                  122
% identity
                   66
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   222912
Seq. No.
                  LIB3165-034-P1-K6-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3257810
BLAST score
                   206
                   3.0e-16
E value
Match length
                   126
% identity
                   37
                  (AP000006) 307aa long hypothetical phosphoglycerate
NCBI Description
                  dehydrogenase [Pyrococcus horikoshii]
                   222913
Seq. No.
Seq. ID
                   LIB3165-034-P1-K6-G9
Method
                   BLASTX
NCBI GI
                   q482311
BLAST score
                   111
                   5.0e-10
E value
Match length
                   67
                   54
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   222914
Seq. No.
                   LIB3165-034-P1-K6-H1
Seq. ID
                   BLASTX
Method
                   g4324714
NCBI GI
BLAST score
                   459
                   6.0e-46
E value
                   128
Match length
                   72
% identity
NCBI Description (AF110771) ammonium transporter [Arabidopsis thaliana]
```

Seq. ID LIB3165-034-P1-K6-H11

Method BLASTX
NCBI GI g1352821
BLAST score 527
E value 7.0e-54
Match length 102
% identity 99



% identity

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  222916
Seq. No.
Seq. ID
                  LIB3165-034-P1-K6-H12
                  BLASTX
Method
NCBI GI
                  g1181599
BLAST score
                  394
                  2.0e-38
E value
Match length
                  107
                  73
% identity
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                  222917
                  LIB3165-034-P1-K6-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262250
BLAST score
                  410
                  3.0e-40
E value
                  117
Match length
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
                  222918
Seq. No.
                  LIB3165-034-P1-K6-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  350
                  4.0e-33
E value
Match length
                  116
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  222919
Seq. No.
                  LIB3165-034-P1-K6-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  615
                  3.0e-64
E value
Match length
                  125
                  93
% identity
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  222920
Seq. No.
                  LIB3165-034-P1-K6-H6
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                  450
                  7.0e-45
E value
Match length
                  89
```

31580

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

222921 Seq. No. LIB3165-034-P1-K6-H8 Seq. ID BLASTX Method q1352821 NCBI GI BLAST score 379 1.0e-36 E value 102 Match length 71 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 222922 Seq. No. LIB3165-036-P1-K1-A1 Seq. ID BLASTX Method q1076524 NCBI GI BLAST score 415 7.0e-41E value 120 Match length 62 % identity chloroplast outer envelope protein OEP86 precursor - garden NCBI Description pea >gi 599958 emb CAA83453 (Z31581) chloroplast outer envelope protein 86 [Pisum sativum] 222923 Seq. No. Seq. ID LIB3165-036-P1-K1-A10 BLASTX Method q3687303 NCBI GI BLAST score 215 2.0e-17 E value Match length 95 % identity (AJ006377) subtilisin-like protease [Lycopersicon NCBI Description esculentum] Seq. No. 222924 LIB3165-036-P1-K1-A11 Seq. ID BLASTX Method q2493689 NCBI GI BLAST score 287 E value 8.0e-26 59 Match length 93 % identity NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_1070377_emb_CAA63670_ (X93203) 10 kDa phosphoprotein
[Populus deltoides] >gi_2143326_emb_CAA73768_ (Y13328) 10kDa phosphoprotein [Populus deltoides]

31581

222925

BLASTX

LIB3165-036-P1-K1-A12

Seq. No.

Seq. ID

Method



```
NCBI GI
                  g1351408
BLAST score
                  460
                  4.0e-46
E value
                  121
Match length
                  73
% identity
                  VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                  >gi 1076563_pir__S51117 cystein proteinase - sweet orange
                  >qi 633185 emb CAA87720 (Z47793) cystein proteinase (by
                  similarity) [Citrus sinensis] >gi 1588548 prf 2208463A
                  vascular processing protease [Citrus sinensis]
                  222926
Seq. No.
Seq. ID
                  LIB3165-036-P1-K1-A3
                  BLASTX
Method
NCBI GI
                  g2495365
BLAST score
                  624
                  3.0e-65
E value
Match length
                  129
                  92
% identity
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  222927
Seq. No.
Seq. ID
                  LIB3165-036-P1-K1-A4
                  BLASTX
Method
                  g3033513
NCBI GI
BLAST score
                  350
                  4.0e-33
E value
Match length
                  100
% identity
NCBI Description (AF041068) rubisco activase [Phaseolus vulgaris]
                  222928
Seq. No.
                  LIB3165-036-P1-K1-A5
Sea. ID
Method
                  BLASTX
NCBI GI
                  g2501578
BLAST score
                  339
                  7.0e-32
E value
Match length
                  88
% identity
                  77
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913 pir__S60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  222929
Seq. No.
                  LIB3165-036-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914005
                  278
BLAST score
E value
                  2.0e-28
Match length
                  93
                  78
% identity
```

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586

(U85494) LON1 protease [Zea mays]



```
LIB3165-036-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g4490748
NCBI GI
BLAST score
                  155
E value
                   2.0e-10
Match length
                   36
                   67
% identity
NCBI Description
                  (AL035708) putative protein [Arabidopsis thaliana]
                  222931
Seq. No.
                  LIB3165-036-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  g131385
NCBI GI
BLAST score
                   381
E value
                   9.0e-37
Match length
                  109
                   74
% identity
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
                  222932
Seq. No.
                  LIB3165-036-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3834310
BLAST score
                   349
E value
                   4.0e-33
Match length
                  71
                  94
% identity
NCBI Description
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                  gb_D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,
                  gb_N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                   222933
Seq. ID
                  LIB3165-036-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q2924258
BLAST score
                  556
E value
                  2.0e-57
Match length
                  131
% identity
                  82
NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                   222934
Seq. ID
                  LIB3165-036-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  638
E value
                   7.0e-67
Match length
                  123
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
```

222935

LIB3165-036-P1-K1-B6

Seq. No. Seq. ID



Method BLASTX NCBI GI g289920 BLAST score 557 4.0e-61 E value Match length 123 97 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 222936 Seq. No. Seq. ID LIB3165-036-P1-K1-B7 BLASTX Method NCBI GI g4406530 349 BLAST score 4.0e-33 E value 93 Match length 76 % identity (AF126870) rubisco activase [Vigna radiata] NCBI Description 222937 Seq. No. LIB3165-036-P1-K1-B9 Seq. ID BLASTX Method NCBI GI g1170898 BLAST score 293 8.0e-27 E value 74 Match length 81 % identity MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR NCBI Description >gi 629659 pir S44167 malate dehydrogenase, mitochondrial - cider tree >gi 473206 emb CAA55383 (X78800) mitochondrial malate dehydrogenase [Eucalyptus gunnii] 222938 Seq. No. LIB3165-036-P1-K1-C10 Seq. ID Method BLASTX NCBI GI g228403 BLAST score 476 6.0e-48E value Match length 111 % identity 82 NCBI Description glycolate oxidase [Lens culinaris] 222939 Seq. No. LIB3165-036-P1-K1-C11 Seq. ID BLASTX Method NCBI GI g68200 BLAST score 456 1.0e-45 E value

Match length 115 80 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

222940 Seq. No.

LIB3165-036-P1-K1-C4 Seq. ID

Method BLASTX



```
NCBI GI
                  g4406530
                  152
BLAST score
                  2.0e-10
E value
                  60
Match length
                   53
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
Seq. No.
                  222941
                  LIB3165-036-P1-K1-C7
Seq. ID
                  BLASTX
Method
                   g1332579
NCBI GI
BLAST score
                   503
                   4.0e-51
E value
                   105
Match length
                   10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   222942
Seq. No.
                   LIB3165-036-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4512664
BLAST score
                   306
                   4.0e-28
E value
Match length
                   67
% identity
                   87
                  (AC006931) putative ribose phosphate pyrophosphokinase
NCBI Description
                   [Arabidopsis thaliana]
                   >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative
                   ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
                   222943
Seq. No.
                   LIB3165-036-P1-K1-D10
Seq. ID
                   BLASTX
Method
                   g3914603
NCBI GI
                   588
BLAST score
                   4.0e-61
E value
                   126
Match length
                   87
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                   PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Oryza sativa]
                   222944
Seq. No.
                   LIB3165-036-P1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g430947
BLAST score
                   486
                   4.0e-49
E value
Match length
                   119
                   82
 % identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
```

222945

BLASTX

LIB3165-036-P1-K1-D12

Seq. No.

Seq. ID

Method

E value Match length

% identity

114 91



```
q1781348
NCBI GI
BLAST score
                  592
                  1.0e-61
E value
Match length
                  120
                  93
% identity
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
                  222946
Seq. No.
                  LIB3165-036-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  q3850111
NCBI GI
BLAST score
                  218
                  1.0e-17
E value
                  72
Match length
% identity
                  (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                  involvement in lipid metabolism [Schizosaccharomyces pombe]
                  222947
Seq. No.
Seq. ID
                  LIB3165-036-P1-K1-D3
                  BLASTX
Method
                  g2970051
NCBI GI
BLAST score
                  401
                   4.0e-39
E value
                  100
Match length
                  75
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  222948
                  LIB3165-036-P1-K1-D4
Seq. ID
                  BLASTX
Method
                   g1168411
NCBI GI
BLAST score
                   381
                   6.0e-37
E value
                   100
Match length
                   80
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   222949
Seq. No.
                   LIB3165-036-P1-K1-D5
Seq. ID
                   BLASTX
Method
                   g20559
NCBI GI
                   497
BLAST score
                   2.0e-50
E value
                   130
Match length
                   81
% identity
NCBI Description (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]
                   222950
Seq. No.
                   LIB3165-036-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g266944
NCBI GI
BLAST score
                   560
                   8.0e-58
```

31586



72

Match length

% identity

```
60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
NCBI Description
                  >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic -
                  tomato >gi 19343 emb CAA45863 (X64562) ribosomal protein
                  L2 [Lycopersicon esculentum]
                  222951
Seq. No.
                  LIB3165-036-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  q100615
NCBI GI
                  502
BLAST score
                  5.0e-51
E value
                  126
Match length
                  77
% identity
                  ribulose-bisphosphate carboxylase activase A short form
NCBI Description
                  precursor - barley >gi_167091 (M55447) ribulose
                  1,5-bisphosphate carboxylase activase [Hordeum vulgare]
                  222952
Seq. No.
Seq. ID
                  LIB3165-036-P1-K1-D8
                  BLASTX
Method
                  q3063392
NCBI GI
                  386
BLAST score
                  2.0e-37
E value
                  106
Match length
                  75
% identity
NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]
                   222953
Seq. No.
Seq. ID
                  LIB3165-036-P1-K1-D9
                  BLASTX
Method
NCBI GI
                   q4455180
                   255
BLAST score
                   5.0e-22
E value
                   106
Match length
                   51
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                   222954
Seq. No.
                   LIB3165-036-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539351
BLAST score
                   185
                   7.0e-14
E value
                   51
Match length
% identity
                   63
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                   222955
Seq. No.
                   LIB3165-036-P1-K1-E3
Seq. ID
Method
                   BLASTX
                   g100200
NCBI GI
                   371
BLAST score
                   1.0e-35
E value
```

31587

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato



Seq. ID LIB3165-036-P1-K1-E4

Method BLASTX
NCBI GI g1352821
BLAST score 535
E value 7.0e-55
Match length 101
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222957

Seq. ID LIB3165-036-P1-K1-E5

Method BLASTX
NCBI GI g2190551
BLAST score 272
E value 4.0e-24
Match length 56
% identity 89

NCBI Description (AC001229) Similar to C. elegans hypothetical protein

K07C5.6 (gb Z71181). ESTs gb_H36844,gb_AA394956 come from

this gene. [Arabidopsis thaliana]

Seq. No. 222958

Seq. ID LIB3165-036-P1-K1-E7

Method BLASTX
NCBI GI g2129538
BLAST score 299
E value 3.0e-27
Match length 62
% identity 90

NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No. 222959

Seq. ID LIB3165-036-P1-K1-F1

Method BLASTX
NCBI GI g100616
BLAST score 419
E value 3.0e-41
Match length 113
% identity 73

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 222960

Seq. ID LIB3165-036-P1-K1-F11

Method BLASTX
NCBI GI g4107276
BLAST score 651
E value 2.0e-68



```
Match length
                  125
% identity
                  (X98506) acetyl-CoA synthetase [Solanum tuberosum]
NCBI Description
Seq. No.
                  222961
                  LIB3165-036-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1181599
BLAST score
                  421
                  2.0e-41
E value
Match length
                  112
                  74
% identity
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                  222962
Seq. No.
                  LIB3165-036-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1353352
BLAST score
                  183
                  1.0e-13
E value
Match length
                  48
% identity
                  75
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  222963
Seq. No.
                  LIB3165-036-P1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2253415
BLAST score
                   418
                   3.0e-41
E value
                  81
Match length
                   90
% identity
                  (AF007215) stress-induced cysteine proteinase [Lavatera
NCBI Description
                   thuringiaca]
                   222964
Seq. No.
                   LIB3165-036-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129698
                   470
BLAST score
                   3.0e-47
E value
                   115
Match length
                   77
% identity
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi 1054633 emb CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
                   222965
Seq. No.
Seq. ID
                   LIB3165-036-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g4406530
BLAST score
                   312
E value
                   1.0e-28
Match length
                   108
```

(AF126870) rubisco activase [Vigna radiata]

62

% identity

NCBI Description



Seq. No. Seq. ID 222966

LIB3165-036-P1-K1-G11

```
BLASTX
 Method
                    q3193286
 NCBI GI
                    179
 BLAST score
                    3.0e-13
 E value
                    55
 Match length
                    58
 % identity
                   (AF069298) T14P8.22 gene product [Arabidopsis thaliana]
 NCBI Description
                    222967
 Seq. No.
 Seq. ID
                    LIB3165-036-P1-K1-G2
                    BLASTX
 Method
                    g445116
 NCBI GI
                    405
 BLAST score
                    8.0e-40
 E value
                    86
 Match length
                    91
  % identity
 NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]
                    222968
  Seq. No.
                    LIB3165-036-P1-K1-G3
  Seq. ID
                    BLASTX
  Method
                    q1532135
· NCBI GI
                    242
  BLAST score
                    2.0e-20
  E value
                    49
  Match length
                    92
  % identity
                   (U49442) chloroplast mRNA-binding protein CSP41 precursor
  NCBI Description
                    [Spinacia oleracea]
                    222969
  Seq. No.
  Seq. ID
                    LIB3165-036-P1-K1-G6
                    BLASTX
  Method
                     g3687652
  NCBI GI
  BLAST score
                    577
                     9.0e-60
  E value
  Match length
                     119
  % identity
  NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]
                     222970
  Seq. No.
                     LIB3165-036-P1-K1-G7
  Seq. ID
                     BLASTX
  Method
                     g1352821
  NCBI GI
  BLAST score
                     565
                     2.0e-58
  E value
  Match length
                     113
                     97
  % identity
  NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                     (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                     ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                     precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                     ribulose bisphosphate carboxylase [Gossypium hirsutum]
                     222971
   Seq. No.
```

Match length

NCBI Description

% identity

103



```
LIB3165-036-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829204
BLAST score
                  257
                  3.0e-22
E value
                  107
Match length
                  50
% identity
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                  222972
Seq. No.
                  LIB3165-036-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82080
                  489
BLAST score
                  2.0e-49
E value
Match length
                  121
% identity
                  79
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                  222973
Seq. No.
                  LIB3165-036-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g267122
                  442
BLAST score
                  5.0e-44
E value
                  104
Match length
                  78
% identity
                  THIOREDOXIN H-TYPE (TRX-H) >gi 478400 pir JQ2242
NCBI Description
                  thioredoxin h - Arabidopsis thaliana
                  >gi 16552 emb CAA78462 (Z14084) Thioredoxin H [Arabidopsis
                  thaliana] >gi 1388080 (U35827) thioredoxin h [Arabidopsis
                   thaliana]
                   222974
Seq. No.
                  LIB3165-036-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249382
                   397
BLAST score
E value
                   1.0e-38
                   91
Match length
% identity
                   82
                  (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   222975
Seq. ID
                   LIB3165-036-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q100200
BLAST score
                   379
E value
                   1.0e-36
```

31591

chlorophyll a/b-binding protein type I precursor - tomato

% identity



```
222976
Seq. No.
                  LIB3165-036-P1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q231610
                  285
BLAST score
                  1.0e-25
E value
Match length
                  105
                  61
% identity
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
                  222977
Seq. No.
Seq. ID
                  LIB3165-036-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2245005
                  260
BLAST score
                  1.0e-22
E value
                  103
Match length
                  53
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
                  222978
Seq. No.
Seq. ID
                  LIB3165-037-P1-K1-A1
                  BLASTX
Method
NCBI GI
                  q1168411
BLAST score
                   471
                   3.0e-47
E value
Match length
                  113
                  86
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   222979
Seq. No.
                  LIB3165-037-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q115813
BLAST score
                   301
E value
                   2.0e-27
                   98
Match length
                   63
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                   (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   222980
Seq. No.
                   LIB3165-037-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g1895084
NCBI GI
                   587
BLAST score
E value
                   6.0e-61
                   115
Match length
```

NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

222986

```
Seq. No.
                   222981
Seq. ID
                   LIB3165-037-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   675
E value
                   3.0e-71
Match length
                   130
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                   222982
Seq. ID
                   LIB3165-037-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4559339
BLAST score
                  595
E value
                  7.0e-62
Match length
                  136
% identity
                  85
                  (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  222983
Seq. ID
                  LIB3165-037-P1-K1-A8
Method
                  BLASTX
                  q3738285
NCBI GI
BLAST score
                  273
E value
                  4.0e-24
Match length
                  69
% identity
                  74
NCBI Description
                 (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  222984
Seq. ID
                  LIB3165-037-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3452497
BLAST score
                  589
E value
                  4.0e-61
Match length
                  134
% identity
                  86
                 (Y17796) ketol-acid reductoisomerase [Pisum sativum]
NCBI Description
Seq. No.
                  222985
Seq. ID
                  LIB3165-037-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1171866
BLAST score
                  366
E value
                  5.0e-35
Match length
                  111
% identity
                  64
NCBI Description
                  NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
                  (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH
                  dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild
                  cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of
                  NADH: ubiquinone oxidoreductase [Brassica oleracea]
```

31593

```
LIB3165-037-P1-K1-B12
Seq. ID
                  BLASTX
Method
                  g3335355
NCBI GI
BLAST score
                  529
                  3.0e-54
E value
                  109
Match length
                  27
% identity
                  (AC004512) Match to polyubiquitin DNA gb_L05401 from A.
NCBI Description
                  thaliana. Contains insertion of mitochondrial NADH
                  dehydrogenase gb X82618 and gb_X98301. May be a pseudogene
                  with an expressed insert. EST gb_AA586248 comes from this
                  region. [Arabi
                  222987
Seq. No.
                  LIB3165-037-P1-K1-B2
Seq. ID
                  BLASTX
Method
                  g2244847
NCBI GI
                  284
BLAST score
                  2.0e-25
E value
                  88
Match length
% identity
                  61
                  (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                  [Arabidopsis thaliana]
                  222988
Seq. No.
                  LIB3165-037-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4545262
BLAST score
                  234
E value
                  1.0e-19
Match length
                  44
% identity
                  (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                  hirsutum]
                   222989
Seq. No.
                   LIB3165-037-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   q3694872
NCBI GI
BLAST score
                   239
                   2.0e-20
E value
Match length
                   89
                   57
% identity
NCBI Description (AF092547) profilin [Ricinus communis]
Seq. No.
                   222990
                   LIB3165-037-P1-K1-B7
Seq. ID
Method
                   BLASTX
                   q1352821
NCBI GI
BLAST score
                   555
                   3.0e-57
E value
                   105
Match length
% identity
                   100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
```



ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222991 LIB3165-037-P1-K1-B8 Seq. ID Method BLASTX q3914605 NCBI GI BLAST score 552 7.0e-57 E value 122 Match length 88 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE NCBI Description PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase apple tree >gi 415852 emb CAA79857 (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica] Seq. No. 222992 LIB3165-037-P1-K1-C12 Seq. ID Method BLASTX g2970051 NCBI GI BLAST score 461 E value 4.0e-46 Match length 118 74 % identity NCBI Description (AB012110) ARG10 [Vigna radiata] Seq. No. 222993 LIB3165-037-P1-K1-C7 Seq. ID Method BLASTX NCBI GI g20729 BLAST score 368 E value 3.0e - 35104 Match length 72 % identity NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum] Seq. No. 222994 LIB3165-037-P1-K1-C8 Seq. ID Method BLASTX g289920 NCBI GI BLAST score 696 E value 1.0e-73 133 Match length 96 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 222995 Seq. No. Seq. ID LIB3165-037-P1-K1-C9 Method BLASTX NCBI GI g4262236

NCBI GI g4262236
BLAST score 302
E value 1.0e-27
Match length 85
% identity 73

NCBI Description (AC006200) putative ribose 5-phosphate isomerase



[Arabidopsis thaliana]

222996 Seq. No. Seq. ID LIB3165-037-P1-K1-D1 Method BLASTX NCBI GI q20729 BLAST score 385 3.0e-37 E value 109 Match length 72 % identity (X15190) precursor (AA -68 to 337) [Pisum sativum] NCBI Description Seq. No. 222997 LIB3165-037-P1-K1-D4 Seq. ID BLASTX Method NCBI GI g3738298 BLAST score 322 6.0e-30 E value Match length 107 % identity (AC005309) unknown protein [Arabidopsis thaliana] NCBI Description >qi 4249394 (AC006072) unknown protein [Arabidopsis thaliana] 222998 Seq. No. LIB3165-037-P1-K1-D6 Seq. ID BLASTX Method NCBI GI q120669 BLAST score 560 9.0e-58 E value Match length 112 93 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi 66014 pir DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora] Seq. No. 222999 LIB3165-037-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g1814405 BLAST score 151 8.0e-10 E value 71 Match length 52 % identity (U84890) putative phosphate permease [Mesembryanthemum NCBI Description crystallinum] 223000 Seq. No. LIB3165-037-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 574

31596

2.0e-59

108 98

E value Match length

% identity



RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223001 Seq. No. Seq. ID LIB3165-037-P1-K1-E12

BLASTX Method NCBI GI g1168411 BLAST score 481 2.0e-48 E value 120 Match length % identity 82

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

223002 Seq. No.

LIB3165-037-P1-K1-E2 Seq. ID

Method BLASTX NCBI GI q3738261 BLAST score 352 E value 5.0e-62 Match length 133 95

% identity NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 223003

LIB3165-037-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI g2275196 BLAST score 437 E value 3.0e-43Match length 88

94 % identity

NCBI Description (AC002337) water stress-induced protein, WSI76 isolog

[Arabidopsis thaliana]

223004 Seq. No.

LIB3165-037-P1-K1-E5 Seq. ID

Method BLASTX NCBI GI g3738261 BLAST score 264 6.0e - 31E value Match length 76 95 % identity

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 223005

LIB3165-037-P1-K1-E7 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 539 3.0e-55 E value Match length 106 % identity 94

31597



RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223006 Seq. ID LIB3165-037-P1-K1-E9 BLASTX Method NCBI GI g430947 BLAST score 448 1.0e-44 E value Match length 109 % identity 82 NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana] 223007 Seq. No. Seq. ID LIB3165-037-P1-K1-F1 BLASTX Method q4455256 NCBI GI BLAST score 544 6.0e-56 E value Match length 110 % identity 87 (AL035523) protein-methionine-S-oxide reductase NCBI Description [Arabidopsis thaliana] Seq. No. 223008 LIB3165-037-P1-K1-F12 Seq. ID BLASTX Method NCBI GI g1352821 BLAST score 531 E value 2.0e-54 100 Match length 100 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223009 Seq. No. LIB3165-037-P1-K1-F3 Seq. ID Method BLASTX g289920 NCBI GI 528 BLAST score 5.0e-54E value

107 Match length 93 % identity

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

223010 Seq. No.

LIB3165-037-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI g3150412



```
BLAST score
                  336
                  4.0e-35
E value
Match length
                  95
                  76
% identity
                  (AC004165) putative Fe(II) transport protein [Arabidopsis
NCBI Description
                  thaliana] >gi 3420044 (AC004680) putative Fe(II) transport
                  protein [Arabidopsis thaliana]
                  223011
Seq. No.
Seq. ID
                  LIB3165-037-P1-K1-F5
                  BLASTX
Method
                  g3080371
NCBI GI
BLAST score
                  285
                  6.0e-26
E value
                  77
Match length
                  61
% identity
                  (AL022580) putative pectinacetylesterase protein
NCBI Description
                  [Arabidopsis thaliana]
                  223012
Seq. No.
Seq. ID
                  LIB3165-037-P1-K1-F6
                  BLASTX
Method
                  q3928099
NCBI GI
                  282
BLAST score
                  4.0e-25
E value
                  136
Match length
                  24
% identity
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
                  223013
Seq. No.
Seq. ID
                  LIB3165-037-P1-K1-F8
                  BLASTX
Method
NCBI GI
                  g2828292
                  481
BLAST score
                  1.0e-48
E value
Match length
                  114
                  77
% identity
NCBI Description (AL021687) neoxanthin cleavage enzyme-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  223014
Seq. ID
                  LIB3165-037-P1-K1-F9
                  BLASTX
Method
                  g481131
NCBI GI
BLAST score
                   293
E value
                   2.0e-26
                   111
Match length
% identity
                   51
                  sucrose transport protein SUC2 - Arabidopsis thaliana
NCBI Description
                   >gi 407092 emb CAA53150 (X75382) sucrose-proton symporter
                   [Arabidopsis thaliana]
```

Seq. No. 223015

Seq. ID LIB3165-037-P1-K1-G11

Method BLASTX NCBI GI g1403522 BLAST score 401



4.0e-39 E value 128 Match length 62 % identity

NCBI Description (X57187) chitinase [Phaseolus vulgaris]

Seq. No. Seq. ID

LIB3165-037-P1-K1-G2

Method NCBI GI BLASTX g3377802 427

223016

BLAST score E value

3.0e-42102

Match length % identity

79 (AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis NCBI Description

thaliana]

Seq. No.

223017

Seq. ID

LIB3165-037-P1-K1-G4

BLASTX Method g1709846 NCBI GI BLAST score 329 1.0e-30 E value 124 Match length % identity 46

PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336) NCBI Description

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq. No.

223018

Seq. ID

LIB3165-037-P1-K1-G5

BLASTX Method g461550 NCBI GI 218 BLAST score 1.0e-17 E value 47 Match length 98 % identity

NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR

>gi_81635_pir__B39732 H+-transporting ATP synthase (EC

3.6.1.34) gamma-1 chain precursor, chloroplast -Arabidopsis thaliana >gi 166632 (M61741) ATP synthase

gamma-subunit [Arabidopsis thaliana]

223019 Seq. No.

Seq. ID LIB3165-037-P1-K1-G7

BLASTX Method NCBI GI q1495259 424 BLAST score 6.0e-42E value Match length 119 % identity

NCBI Description (X97826) orf04 [Arabidopsis thaliana]

Seq. No.

223020

Seq. ID

LIB3165-037-P1-K1-G9

Method BLASTX q4406530 NCBI GI BLAST score 342

```
3.0e-32
E value
Match length
                  92
                  76
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  223021
Seq. No.
Seq. ID
                  LIB3165-037-P1-K1-H11
                  BLASTX
Method
NCBI GI
                  q4406530
                  350
BLAST score
                  4.0e-33
E value
                  116
Match length
                  65
% identity
                 (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  223022
Seq. No.
Seq. ID
                  LIB3165-037-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4455251
BLAST score
                  341
                  4.0e-32
E value
                  103
Match length
                  64
% identity
                  (AL035523) magnesium-protoporphyrin IX
NCBI Description
                  methyltransferase-like protein [Arabidopsis thaliana]
                  223023
Seq. No.
                  LIB3165-037-P1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3738285
BLAST score
                  159
                   9.0e-11
E value
                   52
Match length
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                   223024
Seq. No.
                   LIB3165-037-P1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1352821
BLAST score
                   548
                   2.0e-56
E value
Match length
                   105
                   99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223025
Seq. No.
                   LIB3165-038-Q1-K1-A1
Seq. ID
Method
                   BLASTX
                   g3482918
NCBI GI
                   590
BLAST score
E value
                   3.0e-61
```

31601

134

Match length



% identity (AC003970) Similar to ATP-citrate-lyase [Arabidopsis NCBI Description thaliana] 223026 Seq. No. Seq. ID LIB3165-038-Q1-K1-A12 BLASTX Method NCBI GI g1352821 557 BLAST score 2.0e-57 E value 108 Match length 95 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase $\overline{\text{(EC 4.1.1.39)}}$ small chain precursor - upland cotton >gi_450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223027 Seq. No. Seq. ID LIB3165-038-Q1-K1-A2 Method BLASTX NCBI GI g20729 348 BLAST score 5.0e-33 E value 101 Match length 70 % identity NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum] 223028 Seq. No. LIB3165-038-Q1-K1-A4 Seq. ID BLASTX Method g2827551 NCBI GI 199 BLAST score 2.0e-15 E value 60 Match length 67 % identity NCBI Description (AL021635) predicted protein [Arabidopsis thaliana] 223029 Seq. No. Seq. ID LIB3165-038-Q1-K1-A5 BLASTX Method g1352821 NCBI GI BLAST score 621 6.0e-65 E value Match length 121 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223030 Seq. No.

Seq. ID LIB3165-038-Q1-K1-A6

Method BLASTX NCBI GI g2979553 BLAST score 243



```
E value
                  1.0e-20
Match length
                  117
% identity
                  45
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
                  223031
Seq. No.
                  LIB3165-038-Q1-K1-A8
Seg. ID
Method
                  BLASTX
NCBI GI
                  q3023752
BLAST score
                  223
                  2.0e-18
E value
                  92
Match length
% identity
                  55
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb CAA99756_ (Z75520)
                  ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                  223032
                  LIB3165-038-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131147
BLAST score
                  150
                  3.0e-10
E value
Match length
                  53
% identity
                  53
                  PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2
NCBI Description
                  >gi 72675 pir A2LVP7 photosystem I P700 apoprotein A2 -
                  liverwort (Marchantia polymorpha) chloroplast
                  >gi 11671 emb CAA28084_ (X04465) psaB [Marchantia
                  polymorpha]
Seq. No.
                  223033
                  LIB3165-038-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  357
                  6.0e - 34
E value
Match length
                  117
% identity
                   65
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                   223034
                  LIB3165-038-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2765081
                   395
BLAST score
                  2.0e-38
E value
Match length
                  119
% identity
                   66
NCBI Description (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                   223035
                  LIB3165-038-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q285317
                  157
BLAST score
```

31603

7.0e-11

77

E value

Match length

```
% identity
                 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea
NCBI Description
                  223036
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-B3
                  BLASTX
Method
                  q2827551
NCBI GI
BLAST score
                  182
                  2.0e-13
E value
                  83
Match length
                  54
% identity
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
                  223037
Seq. No.
                 ·LIB3165-038-Q1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q586858
BLAST score
                  270
E value
                  8.0e-24
                  118
Match length
% identity
                  46
                  HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION
NCBI Description
                  >gi 2127020 pir S66042 hypothetical protein - Bacillus
                  subtilis >gi 467402 dbj BAA05248_ (D26185) unknown
                  [Bacillus subtilis] > gi 2632279 emb CAB11788 (Z99104)
                  similar to hypothetical proteins [Bacillus subtilis]
                  223038
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-B6
Method
                  BLASTX
                  q2244905
NCBI GI
BLAST score
                  388
                  1.0e-37
E value
Match length
                  112
% identity
                  61
                  (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. No. 223039

LFB3165-038-Q1-K1-B7 Seq. ID

Method BLASTX q4559372 NCBI GI 228 BLAST score 6.0e-19E value 57 Match length % identity 81

NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]

223040 Seq. No.

LIB3165-038-Q1-K1-B9 Seq. ID

Method BLASTX g1352821 NCBI GI 193 BLAST score 5.0e-15 E value 51 Match length 76 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

Seq. ID Method

NCBI GI



(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. LIB3165-038-Q1-K1-C10 Seq. ID BLASTX Method q4406530 NCBI GI 328 BLAST score 1.0e-30 E value 91 Match length 75 % identity (AF126870) rubisco activase [Vigna radiata] NCBI Description 223042 Seq. No. Seq. ID LIB3165-038-Q1-K1-C12 Method BLASTX NCBI GI q1352821 481 BLAST score 2.0e-48 E value 98 Match length 92 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223043 Seq. ID LIB3165-038-Q1-K1-C3 BLASTX Method g3319921 NCBI GI BLAST score 283 E value 3.0e-25 Match length 105 58 % identity (AJ223388) Hev b 3 [Hevea brasiliensis] NCBI Description >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliens \overline{i} s] >gi $\overline{3}$ 818 $\overline{4}$ 75 (AF05 $\overline{1}$ 317) small rubber particle protein [Hevea brasiliensis] 223044 Seq. No. Seq. ID LIB3165-038-Q1-K1-C4 Method BLASTX g2970051 NCBI GI 316 BLAST score 4.0e-29 E value 75 Match length 81 % identity NCBI Description (AB012110) ARG10 [Vigna radiata] 223045 Seq. No.

31605

LIB3165-038-Q1-K1-C5

BLASTX g2739375



```
BLAST score
                  192
E value
                  1.0e-14
Match length
                  102
                  47
% identity
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223046
                  LIB3165-038-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g133085
BLAST score
                  183
                  1.0e-13
E value
                  110
Match length
                  45
% identity
                  50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12)
NCBI Description
                  >gi_71136_pir__R7SP12 ribosomal protein L12, chloroplast -
                  spinach >gi 170115 (J02849) ribosomal L12 precursor
                  [Spinacia oleracea]
                  223047
Seq. No.
                  LIB3165-038-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913651
BLAST score
                  569
                  8.0e-59
E value
Match length
                  139
                  76
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                  223048
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-D1
                  BLASTX
Method
NCBI GI
                  q1255954
BLAST score
                  534
E value
                  1.0e-54
                  118
Match length
                  83
% identity
NCBI Description (Z70677) thioredoxin [Ricinus communis]
Seq. No.
                  223049
Seq. ID
                  LIB3165-038-Q1-K1-D11
                  BLASTX
Method
NCBI GI
                  q117822
BLAST score
                  392
                  4.0e-38
E value
Match length
                  74
% identity
                  100
NCBI Description
                 CYTOCHROME B6 >gi 65635 pir CBNT6
```

plastoquinol--plastocyanin reductase (EC 1.10.99.1)

cytochrome b6 - common tobacco chloroplast

>gi_11858_emb_CAA77375_ (Z00044) cytochrome b6 [Nicotiana tabacum] >gi_225226_prf__1211235BH cytochrome b6 [Nicotiana

tabacum]

Seq. No. 223050

31606



LIB3165-038-Q1-K1-D12 Seq. ID

Method BLASTX q2493694 NCBI GI BLAST score 261 1.0e-22 E value 105 Match length 54 % identity

PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII NCBI Description

6.1 KD PROTEIN) >gi 1076268 pir_S53025 photosystem II protein - spinach >gi 728716 emb CAA59409 (X85038) protein

of photosystem II [Spinacia oleracea]

223051 Seq. No.

Seq. ID LIB3165-038-Q1-K1-D7

BLASTX Method q1352821 NCBI GI BLAST score 588 5.0e-61 E value Match length 111 % identity 97

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >qi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223052 Seq. No.

Seq. ID LIB3165-038-Q1-K1-D8

Method BLASTX NCBI GI q282865 BLAST score 627 1.0e-65 E value Match length 136 87 % identity

chlorophyll a/b-binding protein - Arabidopsis thaliana NCBI Description

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >gi 166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana]

223053 Seq. No.

LIB3165-038-Q1-K1-E1 Seq. ID

BLASTX Method g1352821 NCBI GI 636 BLAST score E value 1.0e-66 123 Match length 99 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

223054 Seq. No.

LIB3165-038-Q1-K1-E10 Seq. ID

Method BLASTX NCBI GI g1360088

31607

NCBI Description

```
BLAST score
                  310
                  2.0e-28
E value
Match length
                  88
% identity
                  65
NCBI Description
                 (X97947) Zn finger protein [Nicotiana tabacum]
                  223055
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-E11
                  BLASTX
Method
                  q4056568
NCBI GI
                  249
BLAST score
                  2.0e-21
E value
Match length
                  91
% identity
                  18
NCBI Description (U90944) PDI-like protein [Zea mays]
                  223056
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3334138
BLAST score
                  267
                  2.0e-23
E value
Match length
                  99
                  53
% identity
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin
                  [Glycine max]
                  223057
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-E2
Method
                  BLASTX
                  q4572673
NCBI GI
BLAST score
                  483
                  1.0e-48
E value
Match length
                  117
% identity
                  77
NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  223058
                  LIB3165-038-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g945081
BLAST score
                  541
                  2.0e-55
E value
Match length
                  135
% identity
                  78
NCBI Description (U31094) P21 [Petunia hybrida]
                  223059
Seq. No.
                  LIB3165-038-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512653
                  298
BLAST score
                  4.0e-39
E value
Match length
                  126
% identity
                  71
```

31608

(AC007048) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                  223060
                  LIB3165-038-Q1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4406530
BLAST score
                  242
                  4.0e-26
E value
Match length
                  111
                  64
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  223061
Seq. No.
                  LIB3165-038-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  q3668085
NCBI GI
                   142
BLAST score
                   8.0e-09
E value
                   76
Match length
                   42
% identity
                  (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   223062
Seq. No.
Seq. ID
                   LIB3165-038-Q1-K1-E9
                   BLASTX
Method
                   q2811025
NCBI GI
                   187
BLAST score
                   8.0e-28
E value
Match length
                   105
                   68
% identity
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
                   223063
Seq. No.
                   LIB3165-038-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   509
                   9.0e-57
E value
Match length
                   121
% identity
                   10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   223064
Seq. No.
                   LIB3165-038-Q1-K1-F11
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g289920
BLAST score 680
E value 7.0e-72
Match length 128
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 223065

Seq. ID LIB3165-038-Q1-K1-F2

Method BLASTX NCBI GI g421843

31609



457 BLAST score E value 9.0e-46111 Match length 74 % identity

protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana NCBI Description >qi 217861 dbj BAA01715 (D10909) serine/threonine protein

kinase [Arabidopsis thaliana]

223066 Seq. No.

Seq. ID LIB3165-038-Q1-K1-F3

BLASTX Method q464986 NCBI GI BLAST score 514 2.0e-52 E value 95 Match length 98 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi 297884 emb_CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 223067

LIB3165-038-Q1-K1-F4 Seq. ID

BLASTX Method NCBI GI g3319921 BLAST score 184 2.0e-21 E value 109 Match length % identity 54

(AJ223388) Hev b 3 [Hevea brasiliensis] NCBI Description

>gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3

[Hevea brasiliensis] >gi 3818475 (AF051317) small rubber

particle protein [Hevea brasiliensis]

223068 Seq. No.

LIB3165-038-Q1-K1-F5 Seq. ID

Method BLASTX g20729 NCBI GI 452 BLAST score 1.0e-45 E value Match length 129 % identity 76

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

223069 Seq. No.

LIB3165-038-Q1-K1-F9 Seq. ID

Method BLASTX g2677828 NCBI GI BLAST score 393

Match length

% identity

122 69



```
3.0e-38
E value
Match length
                  114
                  67
% identity
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  223070
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-G1
                  BLASTX
Method
NCBI GI
                  q3822036
BLAST score
                  214
                  3.0e-17
E value
                  93
Match length
                  49
% identity
                 (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
NCBI Description
                  223071
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-G12
                  BLASTX
Method
NCBI GI
                  g1723730
BLAST score
                  184
                  1.0e-13
E value
                  80
Match length
                  51
% identity
                  HYPOTHETICAL 78.8 KD PROTEIN IN ATF2-RNR4 INTERGENIC REGION
NCBI Description
                  >gi 2131694_pir__S64492 hypothetical protein YGR178c -
                  yeast (Saccharomyces cerevisiae) >gi 1323315 emb CAA97204
                   (Z72963) PBP1 [Saccharomyces cerevisiae] >gi 2737884
                   (U46931) Mrs16p [Saccharomyces cerevisiae]
Seq. No.
                  223072
                  LIB3165-038-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                   a1871577
NCBI GI
                   314
BLAST score
E value
                   7.0e-29
                   115
Match length
                   49
% identity
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.
                   223073
                   LIB3165-038-Q1-K1-G4
Seq. ID
Method
                   BLASTX
                   g3618316
NCBI GI
BLAST score
                   226
                   1.0e-18
E value
Match length
                   113
                   44
% identity
NCBI Description (AB001886) zinc finger protein [Oryza sativa]
Seq. No.
                   223074
                   LIB3165-038-Q1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402713
                   415
BLAST score
                   9.0e-41
E value
```

31611



```
(AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223075
Seq. ID
                  LIB3165-038-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  q3023752
BLAST score
                  281
                  4.0e-25
E value
Match length
                  111
                  54
% identity
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
                  223076
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-G8
                  BLASTX
Method
                  q1617206
NCBI GI
BLAST score
                  400
                  5.0e-39
E value
Match length
                  122
                  66
% identity
NCBI Description (Z72489) CP12 [Pisum sativum]
                  223077
Seq. No.
Seq. ID
                  LIB3165-038-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  561
                  5.0e-58
E value
Match length
                  118
% identity
                  87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Oryza sativa]
                  223078
Seq. No.
                  LIB3165-038-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  503
E value
                  1.0e-60
Match length
                  124
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223079
                  LIB3165-038-Q1-K1-H2
```

Seq. ID

Method BLASTX NCBI GI q2275196 BLAST score 272 3.0e-34 E value 81 Match length



% identity 95

NCBI Description (AC002337) water stress-induced protein, WSI76 isolog

[Arabidopsis thaliana]

Seq. No. 223080

Seq. ID LIB3165-038-Q1-K1-H3

Method BLASTX
NCBI GI g1352821
BLAST score 622
E value 5.0e-65
Match length 117

% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223081

Seq. ID LIB3165-038-Q1-K1-H7

Method BLASTX
NCBI GI g1352821
BLAST score 424
E value 6.0e-42
Match length 90
% identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223082

Seq. ID LIB3165-038-Q1-K1-H8

Method BLASTX
NCBI GI g1439609
BLAST score 521
E value 3.0e-53
Match length 105
% identity 98

NCBI Description (U62778) delta-tonoplast intrinsic protein [Gossypium

hirsutum]

Seq. No. 223083

Seq. ID LIB3165-038-Q1-K1-H9

Method BLASTX
NCBI GI g2924520
BLAST score 601
E value 1.0e-62
Match length 130
% identity 88

NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)

[Arabidopsis thaliana]

Seq. No. 223084

Seq. ID LIB3165-039-Q1-K1-A1

Method BLASTX



```
NCBI GI
                  g166702
BLAST score
                  516
                  1.0e-52
E value
Match length
                  140
                  75
% identity
                  (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit
NCBI Description
                   [Arabidopsis thaliana]
                   223085
Seq. No.
                  LIB3165-039-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  q3023752
NCBI GI
BLAST score
                   334
                   3.0e - 31
E value
                   113
Match length
                   62
% identity
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
                   223086
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-A11
                   BLASTX
Method
                   q1352821
NCBI GI
BLAST score
                   535
                   1.0e-55
E value
                   110
Match length
                   97
% identity
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223087
Seq. No.
                   LIB3165-039-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g3688174
NCBI GI
BLAST score
                   426
E value
                   5.0e-42
Match length
                   111
% identity
                   74
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                   223088
Seq. No.
                   LIB3165-039-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g1169494
NCBI GI
BLAST score
                   234
                   2.0e-19
E value
                   81
Match length
                   59
% identity
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
```

Seq. No. 223089

max]

>gi_2119915_pir__S60659 EF-Tu protein precursor - soybean >gi_949873 emb CAA61444 (X89058) EF-Tu protein [Glycine



LIB3165-039-Q1-K1-A7 Seq. ID BLASTX Method q3036944 NCBI GI 580 BLAST score 4.0e-60 E value 126 Match length % identity 95 (AB012637) light harvesting chlorophyll a/b-binding protein NCBI Description [Nicotiana sylvestris] 223090 Seq. No. LIB3165-039-Q1-K1-A8 Seq. ID BLASTX Method q1352821 NCBI GI 586 BLAST score E value 8.0e-61 110 Match length 100 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223091 Seq. No. LIB3165-039-Q1-K1-A9 Seq. ID Method BLASTX NCBI GI g167367 BLAST score 547 3.0e-56E value 136 Match length 79 % identity (L08199) peroxidase [Gossypium hirsutum] NCBI Description 223092 Seq. No. LIB3165-039-Q1-K1-B1 Seq. ID Method BLASTX g3913295 NCBI GI 311 BLAST score 1.0e-28 E value Match length 118 % identity CAFFEIC ACID 3-O-METHYLTRANSFERASE NCBI Description (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_ (X83217) caffeic O-methyltransferase [Prunus dulcis] Seq. No. 223093 Seq. ID LIB3165-039-Q1-K1-B10 BLASTX Method NCBI GI q1781348 BLAST score 483 E value 1.0e-48

Match length 97 94 % identity

(Y10380) homologous to plastidic aldolases [Solanum NCBI Description

tuberosum]



Seq. No. 223094 LIB3165-039-Q1-K1-B11 Seq. ID Method BLASTX NCBI GI q4406814 456 BLAST score 1.0e-45 E value Match length 107 % identity 81 (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis NCBI Description thaliana] Seq. No. 223095

Seq. ID LIB3165-039-Q1-K1-B2
Method BLASTX
NCBI GI g1702986
BLAST score 302
E value 6.0e-32

E value 6.0e-3
Match length 97
% identity 85

NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi 1256534 (L09112) GF14

chi chain [Arabidopsis thaliana]

Seq. No. 223096

Seq. ID LIB3165-039-Q1-K1-B3

Method BLASTX
NCBI GI g166834
BLAST score 296
E value 8.0e-31
Match length 104
% identity 68

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000)

Rubisco activase [Arabidopsis thaliana]

Seq. No. 223097

Seq. ID LIB3165-039-Q1-K1-B5

Method BLASTX
NCBI GI g3914605
BLAST score 695
E value 1.0e-73
Match length 141
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 223098

Seq. ID LIB3165-039-Q1-K1-B6

Method BLASTX
NCBI GI g2129511
BLAST score 657
E value 4.0e-69



```
141
Match length
                  89
% identity
                  glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1,
NCBI Description
                  microbody - cucurbit >gi_1304042_dbj_BAA08410_ (D49432)
                  hydroxypyruvate reductase [Cucurbita sp.]
                  223099
Seq. No.
                  LIB3165-039-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115357
BLAST score
                  363
                  1.0e-34
E value
                  134
Match length
% identity
                  51
                 (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223100
                  LIB3165-039-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3420052
                  350
BLAST score
E value
                  4.0e-33
                  118
Match length
% identity
                  62
                  (AC004680) putative ubiqinone reductase [Arabidopsis
NCBI Description
                  thaliana]
                  223101
Seq. No.
                  LIB3165-039-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  361
E value
                  2.0e-34
                  98
Match length
                  76
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  223102
Seq. No.
                  LIB3165-039-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  453
E value
                  4.0e-45
Match length
                  122
                  77
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
```

Seq. No. 223103

Seq. ID LIB3165-039-Q1-K1-C10

Method BLASTX
NCBI GI 94566614
BLAST score 414
E value 1.0e-40
Match length 108
% identity 74

NCBI Description (AF112887) actin depolymerizing factor [Populus alba x

Populus tremula]



```
Seq. No.
                  223104
Seq. ID
                  LIB3165-039-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g266893
BLAST score
                  730
                  1.0e-77
E value
Match length
                  141
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                  sativus]
Seq. No.
                  223105
                  LIB3165-039-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g294060
BLAST score
                  174
                  2.0e-12
E value
Match length
                  128
% identity
                  33
NCBI Description (L06467) major latex protein [Papaver somniferum]
Seq. No.
                  223106
                  LIB3165-039-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244924
BLAST score
                  334
                  3.0e-31
E value
                  93
Match length
                  65
% identity
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]
                  223107
Seq. No.
                  LIB3165-039-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500378
                  423
BLAST score
                  1.0e-41
E value
                  87
Match length
                  89
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
                  223108
Seq. No.
                  LIB3165-039-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
```

BLAST score 641 3.0e-67 E value Match length 124 99 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

Seq. No.

223114



ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
223109
Seq. No.
                  LIB3165-039-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  q1408471
NCBI GI
BLAST score
                  531
                  2.0e-54
E value
                  117
Match length
                  82
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
                  223110
Seq. No.
                  LIB3165-039-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  q68200
NCBI GI
BLAST score
                  531
                  2.0e-54
E value
                  131
Match length
                  82
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633_emb_CAA47293_ (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
                   223111
Seq. No.
                  LIB3165-039-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  361
                  2.0e-34
E value
                  98
Match length
% identity
                  76
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   223112
Seq. No.
                  LIB3165-039-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4559292
BLAST score
                   370
                   2.0e-35
E value
                  109
Match length
% identity
                   63
NCBI Description (AF124148) trehalase 1 GMTRE1 [Glycine max]
                   223113
Seq. No.
                   LIB3165-039-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   g4454458
NCBI GI
BLAST score
                   186
                   6.0e-14
E value
                   125
Match length
                   43
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
```

31619



```
Seq. ID
                  LIB3165-039-Q1-K1-E11
                  BLASTX
Method
                  q2677828
NCBI GI
BLAST score
                  484
                  8.0e-49
E value
                  135
Match length
                  68
% identity
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  223115
Seq. No.
                  LIB3165-039-Q1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q228403
                  542
BLAST score
                  1.0e-55
E value
                  121
Match length
                   87
% identity
NCBI Description glycolate oxidase [Lens culinaris]
                   223116
Seq. No.
                  LIB3165-039-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g1061040
NCBI GI
BLAST score
                   644
                   1.0e-67
E value
                   128
Match length
                   91
% identity
                  (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
NCBI Description
                   >qi 1587694 prf 2207220A sterol C-methyltransferase
                   [Arabidopsis thaliana]
                   223117
Seq. No.
                   LIB3165-039-Q1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3953473
BLAST score
                   451
                   6.0e-45
E value
Match length
                   141
                   72
% identity
NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]
                   223118
Seq. No.
                   LIB3165-039-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   g1788965
NCBI GI
                   187
BLAST score
                   5.0e-14
E value
                   124
Match length
                   37
% identity
NCBI Description (AE000347) orf, hypothetical protein [Escherichia coli]
                   223119
Seq. No.
                   LIB3165-039-Q1-K1-E5
Seq. ID
                   BLASTX
Method
```

31620

g421843

2.0e-30

327

NCBI GI

E value

BLAST score



```
131
Match length
% identity
                  protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
NCBI Description
                  >gi 217861_dbj_BAA01715_ (D10909) serine/threonine protein
                  kinase [Arabidopsis thaliana]
                  223120
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-E7
                  BLASTX
Method
                  q3687652
NCBI GI
                  639
BLAST score
                  5.0e-67
E value
                  133
Match length
                  94
% identity
NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]
                  223121
Seq. No.
                  LIB3165-039-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  q3023752
NCBI GI
                  346
BLAST score
                  1.0e-32
E value
                  113
Match length
                  63
% identity
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
                  ferredoxin-I [Lycopersicon esculentum]
                  223122
Seq. No.
                  LIB3165-039-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  q3059131
NCBI GI
                  226
BLAST score
                  1.0e-18
E value
Match length
                  69
                  62
% identity
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]
                   223123
Seq. No.
                   LIB3165-039-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   q1168411
NCBI GI
BLAST score
                   525
                   1.0e-53
E value
Match length
                   127
                   83
 % identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   223124
 Seq. No.
                   LIB3165-039-Q1-K1-F12
 Seq. ID
                   BLASTX
 Method
```

Method BLASTX
NCBI GI g1354515
BLAST score 317
E value 3.0e-29
Match length 139
% identity 50

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]



Seq. No. 223125

Seq. ID LIB3165-039-Q1-K1-F3

BLASTX Method NCBI GI q2499966 BLAST score 159 1.0e-10 E value Match length 107 42 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E NCBI Description

> A) >gi 632722 bbs 151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

141 aa] [Nicotiana sylvestris]

223126 Seq. No.

Seq. ID LIB3165-039-Q1-K1-F4

Method BLASTX NCBI GI q231688 BLAST score 672 1.0e-70 E value Match length 134 100 % identity

NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC

1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

223127 Seq. No.

LIB3165-039-Q1-K1-F5 Seq. ID

Method BLASTX NCBI GI g1168411 BLAST score 147 2.0e-09 E value 90 Match length 43

% identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

223128 Seq: No.

LIB3165-039-Q1-K1-F6 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 495 4.0e-50 E value 95 Match length % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223129 Seq. No.

LIB3165-039-Q1-K1-F7 Seq. ID

Method BLASTX NCBI GI q1354515 BLAST score 310 2.0e-28 E value 139 Match length



```
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  223130
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  531
E value
                  2.0e-54
                  103
Match length
                  99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223131
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2905643
BLAST score
                  265
                  4.0e-23
E value
                  108
Match length
                  48
% identity
NCBI Description (AF045244) ribitol kinase [Klebsiella pneumoniae]
                  223132
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q4415908
BLAST score
                  163
                  3.0e-11
E value
Match length
                  48
                  54
% identity
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]
                  223133
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q4455208
BLAST score
                  305
                  7.0e-28
E value
Match length
                  100
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  223134
Seq. ID
                  LIB3165-039-Q1-K1-G3
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3885513
BLAST score 329
E value 1.0e-30
Match length 68
% identity 87

NCBI Description (AF084201) similar to chloroplast 50S ribosomal protein L31

Seq. ID

Method



[Medicago sativa]

```
Seq. No.
                  223135
Seq. ID
                  LIB3165-039-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q1352821
                  590
BLAST score
                  3.0e-61
E value
                  110
Match length
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) > gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223136
Seq. No.
                  LIB3165-039-Q1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q131167
                  447
BLAST score
                  2.0e-44
E value
                  138
Match length
                  67
% identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 100292 pir__S18348 photosystem I chain II precursor -
                  wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2
                  [Nicotiana sylvestris]
                  223137
Seq. No.
Seq. ID
                  LIB3165-039-Q1-K1-G8
                  BLASTX
Method
                  a421826
NCBI GI
BLAST score
                  426
                  5.0e-42
E value
                  125
Match length
% identity
NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  223138
                  LIB3165-039-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3913651
BLAST score
                  381
                  9.0e-37
E value
Match length
                  92
                  76
% identity
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
                  (FNR) >gi_2225993_emb_CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                  223139
Seq. No.
```

31624

LIB3165-039-Q1-K1-H10

BLASTX

```
q1332579
NCBI GI
BLAST score
                  507
                  1.0e-67
E value
                  140
Match length
                  10
% identity
                 (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  223140
Seq. No.
                  LIB3165-039-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  g3914605
NCBI GI
BLAST score
                  171
E value
                  2.0e-12
                  97
Match length
                  42
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857_ (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Malus domestica]
                  223141
Seq. No.
                  LIB3165-039-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  q3417451
NCBI GI
                   417
BLAST score
                  3.0e-41
E value
                  89
Match length
                  89
% identity
                  (AB013728) light-harvesting chlorophyll a/b-binding protein
NCBI Description
                  of photosystem II [Cryptomeria japonica]
Seq. No.
                   223142
                   LIB3165-039-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
BLAST score
                   375
                   5.0e-36
E value
Match length
                   67
                   100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223143
Seq. No.
Seq. ID
                   LIB3165-039-Q1-K1-H6
                   BLASTX
Method
                   g1352821
NCBI GI
BLAST score
                   627
```

31625

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

1.0e-65

124

98

E value

Match length

% identity



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223144 Seq. No. Seq. ID LIB3165-039-Q1-K1-H7 BLASTX Method g68200 NCBI GI 512 BLAST score 4.0e-52 E value 125 Match length 83 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 223145

Seq. ID LIB3165-039-Q1-K1-H8
Method BLASTX
NCBI GI g1168411
BLAST score 500
E value 1.0e-50
Match length 124
% identity 82

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 223146

Seq. ID LIB3165-039-Q1-K1-H9

Method BLASTX
NCBI GI g100200
BLAST score 488
E value 3.0e-49
Match length 123
% identity 76

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 223147

Seq. ID LIB3165-040-Q1-K1-A1

Method BLASTX
NCBI GI g1352821
BLAST score 666
E value 3.0e-70
Match length 125
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223148

Seq. ID LIB3165-040-Q1-K1-A10

Method BLASTX
NCBI GI g2618721
BLAST score 169
E value 6.0e-12
Match length 77



```
% identity
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223149
Seq. ID
                  LIB3165-040-Q1-K1-A11
                  BLASTX
Method
NCBI GI
                  q4103987
BLAST score
                  414
                  1.0e-50
E value
Match length
                  122
                  84
% identity
                  (AF030516) 5,10-methylenetetrahydrofolate
NCBI Description
                  dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum]
                  223150
Seq. No.
                  LIB3165-040-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g3355480
NCBI GI
BLAST score
                  312
                  9.0e-29
E value
Match length
                  101
                  58
% identity
                  (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   223151
Seq. ID
                  LIB3165-040-Q1-K1-A5
Method
                  BLASTX
                   q68200
NCBI GI
                   468
BLAST score
                   5.0e-47
E value
                   115
Match length
% identity
                   82
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                   223152
                   LIB3165-040-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g3913414
NCBI GI
                   507
BLAST score
                   2.0e-51
E value
                   135
Match length
                   76
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2)
NCBI Description
                   (SAMDC 2) (SAMDC16) >gi_1155242 (U38527)
                   S-adenosylmethionine decarboxylase 2 [Dianthus
                   caryophyllus]
```

Seq. No. 223153
Seq. ID LIB3165-040-Q1-K1-A7

Method BLASTX NCBI GI g82188

NCBI GI g82188 BLAST score 383 E value 5.0e-37

```
Match length
                  114
% identity
                  photosystem II oxygen-evolving complex protein 2 precursor
NCBI Description
                  - common tobacco (fragment) >gi 19896 emb CAA41713
                  (X58910) photosystem II 23 kDa polypeptide [Nicotiana
                  tabacum]
Seq. No.
                  223154
                  LIB3165-040-Q1-K1-B1
Seq. ID
Method
                  BLASTX
                  q1170897
NCBI GI
BLAST score
                  311
E value
                  1.0e-28
                  86
Match length
                  72
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >qi 1076276 pir S52039 NAD-malate dehydrogenase - cucumber
                  >gi 695311 (L31900) glyoxysomal malate dehydrogenase
                  [Cucumis sativus]
                  223155
Seq. No.
                  LIB3165-040-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g1532135
NCBI GI
BLAST score
                  601
                  1.0e-62
E value
                  138
Match length
% identity
NCBI Description
                  (U49442) chloroplast mRNA-binding protein CSP41 precursor
                  [Spinacia oleracea]
Seq. No.
                  223156
                  LIB3165-040-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928099
BLAST score
                  288
                  7.0e-26
E value
Match length
                  139
% identity
                  23
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
                  223157
Seq. No.
                  LIB3165-040-Q1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2213590
BLAST score
                  203
                  7.0e-16
E value
                  106
Match length
% identity
                  40
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
```

Seq. No. 223158

Seq. ID LIB3165-040-Q1-K1-B5 Method BLASTX

Method BLASTX
NCBI GI g1076708
BLAST score 552
E value 8.0e-57



Match length 126 % identity 25 NCBI Description

seed tetraubiquitin - common sunflower

>gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi 994785 dbj BAA05085 (D26092)

Ubiquitin [Glycine max] >gi_4263514 gb AAD15340 (AC004044)

putative polyubiquitin [Arabidopsis thaliana]

>gi 1096513 prf 2111434A tetraubiquitin [Helianthus

annuus]

Seq. No.

223159

LIB3165-040-Q1-K1-B7 Seq. ID

BLASTX Method NCBI GI q117822 BLAST score 653 1.0e-68 E value Match length 137 90 % identity

CYTOCHROME B6 >gi 65635 pir CBNT6 NCBI Description

plastoquinol--plastocyanin reductase (EC 1.10.99.1)

cytochrome b6 - common tobacco chloroplast

>gi_11858_emb_CAA77375_ (Z00044) cytochrome b6 [Nicotiana tabacum] >gi 225226 prf 1211235BH cytochrome b6 [Nicotiana

tabacum]

Seq. No.

223160 Seq. ID

LIB3165-040-Q1-K1-B8

Method BLASTX g1419090 NCBI GI 365 BLAST score 7.0e-35 E value Match length 104 70 % identity

(X94968) 37kDa chloroplast inner envelope membrane NCBI Description

polypeptide precursor [Nicotiana tabacum]

Seq. No. 223161

LIB3165-040-Q1-K1-B9 Seq. ID

BLASTX Method g1170507 NCBI GI BLAST score 172 3.0e-12 E value 45 Match length 80 % identity

EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) NCBI Description

>gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 223162

LIB3165-040-Q1-K1-C1 Seq. ID

Method BLASTX NCBI GI g1354515 BLAST score 255



E value 5.0e-22 Match length 103 % identity 55

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 223163

Seq. ID LIB3165-040-Q1-K1-C2

Method BLASTX
NCBI GI g1814403
BLAST score 660
E value 2.0e-69
Match length 140
% identity 89

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 223164

Seq. ID LIB3165-040-Q1-K1-C4

Method BLASTX
NCBI GI 94490297
BLAST score 291
E value 2.0e-42
Match length 127
% identity 64

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 223165

Seq. ID LIB3165-040-Q1-K1-C5

Method BLASTX
NCBI GI g1352821
BLAST score 398
E value 9.0e-39
Match length 107
% identity 76

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223166

Seq. ID LIB3165-040-Q1-K1-C6

Method BLASTX
NCBI GI g166702
BLAST score 250
E value 3.0e-26
Match length 68
% identity 91

NCBI Description (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit

[Arabidopsis thaliana]

Seq. No. 223167

Seq. ID LIB3165-040-Q1-K1-C7

Method BLASTX
NCBI GI g4115357
BLAST score 261



```
E value
                  1.0e-22
Match length
                  137
                  43
% identity
                  (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  223168
Seq. No.
                  LIB3165-040-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                  q20729
NCBI GI
BLAST score
                  508
                  1.0e-51
E value
                  134
Match length
% identity
                  78
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  223169
Seq. No.
Seq. ID
                  LIB3165-040-Q1-K1-D1
                  BLASTX
Method
NCBI GI
                  q3914605
BLAST score
                   440
                   1.0e-43
E value
                   138
Match length
                   64
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                   PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                   apple tree >gi 415852 emb CAA79857 (Z21794)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Malus domestica]
Seq. No.
                   223170
                   LIB3165-040-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1652745
                   260
BLAST score
                   1.0e-22
E value
                   112
Match length
% identity
                   43
                  (D90908) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   223171
                   LIB3165-040-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3928760
                   215
BLAST score
                   3.0e-17
E value
                   104
Match length
                   47
% identity
                  (AB011797) homolog to plastid-lipid-associated protein
NCBI Description
                   [Citrus unshiu]
```

223172 Seq. No. Seq. ID LIB3165-040-Q1-K1-D4

Method BLASTX

NCBI GI g289920 697 BLAST score 8.0e-74 E value



```
131
Match length
                  98
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  223173
Seq. No.
                  LIB3165-040-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g1396054
NCBI GI
                  136
BLAST score
                  1.0e-08
E value
                  39
Match length
                  67
% identity
                  (D86180) phosphoribosylanthranilate transferase [Pisum
NCBI Description
                  sativum]
                  223174
Seq. No.
                  LIB3165-040-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  584
                  1.0e-60
E value
                  110
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223175
                  LIB3165-040-Q1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1170711
BLAST score
                  183
                   9.0e-14
E value
                   65
Match length
% identity
                  SHAGGY RELATED PROTEIN KINASE ASK-ALPHA
NCBI Description
                   >qi 541901 pir S41596 protein kinase ASK-alpha (EC
                   2.7.1.-) - Arabidopsis thaliana >gi 460832 emb CAA53181
                   (X75432) shaggy related kinase [Arabidopsis thaliana]
                   >gi 1769889 emb CAA48538 (X68525) serine /threonine
                   protein kinase [Arabidopsis thaliana]
Seq. No.
                   223176
                   LIB3165-040-Q1-K1-D9
Seq. ID
```

Method BLASTX
NCBI GI g3660471
BLAST score 636
E value 1.0e-66
Match length 135
% identity 88

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 223177



LIB3165-040-Q1-K1-E11 Seq. ID BLASTX Method NCBI GI q2388577 BLAST score 415 E value 9.0e-41Match length 136 56 % identity (AC000098) Similar to Arabidopsis putative ion-channel NCBI Description PID:g2262157 (gb AC002329). [Arabidopsis thaliana] Seq. No. 223178 Seq. ID LIB3165-040-Q1-K1-E2 Method BLASTX NCBI GI q1709651 BLAST score 411 E value 3.0e-40130 Match length 62 % identity NCBI Description PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209 plastocyanin a precursor - black poplar >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus nigra] 223179 Seq. No. Seq. ID LIB3165-040-Q1-K1-E3 Method BLASTX g505482 NCBI GI BLAST score 669 E value 2.0e-70 Match length 136 93 % identity NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum] Seq. No. 223180 Seq. ID LIB3165-040-Q1-K1-E4 Method BLASTX NCBI GI g729668 BLAST score 300 3.0e-27 E value 70 Match length 84 % identity HISTONE H1 >gi 2147479 pir S65059 histone H1, NCBI Description drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii] Seq. No. 223181 Seq. ID LIB3165-040-Q1-K1-E8 Method BLASTX NCBI GI g231688 BLAST score 664 E value 5.0e-72Match length 133

% identity 100

NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

BLAST score

% identity

E value Match length 516 9.0e-55

135 85

```
223182
Seq. No.
Seq. ID
                  LIB3165-040-Q1-K1-F10
Method
                  BLASTX
                  g1255954
NCBI GI
                  534
BLAST score
E value
                  1.0e-54
Match length
                  118
% identity
                  83
                 (Z70677) thioredoxin [Ricinus communis]
NCBI Description
Seq. No.
                  223183
                  LIB3165-040-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  249
                  1.0e-24
E value
Match length
                  72
% identity
                  85
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223184
                  LIB3165-040-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529668
                  652
BLAST score
E value
                  1.0e-68
Match length
                  140
                  87
% identity
                  (AC002535) putative photolyase/blue-light receptor
NCBI Description
                   [Arabidopsis thaliana] >gi_3319288 (AF053366)
                  photolyase/blue light photoreceptor PHR2 [Arabidopsis
                  thaliana]
Seq. No.
                  223185
                  LIB3165-040-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g4539316
NCBI GI
BLAST score
                  301
                  2.0e-33
E value
                  101
Match length
                  81
% identity
                  (AL035679) putative fructose-bisphosphate aldolase
NCBI Description
                   [Arabidopsis thaliana]
                  223186
Seq. No.
                  LIB3165-040-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131385
```



NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No. 223187

Seq. ID LIB3165-040-Q1-K1-G1

Method BLASTX
NCBI GI g1352821
BLAST score 643
E value 2.0e-67
Match length 120
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223188

Seq. ID LIB3165-040-Q1-K1-G10

Method BLASTX
NCBI GI g2129752
BLAST score 344
E value 2.0e-32
Match length 87
% identity 68

NCBI Description thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_

(Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No. 223189

Seq. ID LIB3165-040-Q1-K1-G2

Method BLASTX
NCBI GI g289920
BLAST score 711
E value 2.0e-75
Match length 134
% identity 99

NCBÍ Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 223190

Seq. ID LIB3165-040-Q1-K1-G3

Method BLASTX
NCBI GI g1946367
BLAST score 507
E value 2.0e-51
Match length 118
% identity 81

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 223191

Seq. ID LIB3165-040-Q1-K1-G4

Method BLASTX
NCBI GI g1707017
BLAST score 464
E value 6.0e-61
Match length 136

31635



```
% identity
                  (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223192
                  LIB3165-040-Q1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3334113
BLAST score
                  333
                  4.0e-31
E value
Match length
                  89
                  74
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
NCBI Description
                  acyl-CoA-binding protein [Gossypium hirsutum]
                  223193
Seq. No.
Seq. ID
                  LIB3165-040-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3292831
BLAST score
                  143
                  7.0e-09
E value
Match length
                  124
% identity
                  35
                  (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                  thaliana]
                  223194
Seq. No.
                  LIB3165-040-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g403160
BLAST score
                  333
E value
                  2.0e-43
Match length
                  110
% identity
                  74
                  (L24497) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Pyrus malus X domestica]
                  223195
Seq. No.
                  LIB3165-040-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g4206206
NCBI GI
BLAST score
                   226
                  1.0e-18
E value
                  105
Match length
                   44
% identity
                   (AF071527) putative M-type thioredoxin [Arabidopsis
NCBI Description
                   thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative
                  M-type thioredoxin [Arabidopsis thaliana]
                   223196
Seq. No.
                  LIB3165-040-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2864613
BLAST score
                   349
```

E. value 5.0e-33

Match length 127 % identity 51

NCBI Description (AL021811) S-receptor kinase -like protein [Arabidopsis



thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana]

223197 Seq. No. Seq. ID LIB3165-040-Q1-K1-H2 Method BLASTX q231610 NCBI GI BLAST score 356 7.0e-34 E value 118 Match length % identity 65

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 223198

Seq. ID LIB3165-040-Q1-K1-H3

Method BLASTX
NCBI GI g3869088
BLAST score 583
E value 2.0e-60
Match length 115
% identity 97

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 223199

Seq. ID LIB3165-040-Q1-K1-H5

Method BLASTX
NCBI GI g3885884
BLAST score 585
E value 1.0e-60
Match length 117
% identity 92

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 223200

Seq. ID LIB3165-040-Q1-K1-H8

Method BLASTX
NCBI GI g119748
BLAST score 529
E value 4.0e-54
Match length 114
% identity 91

NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11),

cytosolic - spinach >gi 21245 emb CAA43860 (X61690)

fructose-bisphosphatase [Spinacia oleracea]

Seq. No. 223201

Seq. ID LIB3165-040-Q1-K1-H9

Method BLASTX NCBI GI g4454472 BLAST score 156 E value 1.0e-10



```
Match length 94 % identity 40
```

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 223202

Seq. ID LIB3165-041-Q1-K1-A10

Method BLASTX
NCBI GI 94099835
BLAST score 416
E value 7.0e-41
Match length 112
% identity 63

NCBI Description (U90266) bifunctional nuclease [Zinnia elegans]

Seq. No. 223203

Seq. ID LIB3165-041-Q1-K1-A4

Method BLASTX
NCBI GI g1781348
BLAST score 291
E value 2.0e-26
Match length 64
% identity 86

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 223204

Seq. ID LIB3165-041-Q1-K1-A7

Method BLASTX
NCBI GI g587564
BLAST score 315
E value 2.0e-29
Match length 83
% identity 73

NCBI Description (X80235) mitochondrial processing peptidase [Solanum

tuberosum]

Seq. No. 223205

Seq. ID LIB3165-041-Q1-K1-A8

Method BLASTX
NCBI GI g417544
BLAST score 590
E value 3.0e-61
Match length 112
% identity 98

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi_320209_pir__A60695 photosystem I chain II precursor - cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K protein precursor - cucumber >gi_227772_prf__1710320A

photosystem I 20kD protein [Cucumis sativus]

Seq. No. 223206

Seq. ID LIB3165-041-Q1-K1-A9

Method BLASTX
NCBI GI g4127456
BLAST score 334
E value 3.0e-31

Seq. ID

```
Match length
                  117
% identity
                   62
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
                  223207
Seq. No.
                  LIB3165-041-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4091806
                  545
BLAST score
                  5.0e-56
E value
                  128
Match length
% identity
                  82
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
NCBI Description
Seq. No.
                  223208
                  LIB3165-041-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4090943
                   305
BLAST score
                  7.0e-28
E value
                  123
Match length
% identity
                   46
NCBI Description
                  (AF029984) COP1 homolog [Lycopersicon esculentum]
                   223209
Seq. No.
                  LIB3165-041-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885884
BLAST score
                   523
                  2.0e-53
E value
                  105
Match length
                   90
% identity
NCBI Description
                 (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                   223210
Seq. No.
                  LIB3165-041-Q1-K1-B7
Seq. ID
Method -
                  BLASTX
                  g1353352
NCBI GI
BLAST score
                   320
                   1.0e-29
E value
                   90
Match length
% identity
                   73
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
                   223211
Seq. No.
                  LIB3165-041-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2980770
NCBI GI
BLAST score
                   395
E value
                   1.0e-38
                   84
Match length
% identity
                   88
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   223212
```

31639

LIB3165-041-Q1-K1-C11



BLASTX Method NCBI GI q2262164 168 BLAST score 9.0e-12 E value 64 Match length % identity (AC002329) putative obtusifoliol 14-alpha demethylase NCBI Description [Arabidopsis thaliana] 223213 Seq. No. LIB3165-041-Q1-K1-C12 Seq. ID BLASTX Method g2262164 NCBI GI 157 BLAST score 2.0e-10 E value 64 Match length 58 % identity (AC002329) putative obtusifoliol 14-alpha demethylase NCBI Description [Arabidopsis thaliana] 223214 Seq. No. LIB3165-041-Q1-K1-C8 Seq. ID BLASTX Method NCBI GI g3914603 BLAST score 665 4.0e-70 E value 132 Match length 94 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE NCBI Description PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa] Seq. No. 223215 Seq. ID LIB3165-041-Q1-K1-D10 Method BLASTX g289920 NCBI GI BLAST score 743 3.0e-79E value Match length 140 99 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 223216 Seq. No. LIB3165-041-Q1-K1-D11 Seq. ID BLASTX Method g3980394 NCBI GI 182 BLAST score 2.0e-13 E value 94 Match length

46 % identity

NCBI Description (AC004561) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 223217

LIB3165-041-Q1-K1-D2 Seq. ID

BLASTX Method



g289920 NCBI GI BLAST score 242 4.0e-25 E value 80 Match length 76 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 223218 Seq. No. Seq. ID LIB3165-041-Q1-K1-D4 BLASTX Method q115813 NCBI GI 309 BLAST score 1.0e-51 E value 140 Match length 73 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR NCBI Description (CAB-8) >gi 19182_emb CAA33330 (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] 223219 Seq. No. Seq. ID LIB3165-041-Q1-K1-D7 BLASTX Method g3288821 NCBI GI BLAST score 318 1.0e-29 E value 99 Match length 64 % identity (AF063901) alanine:glyoxylate aminotransferase; NCBI Description transaminase [Arabidopsis thaliana] 223220 Seq. No. Seq. ID LIB3165-041-Q1-K1-D8 BLASTX Method NCBI GI q4406530 BLAST score 369 2.0e-35 E value 123 Match length 64 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] Seq. No. 223221 LIB3165-041-Q1-K1-E1 Seq. ID BLASTX Method NCBI GI q126334 BLAST score 171 4.0e-12 _E value Match length 82

46 % identity

NCBI Description LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)

>gi 79925 pir A24075 lipase precursor - Staphylococcus

hyicus >gi 47136 emb CAA26602 (X02844) precursor

[Staphylococcus hyicus]

223222 Seq. No.

LIB3165-041-Q1-K1-E10 Seq. ID

BLASTX Method



```
NCBI GI
                   q3165581
BLAST score
                   187
                   5.0e-14
E value
Match length
                   106
                   39
% identity
                   (AF067942) similar to lysosomal acid lipases (SW:P38571)
NCBI Description
                   [Caenorhabditis elegans]
                   223223
Seq. No.
                   LIB3165-041-Q1-K1-E2
Seq. ID
Method
                   BLASTX
                   q3660471
NCBI GI
BLAST score
                   532
                   1.0e-54
E value
                   116
Match length
% identity
```

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

 Seq. No.
 223224

 Seq. ID
 LIB3165-041-Q1-K1-E7

 Method
 BLASTX

 NCBI GI
 g1352821

 BLAST SCORE
 585

BLAST score 585 E value 1.0e-60 Match length 109 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223225

Seq. ID LIB3165-041-Q1-K1-E8

Method BLASTX
NCBI GI 94220477
BLAST score 281
E value 4.0e-25
Match length 113
% identity 56

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 223226

Seq. ID LIB3165-041-Q1-K1-F1

Method BLASTX
NCBI GI g1708313
BLAST score 555
E value 4.0e-57
Match length 117
% identity 95

NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637

(S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

thaliana]

Seq. No. 223227



Seq. ID LIB3165-041-Q1-K1-F7 Method BLASTX NCBI GI g1352821 BLAST score 630 E value 6.0e-66 116 Match length 100 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223228 Seq. No.

LIB3165-041-Q1-K1-F8 Seq. ID

BLASTX Method NCBI GI g1352821 BLAST score 554 E value 5.0e-57 107 Match length 98 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) > gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223229 Seq. No.

Seq. ID LIB3165-041-Q1-K1-G5

Method BLASTX NCBI GI q2501568 BLAST score 163 E value 3.0e-11 Match length 54 % identity 52

NCBI Description HYPOTHETICAL 28.8 KD PROTEIN SLL0506

>gi_1001342 dbj BAA10829 (D64006) hypothetical protein

[Synechocystis sp.]

Seq. No. 223230

Seq. ID LIB3165-041-Q1-K1-G8

Method BLASTX NCBI GI g3292824 BLAST score 297 E value 6.0e-27 Match length 77 75 % identity

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 223231

Seq. ID LIB3165-041-Q1-K1-G9

Method BLASTX NCBI GI g289920 BLAST score 605 E value 4.0e-63 Match length 112 % identity 100



```
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  223232
Seq. ID
                  LIB3165-041-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q3426043
BLAST score
                  595
E value
                  8.0e-62
Match length
                  134
                  77
% identity
                 (AC005168) putative choline kinase [Arabidopsis thaliana]
NCBI Description
                  223233
Seq. No.
                  LIB3165-041-Q1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2995384
BLAST score
                  162
E value
                  1.0e-11
Match length
                  44
                  73
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                  223234
                  LIB3165-041-Q1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2088651
BLAST score
                  419
E value
                  3.0e-41
Match length
                  125
% identity
                  63
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  223235
                  LIB3165-041-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2815246
BLAST score
                  225
E value
                  2.0e-18
Match length
                  55
                  73
% identity
NCBI Description
                 (X95709) class I type 2 metallothionein [Cicer arietinum]
                  223236
Seq. No.
                  LIB3165-041-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2969887
BLAST score
                  454
                  3.0e-45
E value
Match length
                  138
% identity
                  65
                  (Y16766) sucrose/H+ symporter [Daucus carota]
NCBI Description
```

>gi_2969889_emb_CAA76368_ (Y16767) sucrose/H+ symporter

[Daucus carota]

Seq. No. 223237

E value

Match length

% identity

2.0e-51

128

80



```
Seq. ID
                  LIB3165-042-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  342
E value
                  2.0e-32
Match length
                  67
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223238
Seq. ID
                  LIB3165-042-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  q2864617
BLAST score
                  141
E value
                  1.0e-08
                  110
Match length
                  36
% identity
NCBI Description (ALO21811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana]
Seq. No.
                  223239
                  LIB3165-042-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q266893
BLAST score
                  699
E value
                  5.0e-74
Match length
                  134
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                  sativus]
Seq. No.
                  223240
                  LIB3165-042-Q1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1353352
BLAST score
                  167
E value
                  3.0e-12
                  71
Match length
                  52
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  223241
Seq. No.
                  LIB3165-042-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q430947
BLAST score
                  507
```

31645

NCBI Description

Seq. No.

223247



```
(U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  223242
Seq. No.
Seq. ID
                  LIB3165-042-Q1-K1-A6
                  BLASTX
Method
                  g131385
NCBI GI
BLAST score
                  463
                  2.0e-46
E value
                  116
Match length
                  83
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
                  223243
Seq. No.
                  LIB3165-042-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  g1354515
NCBI GI
BLAST score
                  213
                  2.0e-17
E value
                  82
Match length
                  61
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  223244
Seq. No.
Seq. ID
                  LIB3165-042-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                  g4455177
BLAST score
                  271
                  7.0e-24
E value
                  102
Match length
                  53
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                  223245
                  LIB3165-042-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3413167
BLAST score
                   369
E value
                   2.0e-35
                  73
Match length
% identity
                   99
NCBI Description (AJ010225) elongation factor 1-alpha [Cicer arietinum]
Seq. No.
                   223246
                  LIB3165-042-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3386621
BLAST score
                   632
                   3.0e-66
E value
Match length
                  135
                   90
% identity
```

31646

(AC004665) unknown protein [Arabidopsis thaliana]



```
LIB3165-042-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  570
                  6.0e-59
E value
                  108
Match length
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223248
Seq. No.
                  LIB3165-042-Q1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q416681
                  318
BLAST score
E value
                  2.0e-29
                  99
Match length
                  65
% identity
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_280404_pir__S26198 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain precursor, chloroplast - common
                  tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP
                  synthase (delta subunit) [Nicotiana tabacum]
                  223249
Seq. No.
Seq. ID
                  LIB3165-042-Q1-K1-B6
Method
                  BLASTX
                  q289920
NCBI GI
                  586
BLAST score
                  7.0e-61
E value
Match length
                  114
                  96
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  223250
Seq. No.
                  LIB3165-042-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                   343
                   2.0e-32
E value
                   68
Match length
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505_emb CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

Seq. No. 223251

Seq. ID LIB3165-042-Q1-K1-B8

Method BLASTX NCBI GI g1168411 BLAST score 295



```
E value
                  2.0e-43
Match length
                  117
                  81
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  223252
Seq. No.
                  LIB3165-042-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  602
                  1.0e-62
E value
Match length
                  115
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  223253
Seq. No.
Seq. ID
                  LIB3165-042-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  577
                  8.0e-60
E value
Match length
                  110
                  97
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  223254
Seq. ID
                  LIB3165-042-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g542020
BLAST score
                  479
                  3.0e-48
E value
Match length
                  117
% identity
                  77
                  sucrose transport protein - castor bean
NCBI Description
                  >gi 468562 emb CAA83436 (Z31561) sucrose carrier [Ricinus
                  communis]
Seq. No.
                  223255
                  LIB3165-042-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  482
E value
                  1.0e-48
                  122
Match length
% identity
                  76
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  223256
                  LIB3165-042-Q1-K1-C4
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g417103
BLAST score 618
E value 2.0e-64
Match length 125
% identity 99

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone



H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >qi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi 4038469 gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 223257 Seq. ID LIB3165-042-Q1-K1-C6 BLASTX Method NCBI GI g505482 BLAST score 357 3.0e-35 E value Match length 104 82 % identity

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

223258 Seq. No. LIB3165-042-Q1-K1-C7 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 529 4.0e-54E value 101 Match length 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223259

% identity

LIB3165-042-Q1-K1-D5 Seq. ID

Method BLASTX NCBI GI g100200 BLAST score 263 E value 4.0e-32 Match length 105 % identity 71

NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

223260 Seq. No.

LIB3165-042-Q1-K1-D9 Seq. ID

Method BLASTX

31649

```
NCBI GI
                  g1483218
BLAST score
                   229
E value
                   5.0e-19
Match length
                   105
% identity
                   50
NCBI Description
                   (X99793) induced upon wounding stress [Arabidopsis
                   thaliana]
Seq. No.
                   223261
                  LIB3165-042-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4234941
BLAST score
                   513
                   3.0e-52
E value
Match length
                   121
                   88
% identity
NCBI Description
                   (AF097938) cytosolic phosphoglucomutase [Populus tremula x
                  Populus tremuloides]
Seq. No.
                   223262
Seq. ID
                  LIB3165-042-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                   g430947
BLAST score
                   442
                   7.0e-44
E value
Match length
                   108
                   81
% identity
NCBI Description
                   (U01103) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   223263
                   LIB3165-042-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3243234
BLAST score
                   270
                   1.0e-23
E value
Match length
                   123
% identity
                   44
NCBI Description
                   (AF071477) isoflavone reductase related protein [Pyrus
                   communis]
                   223264
Seq. No.
                  LIB3165-042-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1352821
BLAST score
                   614
                   4.0e-64
E value
Match length
                   114
% identity
                   100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
```

31650

223265

LIB3165-042-Q1-K1-E3

Seq. No. Seq. ID

ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
Method
                  BLASTX
NCBI GI
                  g100616
                  232
BLAST score
                  2.0e-19
E value
                  57
Match length
                  81
% identity
                  ribulose-bisphosphate carboxylase activase B precursor -
NCBI Description
                  barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                  carboxylase activase [Hordeum vulgare] >gi 167095 (M55449)
                  ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                  vulgare]
                  223266
Seq. No.
                  LIB3165-042-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363556
BLAST score
                  170
E value
                  4.0e-12
Match length
                  47
% identity
                  64
                  hypothetical protein 58 - maize chloroplast
NCBI Description
                  >gi 902297 emb CAA60361 (X86563) ORF58 [Zea mays]
                  223267
Seq. No.
Seq. ID
                  LIB3165-042-Q1-K1-E8
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  471
                  2.0e-47
E value
Match length
                  89
                  100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >qi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223268
Seq. No.
Seq. ID
                  LIB3165-042-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  543
                  1.0e-55
E value
Match length
                  105
                  99
% identity
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223269 Seq. No.

Seq. ID LIB3165-042-Q1-K1-F11

BLASTX Method NCBI GI g231573 BLAST score 164 7.0e-23E value



```
Match length
                   99
% identity
                   L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi 99970 pir S24757 asparaginase (EC 3.5.1.1) -
                   narrow-leaved blue lupine >gi_19135_emb_CAA43099 (X60691)
                   developing seed L-asparaginase [Lupinus angustifolius]
Seq. No.
                   223270
                   LIB3165-042-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g4115379
NCBI GI
BLAST score
                   314
E value
                   6.0e-29
                   114
Match length
% identity
                   61
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   223271
                   LIB3165-042-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g1352821
NCBI GI
                   594
BLAST score
                   1.0e-61
E value
                   111
Match length
                   98
 % identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
 Seq. No.
                   223272
 Seq. ID
                   LIB3165-042-Q1-K1-F5
 Method
                   BLASTX
 NCBI GI
                   g2213590
 BLAST score
                   268
                   2.0e-23
 E value
 Match length
                   140
 % identity
                   41
                   (AC000348) T7N9.10 [Arabidopsis thaliana]
 NCBI Description
                   223273
 Seq. No.
                   LIB3165-042-Q1-K1-F6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2190012
                   337
 BLAST score
                   1.0e-31
E value
                   108
 Match length
                   63
 % identity
                  (AB004242) din1 [Raphanus sativus]
 NCBI Description
```

Seq. No. 223274

Seq. ID LIB3165-042-Q1-K1-F9

Method BLASTX NCBI GI g1351270 BLAST score 418



E value 4.0e-41 Match length 118 % identity 69

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
5.3.1.1) - rice >gi_169821 (M87064) triosephosphate

isomerase [Oryza sativa]

Seq. No. 223275

Seq. ID LIB3165-042-Q1-K1-G1

Method BLASTX
NCBI GI g4406530
BLAST score 305
E value 7.0e-28
Match length 87

% identity 74

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223276

Seq. ID LIB3165-042-Q1-K1-G3

Method BLASTX
NCBI GI g1352821
BLAST score 546
E value 4.0e-56
Match length 105
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223277

Seq. ID LIB3165-042-Q1-K1-G4

Method BLASTX
NCBI GI g481132
BLAST score 150
E value 1.0e-09
Match length 31
% identity 94

NCBI Description sucrose transport protein SUC1 - Arabidopsis thaliana

>gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter

[Arabidopsis thaliana]

Seq. No. 223278

Seq. ID LIB3165-042-Q1-K1-G6

Method BLASTX
NCBI GI g115471
BLAST score 479
E value 3.0e-48
Match length 139
% identity 67

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792_(X52558) precursor peptide (AA -104 to 224) [Fisum sativum]



```
223279
 Seq. No.
 Seq. ID
                    LIB3165-042-Q1-K1-H12
 Method
                    BLASTX
· NCBI GI
                    g3158476
 BLAST score
                    372
                    7.0e-36
 E value
                    82
 Match length
                    85
 % identity
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                    223280
 Seq. No.
                    LIB3165-042-Q1-K1-H2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1352821
 BLAST score
                    569
                    8.0e-59
 E value
                    107
 Match length
                    100
 % identity
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                    (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                    ribulose bisphosphate carboxylase [Gossypium hirsutum]
 Seq. No.
                    223281
 Seq. ID
                    LIB3165-042-Q1-K1-H3
 Method
                    BLASTX
 NCBI GI
                    g3834388
 BLAST score
                    222
 E value
                    3.0e-18
                    118
 Match length
 % identity
                    45
 NCBI Description (AF038547) beta-1,4-mannanase [Bacillus stearothermophilus]
 Seq. No.
                    223282
 Seq. ID
                    LIB3165-042-Q1-K1-H4
 Method
                    BLASTX
 NCBI GI
                    g3702327
 BLAST score
                    201
 E value
                    1.0e-15
 Match length
                    111
 % identity
                    49
                   (AC005397) unknown protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    223283
                    LIB3165-042-Q1-K1-H6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2369714
 BLAST score
                    577
 E value
                    7.0e-60
 Match length
                    116
                    94
 % identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
 NCBI Description
```

Seq. No. 223284

Seq. ID LIB3165-042-Q1-K1-H7

Method BLASTX



```
NCBI GI
                  g20729
                  331
BLAST score
E value
                  5.0e-31
Match length
                  101
% identity
                  68
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
Seq. No.
                  223285
Seq. ID
                  LIB3165-042-Q1-K1-H8
                  BLASTX
Method
NCBI GI
                  g68064
BLAST score
                  155
                  1.0e-10
E value
Match length
                  56
                  62
% identity
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
NCBI Description
                  precursor - rape >gi_17855_emb_CAA30290_ (X07367) rubisco
                  ssu precursor [Brassica napus]
                  223286
Seq. No.
                  LIB3165-043-Q1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1778095
BLAST score
                  409
                  5.0e-40
E value
Match length
                 118
                  67
% identity
                  (U64903) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   223287
Seq. No.
                  LIB3165-043-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                   g1168411
NCBI GI
                   551
BLAST score
                   1.0e-56
E value
Match length
                  137
% identity
                   82
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   223288
Seq. No.
                  LIB3165-043-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g100616
NCBI GI
                   186
BLAST score
                   4.0e-14
E value
                   43
Match length
                   86
% identity
                  ribulose-bisphosphate carboxylase activase B precursor -
NCBI Description
                   barley >gi_167093 (M55448) ribulose 1,5-bisphosphate
                   carboxylase activase [Hordeum vulgare] >gi 167095 (M55449)
                   ribulose 1,5-bisphosphate carboxylase activase [Hordeum
```

Seq. No. 223289

Seq. ID LIB3165-043-Q1-K1-A7

vulgare]

% identity



```
BLASTX
Method
                  g2739375
NCBI GI
BLAST score
                  225
                  2.0e-18
E value
                  126
Match length
                  45
% identity
                 (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223290
Seq. ID
                  LIB3165-043-Q1-K1-A9
                  BLASTX
Method
                  g3334197
NCBI GI
BLAST score
                  446
                  2.0e-44
E value
Match length
                  113
                  74
% identity
NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T
                  PROTEIN) >gi 2894400 emb CAA94902 (Z71184) T-protein
                  [Flaveria anomala]
                  223291
Seq. No.
                  LIB3165-043-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1709651
BLAST score
                  229
                  5.0e-28
E value
                  124
Match length
                  62
% identity
                  PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
                  223292
Seq. No.
Seq. ID
                  LIB3165-043-Q1-K1-B12
Method
                  BLASTX
                  g1168408
NCBI GI
                  629
BLAST score
                  8.0e-66
E value
Match length
                  134
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
                  >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  223293
Seq. No.
                  LIB3165-043-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g1173347
NCBI GI
BLAST score
                  596
                  6.0e-62
E value
Match length
                  126
```

31656

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >qi 100803 pir S23452 sedoheptulose-bisphosphatase (EC

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR



3.1.3.37) precursor - wheat >gi 14265 emb CAA46507 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 223294

Seq. ID LIB3165-043-Q1-K1-B4

BLASTX Method NCBI GI q231688 282 BLAST score 9.0e-26 E value 59 Match length 90 % identity

CATALASE ISOZYME 2 >gi 99599 pir_S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 223295

LIB3165-043-Q1-K1-B8 Seq. ID

Method BLASTX q3288821 NCBI GI BLAST score 519 E value 6.0e-53 123 Match length 80 % identity

(AF063901) alanine:glyoxylate aminotransferase; NCBI Description

transaminase [Arabidopsis thaliana]

223296 Seq. No.

Seq. ID LIB3165-043-Q1-K1-C11

Method BLASTX NCBI GI g1527219 BLAST score 347 9.0e-33 E value Match length 76 % identity 83

NCBI Description (U68218) ATP sulphurylase [Brassica napus]

Seq. No. 223297

Seq. ID LIB3165-043-Q1-K1-C12

Method BLASTX NCBI GI g1352821 BLAST score 762 2.0e-81 E value Match length 145 % identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223298 Seq. No.

LIB3165-043-Q1-K1-C7 Seq. ID

BLASTX Method g3288821 NCBI GI 488 BLAST score 3.0e-49E value



Match length 117 % identity 79

NCBI Description (AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

Seq. No. 223299

Seq. ID LIB3165-043-Q1-K1-C9

Method BLASTX
NCBI GI g120669
BLAST score 439
E value 1.0e-43
Match length 89

% identity 91 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 223300

Seq. ID LIB3165-043-Q1-K1-D1

Method BLASTX
NCBI GI g3287270
BLAST score 175
E value 3.0e-13
Match length 50
% identity 72

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 223301

Seq. ID LIB3165-043-Q1-K1-D11

Method BLASTX
NCBI GI g1169494
BLAST score 147
E value 2.0e-09
Match length 30
% identity 97

NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)

>gi_2119915_pir__S60659 EF-Tu protein precursor - soybean
>gi_949873_emb_CAA61444 (X89058) EF-Tu protein [Glycine

max]

Seq. No. 223302

Seq. ID LIB3165-043-Q1-K1-D6

Method BLASTX
NCBI GI g120663
BLAST score 279
E value 2.0e-50
Match length 139
% identity 76

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi_66027_pir__DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]



Seq. No. 223303

Seq. ID LIB3165-043-Q1-K1-D9

Method BLASTX
NCBI GI g1352821
BLAST score 593
E value 1.0e-61
Match length 111
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223304

Seq. ID LIB3165-043-Q1-K1-E10

Method BLASTX
NCBI GI g1352821
BLAST score 612
E value 8.0e-64
Match length 114
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223305

Seq. ID LIB3165-043-Q1-K1-E11

Method BLASTX
NCBI GI g1174162
BLAST score 638
E value 7.0e-67
Match length 121
% identity 93

NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis

thaliana] >gi 3746915 (AF091106) E2

ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No. 223306

Seq. ID LIB3165-043-Q1-K1-E12

Method BLASTX
NCBI GI g3242702
BLAST score 333
E value 4.0e-31
Match length 137
% identity 48

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 223307

Seq. ID LIB3165-043-Q1-K1-E3

Method BLASTX
NCBI GI g3080428
BLAST score 239
E value 1.0e-20
Match length 62

```
% identity
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
                  223308
Seq. No.
Seq. ID
                  LIB3165-043-Q1-K1-E4
Method
                  BLASTX
                  q2632109
NCBI GI
BLAST score
                  168
                  2.0e-21
E value
                  132
Match length
                  45
% identity
                  (AJ000508) phospholipid glutathione peroxidase [Pisum
NCBI Description
                  sativum]
                  223309
Seq. No.
Seq. ID
                  LIB3165-043-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  g3334223
BLAST score
                  510
                  7.0e-52
E value
                  143
Match length
                  69
% identity
                  4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                  >qi 2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase
                   [Arabidopsis thaliana] >gi 2392518 (U89267)
                  p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]
                   >gi 3098559 (AF047834) 4-hydroxyphenylpyruvate dioxygenase
                   [Arabidopsis thaliana]
Seq. No.
                   223310
                  LIB3165-043-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  q2605911
NCBI GI
BLAST score
                   349
E value
                   2.0e-66
Match length
                  138
                   91
% identity
NCBI Description
                  (AF029258) plasma membrane H+-ATPase [Kosteletzkya
                   virginica]
Seq. No.
                   223311
                  LIB3165-043-Q1-K1-E9
Seq. ID
Method
                   BLASTX
                   q115705
NCBI GI
BLAST score
                   395
                   6.0e-66
E value
                   128
Match length
                   94
% identity
                  CATALASE >gi 279448 pir CSPM catalase (EC 1.11.1.6) -
NCBI Description
                   garden pea >gi 20677 emb CAA42736 (X60169) catalase [Pisum
                   sativum]
                   223312
Seq. No.
                  LIB3165-043-Q1-K1-F10
Seq. ID
Method
                  BLASTX
                   g285739
NCBI GI
```

31660

392

BLAST score

E value

2.0e-09

```
E value
                  5.0e-38
Match length
                  125
                  57
% identity
NCBI Description
                  (D14605) AX110P [Daucus carota] >gi 740202 prf 2004427A
                  embryogenesis-associated protein [Daucus carota]
                  223313
Seq. No.
Seq. ID
                  LIB3165-043-Q1-K1-F11
Method
                  BLASTX
                  q166834
NCBI GI
BLAST score
                  711
                  2.0e-75
E value
Match length
                  138
                  97
% identity
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
Seq. No.
                  223314
                  LIB3165-043-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1169384
                  490
BLAST score
E value
                  2.0e-49
Match length
                  101
% identity
                  87
                  DNAJ PROTEIN HOMOLOG ANJ1 >gi 543510 pir JQ2142 chaperone
NCBI Description
                  ANJ1 protein - Atriplex nummularia
Seq. No.
                  223315
                  LIB3165-043-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3402705
BLAST score
                  184
E value
                  9.0e-14
Match length
                  104
% identity
                  43
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  223316
Seq. ID
                  LIB3165-043-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g479406
BLAST score
                  275
                  4.0e-51
E value
                  115
Match length
                  59
% identity
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                  >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
Seq. No.
                  223317
                  LIB3165-043-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g3426041
NCBI GI
BLAST score
                  98
```



95 Match length % identity

(AC005168) unknown protein [Arabidopsis thaliana] NCBI Description

223318 Seq. No.

Seq. ID LIB3165-043-Q1-K1-F6

BLASTX Method NCBI GI q1168408 633 BLAST score 3.0e-66 E value 136 Match length

% identity NCBI Description

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >qi 2118268 pir S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

223319 Seq. No.

Seq. ID LIB3165-043-Q1-K1-F7

Method BLASTX NCBI GI a1352821 590 BLAST score 3.0e-61 E value 110 Match length 98 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223320 Seq. No.

LIB3165-043-Q1-K1-G1 Seq. ID

BLASTX Method NCBI GI g1352821 BLAST score 350 1.0e-33 E value Match length 74 82 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir __RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223321

LIB3165-043-Q1-K1-G11 Seq. ID

Method BLASTX g3360289 NCBI GI BLAST score 129 4.0e-09E value Match length 51 % identity 63

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

223322 Seq. No.



```
LIB3165-043-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  g228403
NCBI GI
BLAST score
                  511
                  5.0e-52
E value
                  119
Match length
                  83
% identity
NCBI Description glycolate oxidase [Lens culinaris]
                  223323
Seq. No.
                  LIB3165-043-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q286122
                  367
BLAST score
                  4.0e-39
E value
                  92
Match length
                  84
% identity
NCBI Description (D14576) glutamine synthetase [Zea mays]
                  223324
Seq. No.
                  LIB3165-043-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q4091806
NCBI GI
BLAST score
                  578
E value
                  7.0e-60
                  137
Match length
                  80
% identity
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                  223325
                  LIB3165-043-Q1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1181599
BLAST score
                   310
                  2.0e-28
E value
Match length
                  135
% identity
                  52
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                   223326
Seq. ID
                  LIB3165-043-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3913651
BLAST score
                   141
                   7.0e-09
E value
Match length
                  58
                   42
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                   ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                   223327
Seq. No.
                   LIB3165-043-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   g4210948
NCBI GI
```

31663

390

7.0e-38

BLAST score

E value



Match length 96 % identity 80

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.

223328

Seq. ID

LIB3165-043-Q1-K1-H4

Method NCBI GI BLAST score BLASTX a120663 255

E value Match length 3.0e-22 82

% identity

65

NCBI Description

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi_66027_pir__DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]

Seq. No.

223329

Seq. ID

LIB3165-043-Q1-K1-H7

Method NCBI GI BLAST score E value

BLASTX q1352821 627

Match length % identity

1.0e-65 116 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

223330

Seq. ID

LIB3165-043-Q1-K1-H8

Method BLASTX NCBI GI g1352681 BLAST score 189 E value 3.0e-14 Match length 115 % identity 43

NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >qi 1076391 pir S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis

thaliana >gi 633028 dbj BAA07287 (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No.

223331

Seq. ID

LIB3165-043-Q1-K1-H9

Method BLASTX NCBI GI g1345698 BLAST score 652 E value 2.0e-68 135 Match length % identity 90

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

a/b-binding protein - upland cotton



>gi 452314 emb CAA38025 (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No. Seq. ID LIB3165-044-Q1-K1-A10 Method BLASTX NCBI GI g226996 BLAST score 609 2.0e-63

E value 132 Match length 89 % identity

NCBI Description petB2 gene [Pisum sativum]

223332

223333 Seq. No.

Seq. ID LIB3165-044-Q1-K1-A11

Method BLASTX NCBI GI g4406530 BLAST score 347 E value 8.0e-33 Match length 118 % identity 63

NCBI Description (AF126870) rubisco activase [Vigna radiata]

223334 Seq. No.

Seq. ID LIB3165-044-Q1-K1-A4

Method BLASTX g124224 NCBI GI BLAST score 483 7.0e-49E value Match length 97 % identity 94

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi 19887 emb CAA45105 (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 223335

Seq. ID LIB3165-044-Q1-K1-A5

Method BLASTX NCBI GI g2493129 BLAST score 243 E value 9.0e-21 Match length 69 % identity 74

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) > qi 459198 (U07052) vacuolar H+-ATPase subunit B

[Gossypium hirsutum]

Seq. No. 223336

Seq. ID LIB3165-044-Q1-K1-A8

Method BLASTX NCBI GI g3023752 BLAST score 279 8.0e-25 E value Match length 101 58 % identity

NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)



ferredoxin-I [Lycopersicon esculentum]

223337 Seq. No. Seq. ID LIB3165-044-Q1-K1-A9 Method BLASTX NCBI GI g1352821 BLAST score 309 1.0e-28 E value 84 Match length 79 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223338 Seq. No. LIB3165-044-Q1-K1-B10 Seq. ID Method BLASTX NCBI GI q3832512 BLAST score 541 E value 2.0e-55 138 Match length 75 % identity (AF097922) granule-bound glycogen (starch) synthase NCBI Description [Astragalus membranaceus] 223339 Seq. No. Seq. ID LIB3165-044-Q1-K1-B11 Method BLASTX q100616 NCBI GI BLAST score 272 6.0e-46E value Match length 129 % identity 77 NCBI Description ribulose-bisphosphate carboxylase activase B precursor barley >gi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] Seq. No. 223340 LIB3165-044-Q1-K1-B12 Seq. ID Method BLASTX NCBI GI q2494076 479 BLAST score 3.0e-48 E value Match length 103 87 % identity NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi 1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase

Seq. No. 223341

[Nicotiana plumbaginifolia]



Seq. ID LIB3165-044-Q1-K1-B3

Method BLASTX
NCBI GI g470373
BLAST score 183
E value 2.0e-13
Match length 112
% identity 36

NCBI Description (U00047) ZK418.5 gene product [Caenorhabditis elegans]

Seq. No. 223342

Seq. ID LIB3165-044-Q1-K1-B6

Method BLASTX
NCBI GI g1928981
BLAST score 507
E value 1.0e-51
Match length 110
% identity 93

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 223343

Seq. ID LIB3165-044-Q1-K1-B8

Method BLASTX
NCBI GI g1856971
BLAST score 524
E value 2.0e-53
Match length 109
% identity 92

NCBI Description (D26058) This gene is specifically expressed at the S phase

during the cell cycle in the synchronous culture of

periwinkle cells. [Catharanthus roseus]

Seq. No. 223344

Seq. ID LIB3165-044-Q1-K1-C1

Method BLASTX
NCBI GI g1352821
BLAST score 645
E value 1.0e-67
Match length 121
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223345

Seq. ID LIB3165-044-Q1-K1-C10

Method BLASTX
NCBI GI g3687652
BLAST score 410
E value 8.0e-63
Match length 135

% identity 88

NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No. 223346



```
Seq. ID
                  LIB3165-044-Q1-K1-C11
Method
                  BLASTX
                  q3914603
NCBI GI
BLAST score
                  582
                  2.0e-60
E value
Match length
                  134
                  80
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Oryza sativa]
                  223347
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1354515
BLAST score
                  216
                  2.0e-17
E value
Match length
                  112
% identity
                  48
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  223348
Seq. No.
                  LIB3165-044-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4454458
                  307
BLAST score
                  4.0e-28
E value
Match length
                  136
                  55
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  223349
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-C4
                  BLASTX
Method
NCBI GI
                  g399082
BLAST score
                  210
E value
                  9.0e-17
Match length
                  134
% identity
                  40
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_322713_pir__S28171 H+-transporting ATP synthase (EC
                   3.6.1.34) delta chain, chloroplast - garden pea >gi_169045
                   (M94558) ATP synthase delta subunit [Pisum sativum]
                  223350
Seq. No.
                  LIB3165-044-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
BLAST score
                  233
                  4.0e-31
E value
```

104 Match length % identity

(AF126870) rubisco activase [Vigna radiata] NCBI Description

223351 Seq. No.

Match length

% identity

137

```
Seq. ID
                  LIB3165-044-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  595
                  8.0e-62
E value
                  114
Match length
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223352
                  LIB3165-044-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2443751
BLAST score
                  447
                  2.0e-44
E value
                  103
Match length
% identity
                  84
NCBI Description
                  (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
                  (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.
                  223353
                  LIB3165-044-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231688
BLAST score
                  727
                  2.0e-77
E value
                  141
Match length
                  97
% identity
NCBI Description
                  CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC
                  1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)
                  subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. Ño.
                  223354
Seq. ID
                  LIB3165-044-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g115471
BLAST score
                  434
E value
                  6.0e - 43
Match length
                  137
                  64
% identity
NCBI Description
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                  DEHYDRATASE) >gi_100078 pir S10200 carbonate dehydratase
                  (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792
                  (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
Seq. No.
                  223355
Seq. ID
                  LIB3165-044-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1354515
BLAST score
                  290
E value
                  4.0e-26
```

Match length

% identity

135 53

```
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
                  223356
Seq. No.
                  LIB3165-044-Q1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4115934
                  443
BLAST score
                  5.0e-44
E value
Match length
                  116
                  74
% identity
NCBI Description
                  (AF118223) contains similarity to Methanobacterium
                  thermoautotrophicum transcriptional regulator (GB:AE000850)
                  [Arabidopsis thaliana]
Seq. No.
                  223357
                  LIB3165-044-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3510256
BLAST score
                  157
                  2.0e-10
E value
                  90
Match length
% identity
                  41
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                  223358
                  LIB3165-044-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100488
BLAST score
                  160
                  7.0e-11
E value
Match length
                  123
% identity
                  35
NCBI Description TNP2 protein - garden snapdragon
                  223359
Seq. No.
                  LIB3165-044-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
                  585
BLAST score
                  1.0e-60
E value
                  109
Match length
% identity
                  98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223360
                  LIB3165-044-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567227
BLAST score
                  395
                  2.0e-38
E value
```



```
(AC007119) putative transport protein [Arabidopsis
NCBI Description
                  thaliana]
                  223361
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q505482
BLAST score
                  508
                  1.0e-56
E value
                  128
Match length
                  89
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                  photosystem II [Nicotiana tabacum]
                  223362
Seq: No.
                  LIB3165-044-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2677828
NCBI GI
BLAST score
                  456
E value
                  1.0e-45
                  118
Match length
                  70
% identity
                 (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  223363
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                  g1346155
BLAST score
                  543
E value
                  8.0e-56
                  119
Match length
                  88
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481942 pir S40212 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                  >qi 437995 emb CAA81078 (Z25859) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
Seq. No.
                  223364
Seq. ID
                  LIB3165-044-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3264759
BLAST score
                  534
E value
                  1.0e-54
Match length
                  126
                   83
% identity
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
Seq. No.
                   223365
```

Seq. ID LIB3165-044-Q1-K1-F1 Method BLASTX

NCBI GI g4091806 BLAST score 484 E value 7.0e-49 Match length 96 % identity 90

% identity

80



```
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]
                  223366
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  g1172873
                  310
BLAST score
                  4.0e-45
E value
                  129
Match length
                  65
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619 dbj_BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
                  223367
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-F2
                  BLASTX
Method
                  g1495366
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
                  124
Match length
                  61
% identity
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
                  223368
Seq. No.
                  LIB3165-044-Q1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2651316
BLAST score
                  115
E value
                  1.0e-10
Match length
                  58
                  71
% identity
NCBI Description (AC002336) unknown protein [Arabidopsis thaliana]
                  223369
Seq. No.
Seq. ID
                  LIB3165-044-Q1-K1-F7
Method
                  BLASTX
                  g128405
NCBI GI
BLAST score
                  318
                  2.0e-29
E value
Match length
                  112
% identity
                   60
NCBI Description NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 -
                   soybean >gi 18694 emb CAA34506 (X16488) nodulin-21 (AA
                   1-201) [Glycine max]
                   223370
Seq. No.
                   LIB3165-044-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q20729
BLAST score
                   483
E value
                  8.0e-49
Match length
                  119
```

31672

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]



Seq. No. 223371 LIB3165-044-Q1-K1-F9 Seq. ID Method BLASTX g3776005 NCBI GI 290 BLAST score 5.0e-38 E value 92 Match length 92 % identity (AJ010466) RNA helicase [Arabidopsis thaliana] NCBI Description Seq. No. 223372 Seq. ID LIB3165-044-Q1-K1-G1 Method BLASTX NCBI GI g3763925 BLAST score 366 E value 4.0e-35 Match length 92 % identity 77 (AC004450) putative Af10-protein [Arabidopsis thaliana] NCBI Description Seq. No. 223373 LIB3165-044-Q1-K1-G10 Seq. ID Method BLASTX NCBI GI g4263711 BLAST score 431 1.0e-42 E value 95 Match length 80 - % identity (AC006223) putative CCR4-associated transcription factor NCBI Description [Arabidopsis thaliana] 223374 Seq. No. LIB3165-044-Q1-K1-G3 Seq. ID Method BLASTX NCBI GI g4033469 390 BLAST score 8.0e-38 E value Match length 114 % identity 44 ARGININE/SERINE-RICH SPLICING FACTOR RSP41 NCBI Description >gi 1707370 emb CAA67799 (X99436) splicing factor [Arabidopsis thaliana] Seq. No. 223375 LIB3165-044-Q1-K1-G4 Seq. ID BLASTX Method g3183088 NCBI GI BLAST score 165 9.0e-12E value

60 Match length 55 % identity

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein -cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer

like protein [Vigna unguiculata]

223376 Seq. No.

Match length

% identity
NCBI Description

75 96

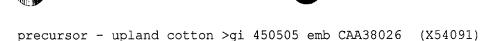


```
LIB3165-044-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                 - g1352821
NCBI GI
BLAST score
                  585
E value
                  1.0e-60
                  109
Match length
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223377
                  LIB3165-044-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1871577
BLAST score
                  192
E value
                  1.0e-14
                  98
Match length
                   43
% identity
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
                  223378
Seq. No.
                  LIB3165-044-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1486472
BLAST score
                   233
E value
                  1.0e-19
Match length
                   53
                  85
% identity
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                   223379
Seq. ID
                  LIB3165-044-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                   g3023501
BLAST score
                   165
E value
                   2.0e-11
Match length
                   46
% identity
                   61
NCBI Description
                  PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP)
                   >gi 2224431 dbj BAA57915 (AB001684) ATP-dependent Clp
                  protease proteolytic subunit [Chlorella vulgaris]
Seq. No.
                   223380
Seq. ID
                  LIB3165-044-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                   g1352821
BLAST score
                   370
                   1.0e-35
E value
```

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223381

Seq. ID LIB3165-044-Q1-K1-H5

Method BLASTX
NCBI GI g3914472
BLAST score 279
E value 5.0e-25
Match length 68
% identity 78

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No. 223382

Seq. ID LIB3165-044-Q1-K1-H8

Method BLASTX
NCBI GI g4115357
BLAST score 323
E value 6.0e-30
Match length 132
% identity 52

NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No. 223383

Seq. ID LIB3165-044-Q1-K1-H9

Method BLASTX
NCBI GI g3287696
BLAST score 201
E value 1.0e-15
Match length 78
% identity 56

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 223384

Seq. ID LIB3165-045-Q1-K1-A11

Method BLASTX
NCBI GI g131384
BLAST score 321
E value 9.0e-30
Match length 74
% identity 82

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA

-81 to 248) [Pisum satīvum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum satīvum] >gi_226937_prf_1611461A 02 evolving

complex 33kD protein [Arachis hypogaea]



```
Seq. No.
                  223385
Seq. ID
                  LIB3165-045-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q20729
BLAST score
                  466
E value
                  1.0e-46
Match length
                  125
                  76
% identity
NCBI Description
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  223386
                  LIB3165-045-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023752
BLAST score
                  202
                  8.0e-16
E value
                  108
Match length
% identity
                  42
                  FERREDOXIN I PRECURSOR >qi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                  223387
Seq. ID
                  LIB3165-045-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q1168411
BLAST score
                  506
E value
                  2.0e-51
Match length
                  126
% identity
                  82
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  223388
Seq. ID
                  LIB3165-045-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3298548
BLAST score
                  404
E value
                  2.0e-39
Match length
                  123
% identity
                  63
NCBI Description
                  (AC004681) putative spliceosomal protein [Arabidopsis
                  thaliana]
Seq. No.
                  223389
Seq. ID
                  LIB3165-045-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  167
E value
                  3.0e-17
Match length
                  49
% identity
                  94
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

Seq. No. 223390

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
LIB3165-045-Q1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  467
                  6.0e-47
E value
                  91
Match length
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223391
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-B2
Method
                  BLASTX
                  g2791834
NCBI GI
BLAST score
                  206
                  5.0e-34
E value
                  85
Match length
% identity
                  80
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  223392
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-B7
                  BLASTX
Method
                  g3158474
NCBI GI
                  478
BLAST score
                  3.0e-48
E value
Match length
                  104
% identity
                  89
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                  223393
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-B9
Method
                  BLASTX
                  q2244847
NCBI GI
BLAST score
                  286
                  1.0e-25
E value
Match length
                  93
                  59
% identity
NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog
                  [Arabidopsis thaliana]
Seq. No.
                  223394
Seq. ID
                  LIB3165-045-Q1-K1-C4
                  BLASTX
Method
NCBI GI
                  g505482
BLAST score
                  359
                  1.0e-38
E value
Match length
                  114
                  77
% identity
NCBI Description
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
                  photosystem II [Nicotiana tabacum]
```

Seq. No. 223395

Seq. ID LIB3165-045-Q1-K1-C7



```
BLASTX
Method
NCBI GI
                  q541951
                  426
BLAST score
                  4.0e-42
E value
                  107
Match length
                  79
% identity
                  SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
NCBI Description
                  [Glycine max]
                  223396
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g3559814
BLAST score
                  495
                  4.0e-50
E value
                  139
Match length
                  70
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
Seq. No.
                  223397
Seq. ID
                  LIB3165-045-Q1-K1-D10
                  BLASTX
Method
NCBI GI
                  q120663
BLAST score
                  326
E value
                  2.0e-35
                  108
Match length
                  72
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 66027 pir DEPMNB
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                   garden pea >qi 309671 (M55147) glyceraldehyde-3-phosphate
                   dehydrogenase B subunit [Pisum sativum]
Seq. No.
                   223398
Seq. ID
                  LIB3165-045-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                   g3059095
BLAST score
                   656
E value
                   5.0e-69
Match length
                  141
% identity
                   91
                 (AJ001091) magnesium chelatase subunit [Glycine max]
NCBI Description
Seq. No.
                   223399
                  LIB3165-045-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1352821
BLAST score
                   645
E value
                   1.0e-67
                  120
Match length
                   97
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb CAA38026_ (X54091)
```

ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
Seq. No.
                  223400
                  LIB3165-045-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
                  709
BLAST score
E value
                  3.0e-75
Match length
                  136
                  99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  223401
                  LIB3165-045-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  q3914442
NCBI GI
BLAST score
                  341
                  4.0e-32
E value
Match length
                  66
                  95
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
                  223402
Seq. No.
                  LIB3165-045-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172664
BLAST score
                  257
E value
                   3.0e-22
Match length
                  55
                   91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_419791_pir__S31165 photosystem I chain III precursor -
                   Flaveria trinervia >gi 298482 bbs 127083 photosystem I
                   reaction center subunit III, PSI-RC PsaF [Flaveria
                   trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                   I subunit III [Flaveria trinervia]
Seq. No.
                  223403
                  LIB3165-045-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  192
                   2.0e-26
E value
                  119
Match length
                   31
```

% identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

223404 Seq. No.

LIB3165-045-Q1-K1-E8 Seq. ID

Method BLASTX

```
q2398679
NCBI GI
BLAST score
                  608
E value
                  2.0e-63
                  127
Match length
                  88
% identity
NCBI Description
                 (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                  synthase [Morinda citrifolia]
Seq. No.
                  223405
Seq. ID
                  LIB3165-045-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  q3885513
BLAST score
                  311
E value
                  1.0e-28
                  69
Match length
                  81
% identity
                  (AF084201) similar to chloroplast 50S ribosomal protein L31
NCBI Description
                  [Medicago sativa]
Seq. No.
                  223406
Seq. ID
                  LIB3165-045-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  358
E value
                  4.0e-34
                  99
Match length
                  71
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  223407
                  LIB3165-045-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730850
BLAST score
                  141
E value
                  1.0e-08
                  123
Match length
                  28
% identity
NCBI Description SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2)
                  >gi_626942_pir_ S48533 SUR2 protein - yeast (Saccharomyces
                  cerevisiae) >gi_458718 (U07171) Sur2p [Saccharomyces
                  cerevisiae] >gi_849215 (U28374) Sur2p: syringomycin
                  response protein 2 [Saccharomyces cerevisiae] >gi 1786173
                  (U10427) Syr2p [Saccharomyces cerevisiae]
Seq. No.
                  223408
Seq. ID
                  LIB3165-045-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2136011
                  188
```

Method BLASTX
NCBI GI g2136011
BLAST score 188
E value 4.0e-14
Match length 76
% identity 42

NCBI Description protein DS 1, 24K - human >gi_1045059_emb_CAA57387_

(X81788) ICT1 protein [Homo sapiens]

>gi 4557657 ref NP 001536.1 pICT1 immature colon carcinoma

transcript

Seq. ID Method

NCBI GI



```
Seq. No.
                  223409
                  LIB3165-045-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850621
BLAST score
                  637
                  8.0e-67
E value
Match length
                  136
% identity
                  85
NCBI Description
                  (Y15382) putative RNA binding protein [Arabidopsis
                  thaliana]
                  223410
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  q2191152
BLAST score
                  495
E value
                  3.0e-50
                  122
Match length
% identity
                  76
                  (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  223411
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  260
                  6.0e-23
E value
Match length
                  52
% identity
                  96
NCBI Description
                 (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana]
Seq. No.
                  223412
                  LIB3165-045-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668080
BLAST score
                  417
E value
                  5.0e-41
Match length
                  135
% identity
                  64
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  223413
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  656
E value
                  5.0e-69
                  135
Match length
% identity
                  90
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                  223414
Seq. No.
```

31681

LIB3165-045-Q1-K1-H12

BLASTX

g4249382

```
282
BLAST score
E value
                  2.0e-25
                  62
Match length
% identity
                  84
                  (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
Seq. No.
                  223415
Seq. ID
                  LIB3165-045-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g136707
BLAST score
                  366
E value
                  5.0e - 35
                  112
Match length
                  65
% identity
                  CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                  (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  iron-sulfur protein precursor - garden pea
                  >gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS
                  protein [Pisum sativum]
                  223416
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-H6
                  BLASTX
Method
                  g2996407
NCBI GI
BLAST score
                  215
E value
                  8.0e-26
Match length
                  84
% identity
                  82
NCBI Description (AJ004940) heat shock cognate 70 [Gallus gallus]
                  223417
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3158476
BLAST score
                  511
```

4.0e-52 E value

Match length 112 86 % identity

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 223418

Seq. ID LIB3165-045-Q1-K1-H8

Method BLASTX NCBI GI g1352821 BLAST score 398 6.0e-39 E value Match length 81 95 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



98

76

Match length

% identity

```
223419
Seq. No.
Seq. ID
                  LIB3165-045-Q1-K1-H9
                  {\tt BLASTX}
Method
NCBI GI
                  g3914603
                  510
BLAST score
                  3.0e-62
E value
                  132
Match length
                  83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Oryza sativa]
                   223420
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-A1
                  BLASTX
Method
                   g166834
NCBI GI
BLAST score
                   557
                   2.0e-57
E value
                   133
Match length
% identity
                   78
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                   activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
                   223421
Seq. No.
Seq. ID
                   LIB3165-046-Q1-K1-A11
                   {\tt BLASTX}
Method
                   g1439609
NCBI GI
BLAST score
                   589
E value
                   3.0e-61
Match length
                   119
                   99
% identity
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                   hirsutum]
                   223422
Seq. No.
                   LIB3165-046-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   443
E value
                   3.0e-44
                   83
Match length
                   99
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
Seq. No.
                   223423
                   LIB3165-046-Q1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4406530
BLAST score
                   364
E value
                   9.0e-35
```

NCBI Description (AF126870) rubisco activase [Vigna radiata]



```
223424
Seq. No.
                  LIB3165-046-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                  618
                  2.0e-64
E value
Match length
                  128
                  93
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223425
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  382
                  7.0e-37
E value
                  103
Match length
% identity
                  70
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
                  223426
Seq. No.
                  LIB3165-046-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023752
                  323
BLAST score
                  5.0e-30
E value
Match length
                  110
% identity
                  63
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
                  223427
Seq. No.
                  LIB3165-046-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g20729
NCBI GI
BLAST score
                  526
E value
                  8.0e-54
                  137
Match length
                  78
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  223428
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-B12
                  BLASTX
Method
                  g266893
NCBI GI
BLAST score
                  707
                  5.0e-75
E value
Match length
                  136
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
```

PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__\$28172 ribulose-bisphosphate carboxylase activase - cucumber >gi 18284 emb CAA47906_ (X67674) rubisco activase [Cucumis



sativus]

```
223429
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-B5
Method
                  BLASTX
                  q2129740
NCBI GI
                  328
BLAST score
                  1.0e-30
E value
Match length
                  123
                  56
% identity
                  small nuclear ribonucleoprotein - Arabidopsis thaliana
NCBI Description
                  >qi 2129756 pir S71411 U1 snRNP 70K protein - Arabidopsis
                  thaliana >gi 1255711 (M93439) small nuclear
                  ribonucleoprotein [Arabidopsis thaliana] >gi 1354469
                   (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
                  223430
Seq. No.
                  LIB3165-046-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982301
BLAST score
                  388
                  1.0e-37
E value
                  94
Match length
                  72
% identity
                  (AF051235) YGL010w-like protein [Picea mariana]
NCBI Description
Seq. No.
                  223431
                  LIB3165-046-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1354515
BLAST score
                  243
                  1.0e-20
E value
Match length
                  127
                  46
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
Seq. No.
                  223432
Seq. ID
                  LIB3165-046-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g4510348
BLAST score
                   385
E value
                   3.0e-37
Match length
                  112
% identity
                   65
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                   223433
Seq. No.
                  LIB3165-046-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1771160
BLAST score
                   472
E value
                   2.0e-47
Match length
                  131
% identity
                   68
NCBI Description (X98929) SBT1 [Lycopersicon esculentum]
```

>gi 3687305 emb CAA06999 (AJ006378) subtilisin-like

NCBI GI

E value

BLAST score

q1352821

2.0e-53

522



protease [Lycopersicon esculentum]

Seq. No. 223434 Seq. ID LIB3165-046-Q1-K1-C12 BLASTX Method NCBI GI g1352821 BLAST score 581 3.0e-60 E value Match length 109 97 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223435 LIB3165-046-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI g3914603 BLAST score 184 9.0e-19 E value 115 Match length 53 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >qi 1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa] Seq. No. 223436 LIB3165-046-Q1-K1-C4 Seq. ID Method BLASTX NCBI GI a4580460 BLAST score 454 2.0e-45 E value 117 Match length 79 % identity (AC006081) putative 26S Protease Subunit 4 [Arabidopsis NCBI Description thaliana] Seq. No. 223437 LIB3165-046-Q1-K1-C5 Seq. ID Method BLASTX NCBI GI q1781348 BLAST score 311 E value 8.0e-36 Match length 130 -% identity 83 NCBI Description (Y10380) homologous to plastidic aldolases [Solanum tuberosum] Seq. No. 223438 Seq. ID LIB3165-046-Q1-K1-C8 Method BLASTX



Match length 100 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223439

Seq. ID LIB3165-046-Q1-K1-D10

Method BLASTX NCBI GI g131399 BLAST score 414 9.0e-41E value Match length 95 % identity 82

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >qi 82277 pir S00411

photosystem II 10K protein precursor - potato

>gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No. 223440

Seq. ID LIB3165-046-Q1-K1-D11

Method BLASTX NCBI GI g1881585 BLAST score 225 E value 1.0e-18 88 Match length

% identity 67

NCBI Description (U72489) remorin [Solanum tuberosum]

Seq. No. 223441

LIB3165-046-Q1-K1-D12 Seq. ID

Method BLASTX NCBI GI g131384 BLAST score 388 E value 1.0e-37 Match length 88 84 % identity

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi 344004_dbj BAA02554 (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi 226937 prf 1611461A 02 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 223442

Seq. ID LIB3165-046-Q1-K1-D5

Method BLASTX NCBI GI q82188 BLAST score 468 E value 5.0e-47Match length 134



% identity 71 ~ photosystem II oxygen-evolving complex protein 2 precursor NCBI Description - common tobacco (fragment) >gi 19896 emb CAA41713 (X58910) photosystem II 23 kDa polypeptide [Nicotiana tabacum] 223443 Seq. No. LIB3165-046-Q1-K1-D6 Seq. ID Method BLASTX NCBI GI g231688 BLAST score 677 2.0e-71 E value Match length 131 98 % identity NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC 1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675) subunit 2 of cotton catalase [Gossypium hirsutum] Seq. No. 223444 Seq. ID LIB3165-046-Q1-K1-D8 Method BLASTX NCBI GI g100200 BLAST score 323 E value 5.0e - 30Match length 94 % identity 68 NCBI Description chlorophyll a/b-binding protein type I precursor - tomato Seq. No. 223445 LIB3165-046-Q1-K1-E12 Seq. ID Method BLASTX NCBI GI q508304 BLAST score 346 1.0e-32 E value 78 Match length 79 % identity NCBI Description (L22305).corC [Medicago sativa] Seq. No. 223446 LIB3165-046-Q1-K1-E2 Seq. ID Method BLASTX NCBI GI g1168258 530 BLAST score E value 2.0e-54 111 Match length 86 % identity ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR NCBI Description (TRANSAMINASE A) >gi 693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No. 223447

Seq. ID LIB3165-046-Q1-K1-E6

Method BLASTX
NCBI GI g2827141
BLAST score 709
E value 3.0e-75
Match length 139



```
% identity
NCBI Description
                  (AF027173) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
                  223448
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  a629597
BLAST score
                  314
                  3.0e-29
E value
                  114
Match length
                  63
% identity
                  proline-rich protein - rape >gi 545029 bbs 142669 (S68113)
NCBI Description
                  proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                  Peptide, 147 aa] [Brassica napus]
                  223449
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q125578
BLAST score
                  448
                  1.0e-44
E value
                  120
Match length
                  73
% identity
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi 167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                  223450
Seq. No.
Seq. ID
                  LIB3165-046-Q1-K1-F1
Method
                  BLASTX
                  g2501578
NCBI GI
                  688
BLAST score
                  9.0e-73
E value
Match length
                  140
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
Seq. No.
                  223451
                  LIB3165-046-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1352821
BLAST score
                  138
                  1.0e-08
E value
Match length
                  47
% identity
                   64
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

31689

223452

LIB3165-046-Q1-K1-F11

Seq. No.

Seg. ID



BLASTX Method NCBI GI q100616 602 BLAST score 1.0e-62 E value Match length 131 % identity ribulose-bisphosphate carboxylase activase B precursor -NCBI Description barley >qi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >qi 167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] 223453 Seq. No. Seq. ID LIB3165-046-Q1-K1-F12 BLASTX Method NCBI GI g1352821 BLAST score 586 8.0e-61 E value Match length 110 % identity 100 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223454 Seq. No. Seq. ID LIB3165-046-Q1-K1-F4 Method BLASTX NCBI GI q4406530 BLAST score 600 2.0e-62 E value 139 Match length 83 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] Seq. No. 223455 LIB3165-046-Q1-K1-F5 Seq. ID Method BLASTX NCBI GI g231688 BLAST score 770 2.0e-82 E value 137 Match length 100 % identity CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton >gi $18\overline{48}8$ emb CAA39998 (X56675) subunit 2 of cotton catalase [Gossypium hirsutum] 223456 Seq. No. LIB3165-046-Q1-K1-F6 Seq. ID Method BLASTX NCBI GI g2780194

Method BLASTX
NCBI GI g2780194
BLAST score 287
E value 7.0e-26
Match length 59
% identity 97

NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]



Seq. No. 223457 LIB3165-046-Q1-K1-F7 Seq. ID Method BLASTX g3044218 NCBI GI 170 BLAST score 8.0e-19 E value 69 Match length 64 % identity (AF057144) signal peptidase [Arabidopsis thaliana] NCBI Description Seq. No. 223458 LIB3165-046-Q1-K1-G10 Seq. ID Method BLASTX NCBI GI g1732411 BLAST score 211 7.0e-17 E value Match length 126 % identity 27 NCBI Description (U47924) isopeptidase T [Homo sapiens] Seq. No. 223459 Seq. ID LIB3165-046-Q1-K1-G2 Method BLASTX NCBI GI g1168411 BLAST score 417 E value 5.0e-41 Match length 107 % identity 80 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR Seq. No. 223460 LIB3165-046-Q1-K1-G3 Seq. ID Method BLASTX NCBI GI g1168411 BLAST score 434 E value 6.0e-43

Match length 111 80 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

223461 Seq. No.

Seq. ID LIB3165-046-Q1-K1-G4

Method BLASTX NCBI GI g4572673 BLAST score 421 E value 2.0e-41 Match length 113 75 % identity

NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis

thaliana]

Seq. No. 223462

LIB3165-046-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI q421826 BLAST score 334



E value 3.0e-31
Match length 105
% identity 62

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 223463

Seq. ID LIB3165-046-Q1-K1-H1

Method BLASTX
NCBI GI g121344
BLAST score 627
E value 1.0e-65
Match length 139
% identity 83

NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR

(GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)

>gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC
6.3.1.2) delta precursor, chloroplast - garden pea

>gi_169059 (M20664) glutamine synthetase (chloroplast GS2)

(EC 6.3.1.2) [Pisum sativum]

Seq. No. 223464

Seq. ID LIB3165-046-Q1-K1-H10

Method BLASTX
NCBI GI g1709651
BLAST score 151
E value 5.0e-10
Match length 73
% identity 47

NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209

plastocyanin a precursor - black poplar

>gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 223465

Seq. ID LIB3165-046-Q1-K1-H11

Method BLASTX
NCBI GI g1352821
BLAST score 697
E value 8.0e-74
Match length 139
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223466

Seq. ID LIB3165-046-Q1-K1-H2

Method BLASTX
NCBI GI g125578
BLAST score 679
E value 1.0e-71
Match length 140
% identity 93



NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase

[Mesembryanthemum crystallinum]

Seq. No. 223467

Seq. ID LIB3165-046-Q1-K1-H4

Method BLASTX NCBI GI g82080 BLAST score 585 E value 1.0e-60 Match length 134 81 % identity

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 223468

LIB3165-046-Q1-K1-H8 Seq. ID

Method BLASTX NCBI GI q1168411 BLAST score 515 E value 2.0e-52 Match length 127 83 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 223469

Seq. ID LIB3165-046-Q1-K1-H9

Method BLASTX NCBI GI g4406530 BLAST score 361 2.0e-34 E value Match length 98

76 % identity

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223470

Seq. ID LIB3165-047-Q1-K1-A1

Method BLASTX NCBI GI q2245107 BLAST score 357 E value 6.0e - 34Match length 133 % identity

NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No. 223471

Seq. ID LIB3165-047-Q1-K1-A10

Method BLASTX NCBI GI g4406530 BLAST score 349 E value 5.0e-33Match length 93 % identity

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223472



```
Seq. ID
                  LIB3165-047-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  593
                  1.0e-61
E value
Match length
                  128
% identity
                  66
NCBI Description
                  chlorophyll a/b-binding protein type I precursor - tomato
                  223473
Seq. No.
                  LIB3165-047-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  594
E value
                  9.0e-62
Match length
                  112
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum] .
Seq. No.
                  223474
Seq. ID
                  LIB3165-047-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q20729
BLAST score
                  408
E value
                  7.0e-40
Match length
                  106
                  77
% identity
NCBI Description
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  223475
                  LIB3165-047-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3033389
BLAST score
                  160
E value
                  8.0e-11
Match length
                  86
% identity
                  4
NCBI Description
                  (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
                  223476
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  574
E value
                  2.0e-59
Match length
                  108
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

E value

Match length

% identity

2.0e-12

127 38

```
223477
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q1168408
BLAST score
                  410
                  2.0e-40
E value
                  89
Match length
                  92
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                  >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  223478
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-A9
                  BLASTX
Method
                  q3023752
NCBI GI
BLAST score
                  291
                  3.0e-26
E value
Match length
                  111
                  56
% identity
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
                  ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                  223479
Seq. ID
                  LIB3165-047-Q1-K1-B1
                  BLASTX
Method
                  g2290528
NCBI GI
BLAST score
                  575
E value
                  2.0e-59
Match length
                  119
% identity
                  88
NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]
Seq. No.
                  223480
                  LIB3165-047-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662341
BLAST score
                  657
E value
                  4.0e-69
Match length
                  131
% identity
                  97
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >qi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                  satīva] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                  [Oryza sativa]
Seq. No.
                  223481
                  LIB3165-047-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512654
BLAST score
                  173
```

31695

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

% identity

98



```
223482
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-B4
                  BLASTX
Method
NCBI GI
                  g3559814
BLAST score
                  294
                  1.0e-26
E value
Match length
                  119
                  5.5
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
                  223483
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-B9
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  540
                  2.0e-55
E value
                  104
Match length
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223484
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  362
                  1.0e-34
E value
Match length
                  100
 % identity
                  71
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  223485
                  LIB3165-047-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  596
E value
                   6.0e-62
Match length
                  118
 % identity
                   97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
 Seq. No.
                   223486
 Seq. ID
                  LIB3165-047-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  590
E value
                  3.0e-61
Match length
                  110
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223487 LIB3165-047-Q1-K1-C7 Seq. ID Method BLASTX NCBI GI q1708312 BLAST score 273 2.0e-24 E value Match length 58 97 % identity NCBI Description HEAT SHOCK PROTEIN 81-1 (HSP81-1) (HEAT SHOCK PROTEIN 83) Seq. No. 223488 Seq. ID LIB3165-047-Q1-K1-C8 Method BLASTX NCBI GI g1332579 BLAST score 592 E value 1.0e-61 Match length 119 % identity 10 NCBI Description (X98063) polyubiquitin [Pinus sylvestris] Seq. No. 223489 Seq. ID LIB3165-047-Q1-K1-D10 Method BLASTX NCBI GI g2765081 BLAST score 364 E value 7.0e-35 Match length 107 % identity 68 NCBI Description (Y10557) g5bf [Arabidopsis thaliana] 223490 Seq. No. Seq. ID LIB3165-047-Q1-K1-D12 Method BLASTX g4406530 NCBI GI BLAST score 293 E value 2.0e-26 Match length 104 % identity 62 NCBI Description (AF126870) rubisco activase [Vigna radiata] Seq. No. 223491 Seq. ID LIB3165-047-Q1-K1-D4 Method BLASTX NCBI GI q3023281 BLAST score 333 E value 5.0e-48 Match length 116 % identity 78

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi_2065194_emb_CAA64475 (X95098) ammonium transporter

[Lycopersicon esculentum]



```
Seq. No.
                   223492
Seq. ID
                  LIB3165-047-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1346155
BLAST score
                  618
E value
                  1.0e-64
                  134
Match length
% identity
                   90
NCBI Description
                 SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481942 pir S40212 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                   >gi 437995 emb CAA81078 (Z25859) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
Seq. No.
                  223493
Seq. ID
                  LIB3165-047-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3511223
BLAST score
                  162
E value
                  3.0e-11
Match length
                  102
% identity
                  41
NCBI Description (AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]
Seq. No.
                  223494
                  LIB3165-047-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q20733
BLAST score
                  560
E value
                  9.0e-58
Match length
                  115
                  88
% identity
NCBI Description (X15188) precursor C-terminal fragment (AA -80 to 367)
                  [Pisum sativum]
Seq. No.
                  223495
                  LIB3165-047-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  389
                  1.0e-37
E value
Match length
                  111
% identity
                  74
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  223496
Seq. ID
                  LIB3165-047-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3869088
                  587
BLAST score
E value
                  6.0e-61
```

Match length 112 % identity 99

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 223497



```
Seq. ID
                  LIB3165-047-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2129921
BLAST score
                  185
                  9.0e-14
E value
Match length
                  51
% identity
                  73
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi 758694
                  (U12573) putative [Catharanthus roseus]
Seq. No.
                  223498
Seq. ID
                  LIB3165-047-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  509
E value
                  9.0e-52
Match length
                  126
% identity
                  83
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  223499
Seq. ID
                  LIB3165-047-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g4512018
BLAST score
                  157
E value
                  1.0e-10
Match length
                  96
% identity
                  45
NCBI Description
                  (AF106660) mRNA binding protein precursor [Lycopersicon
                  esculentum]
Seq. No.
                  223500
Seq. ID
                  LIB3165-047-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g126894
BLAST score
                  580
E value
                  4.0e-60
Match length
                  131
% identity
                  85
NCBI Description
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                  >gi_319832_pir__DEPUGW malate dehydrogenase (EC 1.1.1.37)
                  precursor, glyoxysomal - watermelon >gi 167284 (M33148)
                  glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37)
                  [Citrullus vulgaris]
Seq. No.
                  223501
Seq. ID
                  LIB3165-047-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  598
E value
                  3.0e-62
```

% identity NCBI Description

Match length

(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

112

Seq. No. 223502



```
Seq. ID
                  LIB3165-047-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q3868853
BLAST score
                  141
                  1.0e-08
E value
Match length
                  50
% identity
                  62
NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]
Seq. No.
                  223503
                  LIB3165-047-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131385
```

Method BLASTX
NCBI GI g131385
BLAST score 500
E value 1.0e-50
Match length 125
% identity 83

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 223504

Seq. ID LIB3165-047-Q1-K1-F2

Method BLASTX
NCBI GI g1352821
BLAST score 490
E value 1.0e-49
Match length 104
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223505

Seq. ID LIB3165-047-Q1-K1-F6

Method BLASTX
NCBI GI g729882
BLAST score 268
E value 2.0e-23
Match length 97
% identity 57

NCBI Description CASEIN KINASE II BETA' CHAIN (CK II)

>gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta
chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984)
casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
>gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 223506

Seq. ID LIB3165-047-Q1-K1-F7

Method BLASTX
NCBI GI g3286721
BLAST score 193
E value 4.0e-15
Match length 65

Match length

% identity

123

82



```
% identity
NCBI Description
                  (AJ007449) trans-cinnamic 4-monooxygenase [Cicer arietinum]
                  223507
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q3297815
BLAST score
                  176
                  8.0e-13
E value
Match length
                  42
                  76
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  223508
Seq. ID
                  LIB3165-047-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  522
E value
                  3.0e-53
Match length
                  100
% identity
                  98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223509
Seq. No.
Seq. ID
                  LIB3165-047-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1354515
BLAST score
                  315
E value
                  5.0e-29
Match length
                  138
% identity
                  51
NCBI Description
                 (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
Seq. No.
                  223510
Seq. ID
                  LIB3165-047-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1181599
BLAST score
                  332
E value
                  4.0e-31
Match length
                  111
% identity
                  63
NCBI Description
                  (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                  223511
Seq. ID
                  LIB3165-047-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g231688
BLAST score
                  283
E value
                  1.0e-48
```

NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC



1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 223512 Seq. ID LIB3165-047-Q1-K1-G6 Method BLASTX q1352821 NCBI GI BLAST score 173 1.0e-26 E value Match length 81 80 % identity NCBI Description

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223513 Seq. ID LIB3165-047-Q1-K1-G7 Method BLASTX NCBI GI q2982458 BLAST score 196 E value 4.0e-15 45 Match length 87 % identity

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 223514

Seq. ID LIB3165-047-Q1-K1-G8

Method BLASTX
NCBI GI g505482
BLAST score 399
E value 6.0e-39
Match length 104
% identity 81

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 223515

Seq. ID LIB3165-047-Q1-K1-H10

Method BLASTX
NCBI GI g1652798
BLAST score 259
E value 2.0e-22
Match length 96
% identity 58

NCBI Description (D90908) GcpE [Synechocystis sp.]

Seq. No. 223516

Seq. ID LIB3165-047-Q1-K1-H11

Method BLASTX
NCBI GI g1508783
BLAST score 253
E value 9.0e-22
Match length 123
% identity 48

NCBI Description (Z54351) SecY [Spinacia oleracea]

BLAST score

390

```
Seq. No.
                   223517
Seq. ID
                   LIB3165-047-Q1-K1-H12
Method
                   BLASTX
NCBI GI
                   g1362005
BLAST score
                   231
E value
                   3.0e-19
Match length
                   110
% identity
                   49
NCBI Description secY protein homolog precursor - Arabidopsis thaliana
Seq. No.
                   223518
Seq. ID
                   LIB3165-047-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   g131397
BLAST score
                   298
E value
                   5.0e-27
Match length
                   129
% identity
                   54
                   OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                   SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi 81480 pir S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi_755802_emb_CAA29056 (X05512) 16 kDa protein of the
                   photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi 225597 prf 1307179B luminal protein 16kD
                   [Spinacia oleracea]
Seq. No.
                   223519
Seq. ID
                   LIB3165-047-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3269292
BLAST score
                   245
E value
                   7.0e-21
                   62
Match length
                   73
% identity
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                   223520
Seq. ID
                   LIB3165-047-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   g3319921
BLAST score
                   147
E value
                   2.0e-11
                   89
Match length
                   47
% identity
NCBI Description
                   (AJ223388) Hev b .3 [Hevea brasiliensis]
                   >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
                   [Hevea brasiliensis] >gi 3818475 (AF051317) small rubber
                   particle protein [Hevea brasiliensis]
Seq. No.
                   223521
Seq. ID
                   LIB3165-047-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1168408
```



```
E value
                  5.0e-38
Match length
                  98
                  82
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
                  >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  223522
Seq. No.
                  LIB3165-047-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3559814
BLAST score
                  147
                  2.0e-09
E value
                  48
Match length
                  69
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
Seq. No.
                  223523
                  LIB3165-047-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g228403
BLAST score
                  439
E value
                  1.0e-43
Match length
                  93
                  90
% identity
NCBI Description glycolate oxidase [Lens culinaris]
Seq. No.
                  223524
Seq. ID
                  LIB3165-048-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  q266936
BLAST score
                  455
E value
                  2.0e-45
Match length
                  125
% identity
                  76
NCBI Description
                  50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)
                  >gi 282960 pir A42840 ribosomal protein L27 - common
                  tobacco >gi 170306 (M98473) ribosomal protein L27
                  [Nicotiana tabacum] >gi 170326 (M75731) ribosomal protein
                  L27 [Nicotiana tabacum]
Seq. No.
                  223525
Seq. ID
                  LIB3165-048-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3236248
BLAST score
                  331
                  5.0e-31
E value
Match length
                  93
% identity
                  73
NCBI Description
                 (AC004684) unknown protein [Arabidopsis thaliana]
```

Seq. No. 223526

Seq. ID LIB3165-048-Q1-K1-A11

Method BLASTX NCBI GI g2341045 BLAST score 313



```
E value
                  9.0e-29
                  136
Match length
% identity
                  45
NCBI Description
                 (AC000104) F19P19.16 [Arabidopsis thaliana]
Seq. No.
                  223527
Seq. ID
                  LIB3165-048-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4008159
BLAST score
                  698
E value
                  6.0e-74
Match length
                  137
% identity
                  93
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                  223528
Seq. ID
                  LIB3165-048-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4490313
BLAST score
                  411
E value
                  2.0e-40
Match length
                  111
                  72
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  223529
Seq. ID
                  LIB3165-048-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  632
E value
                  4.0e-66
Match length
                  117
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223530
Seq. No.
                  LIB3165-048-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3980238
BLAST score
                  169
E value
                  7.0e-12
Match length
                  46
% identity
                  63
NCBI Description (Z21677) ribosomal protein L18 [Thermotoga maritima]
                  223531
Seq. No.
                  LIB3165-048-Q1-K1-A6
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1168408
BLAST score 634
E value 2.0e-66
Match length 135
% identity 92



```
NCBI Description
                 FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
                  >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                  223532
Seq. ID
                  LIB3165-048-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1170897
BLAST score
                  497
                  2.0e-50
E value
Match length
                  111
% identity
                  87
NCBI Description
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                  >gi 1076276 pir S52039 NAD-malate dehydrogenase - cucumber
                  >gi 695311 (L31900) glyoxysomal malate dehydrogenase
                  [Cucumis sativus]
Seq. No.
                  223533
Seq. ID
                  LIB3165-048-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3738257
BLAST score
                  346
E value
                  6.0e - 33
Match length
                  79
                  85
% identity
NCBI Description
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                  nigra]
Seq. No.
                  223534
Seq. ID
                  LIB3165-048-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2801536
BLAST score
                  266
                  2.0e-23
E value
                  75
Match length
                  69
% identity
NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]
Seq. No.
                  223535
Seq. ID
                  LIB3165-048-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  q100200
BLAST score
                  649
                  3.0e-68
E value
Match length
                  141
                  69
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  223536
                  LIB3165-048-Q1-K1-B11
Seq. ID
```

Method BLASTX NCBI GI q542157 BLAST score 626 E value 2.0e-65 Match length 144% identity 82



```
NCBI Description ribosomal 5S RNA-binding protein - Rice
```

 Seq. No.
 223537

 Seq. ID
 LIB3165-048-Q1-K1-B2

 Method
 BLASTX

 NCBI GI
 g430947

 BLAST score
 492

 E value
 9.0e-50

E value 9.0 Match length 119 % identity 82

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 223538

Seq. ID LIB3165-048-Q1-K1-B4

Method BLASTX
NCBI GI g400890
BLAST score 194
E value 4.0e-15
Match length 53
% identity 38

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 223539

Seq. ID LIB3165-048-Q1-K1-B5

Method BLASTX
NCBI GI g2190992
BLAST score 378
E value 2.0e-36
Match length 142
% identity 54

NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops

tauschii]

Seq. No. 223540

Seq. ID LIB3165-048-Q1-K1-B6

Method BLASTX
NCBI GI g1352821
BLAST score 464
E value 2.0e-46
Match length 102
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026 (X54091) ribulose bisphosphate carboxylase (Gossypium birgutum)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223541

Seq. ID LIB3165-048-Q1-K1-B8

Method BLASTX NCBI GI q493636

Method

NCBI GI

BLASTX

g4545262



```
382
  BLAST score
                    7.0e-37
  E value
Match length
                    96
                    44
  % identity
                    (D29684) predicted polypeptide for cytokinin-repressed mRNA
  NCBI Description
                     [Cucumis sativus] >gi 746031 prf 2016504A
                    cytokinin-repressed protein CR9 [Cucumis sativus]
                    223542
  Seq. No.
  Seq. ID
                    LIB3165-048-Q1-K1-B9
  Method
                    BLASTX
                    q4406530
  NCBI GI
                    358
  BLAST score
                    4.0e-34
  E value
  Match length
                    104
                    73
  % identity
                    (AF126870) rubisco activase [Vigna radiata]
  NCBI Description
                    223543
  Seq. No.
  Seq. ID
                    LIB3165-048-Q1-K1-C1
  Method
                    BLASTX
  NCBI GI
                    q121344
                    294
  BLAST score
                    1.0e-26
  E value
                    93
  Match length
                     60
  % identity
                    GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR
  NCBI Description
                     (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)
                     >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC
                     6.3.1.2) delta precursor, chloroplast - garden pea
                     >gi 169059 (M20664) glutamine synthetase (chloroplast GS2)
                     (EC 6.3.1.2) [Pisum sativum]
                    223544
  Seq. No.
  Seq. ID
                    LIB3165-048-Q1-K1-C10
  Method
                    BLASTX
  NCBI GI
                    g1332579
  BLAST score
                     496
                     2.0e-70
  E value
  Match length
                    145
  % identity
                    10
  NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                     223545
  Seq. No.
                    LIB3165-048-Q1-K1-C11
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q2760320
  BLAST score
                     360
                     2.0e-34
  E value
  Match length
                     109
  % identity
                     68
  NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
  Seq. No.
                     223546
                    LIB3165-048-Q1-K1-C2
  Seq. ID
```

31708



BLAST score 165 E value 2.0e-11 Match length 44 % identity 66

NCBI Description (AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No. 223547

Seq. ID LIB3165-048-Q1-K1-C4

Method BLASTX
NCBI GI g445116
BLAST score 577
E value 7.0e-60
Match length 120
% identity 88

NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No. 223548

Seq. ID LIB3165-048-Q1-K1-C6

Method BLASTX
NCBI GI g4469014
BLAST score 441
E value 9.0e-44
Match length 141
% identity 67

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 223549

Seq. ID LIB3165-048-Q1-K1-C7

Method BLASTX
NCBI GI g3914603
BLAST score 646
E value 8.0e-68
Match length 137
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

Seq. No. 223550

Seq. ID LIB3165-048-Q1-K1-C8

Method BLASTX
NCBI GI g1730502
BLAST score 251
E value 2.0e-21
Match length 91
% identity 51

NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable

transmembrane protein FT27 - mouse >gi 535682 (M23568)

transmembrane protein [Mus musculus]

Seq. No. 223551

Seq. ID LIB3165-048-Q1-K1-C9

Method BLASTX NCBI GI g1352821 BLAST score 543



E value 9.0e-56 Match length 103 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223552

Seq. ID LIB3165-048-Q1-K1-D1

Method BLASTX NCBI GI q625546 BLAST score 322 6.0e-37 E value Match length 126 % identity 63

photosystem II oxygen-evolving complex protein 2 precursor NCBI Description

- common tobacco >gi_417604 emb CAA45699 (X64347) 23 kDa polypeptide of water-oxidizing complex of photosystem II

[Nicotiana tabacum]

Seq. No. 223553

Seq. ID LIB3165-048-Q1-K1-D10

Method BLASTX NCBI GI g2924520 BLAST score 570 E value 6.0e-59 Match length 124 % identity 88

NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)

[Arabidopsis thaliana]

Seq. No. 223554

Seq. ID LIB3165-048-Q1-K1-D11

Method BLASTX NCBI GI g2894603 BLAST score 186 E value 7.0e-14 Match length 95 23 % identity

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 223555

Seq. ID LIB3165-048-Q1-K1-D12

Method BLASTX NCBI GI g2496789 BLAST score 583 E value 2.0e-60 Match length 139 79 % identity

NCBI Description 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP

REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183_ (D64000)

hypothetical protein [Synechocystis sp.]

Seq. No. 223556

Seq. ID LIB3165-048-Q1-K1-D2



```
Method
                  BLASTX
NCBI GI
                  q4454010
BLAST score
                  442
E value
                  7.0e-44
Match length
                  142
% identity
                  60
NCBI Description
                 (AL035396) putative protein [Arabidopsis thaliana]
Seq. No.
                  223557
Seq. ID
                  LIB3165-048-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q100454
BLAST score
                  620
                  8.0e-65
E value
Match length
                  144
% identity
                  87
                  photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                  >gi_809113_emb_CAA35601 (X17578) 33kDa precursor protein
                  of oxygen-evolving complex [Solanum tuberosum]
Seq. No.
                  223558
Seq. ID
                  LIB3165-048-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  550
E value
                  1.0e-56
Match length
                  133
% identity
                  84
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  223559
Seq. ID
                  LIB3165-048-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3334245
BLAST score
                  446
E value
                  2.0e-44
Match length
                  104
% identity
                  80
NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                  (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi 2909424 emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer
                  arietinum]
Seq. No.
                  223560
Seq. ID
                  LIB3165-048-Q1-K1-D8
Method
                  BLASTX
                  g2832664
                  202
                  9.0e-16
                  82
% identity
                  45
```

NCBI GI BLAST score E value Match length

NCBI Description (AL021710) pollen-specific protein - like [Arabidopsis

thaliana]

Seq. No. 223561

Seq. ID LIB3165-048-Q1-K1-D9



```
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  568
                  1.0e-58
E value
Match length
                  131
% identity
                  83
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  223562
Seq. ID
                  LIB3165-048-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q421809
BLAST score
                  418
E value
                  4.0e-41
Match length
                  143
% identity
                  64
NCBI Description dnaJ protein homolog DnaJ-1 - cucumber
Seq. No.
                  223563
Seq. ID
                  LIB3165-048-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2190012
BLAST score
                  281
E value
                   5.0e-25
Match length
                  90
% identity
                  63
                  (AB004242) din1 [Raphanus sativus]
NCBI Description
Seq. No.
                  223564
                  LIB3165-048-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2347054
BLAST score
                  377
                  2.0e-36
E value
Match length
                  109
% identity
                  70
                  (X96791) arginine decarboxylase [Vitis vinifera]
NCBI Description
```

223565 Seq. No.

Seq. ID LIB3165-048-Q1-K1-E2

Method BLASTX NCBI GI g3341679 BLAST score 266 E value 2.0e-23 Match length 73 78 % identity

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 223566

LIB3165-048-Q1-K1-E3 Seq. ID

Method BLASTX NCBI GI q3298439 BLAST score 442



```
7.0e-44
 E value
Match length
                   129
                   50
 % identity
                   (AB010878) chloroplast ribosomal protein L4 [Nicotiana
 NCBI Description
                   tabacum]
                   223567
 Seq. No.
 Seq. ID
                   LIB3165-048-Q1-K1-E7
 Method
                   BLASTX
 NCBI GI
                   q2708749
 BLAST score
                   351
                   3.0e-33
 E value
Match length
                   111
                   59
 % identity
                   (AC003952) putative senescence-assoc. rhodanese-like
 NCBI Description
                   protein [Arabidopsis thaliana]
                   223568
 Seq. No.
 Seq. ID
                   LIB3165-048-Q1-K1-E8
Method
                   BLASTX
 NCBI GI
                   q421826
 BLAST score
                   409
                   5.0e-40
 E value
Match length
                   83
 % identity
                   86
NCBI Description
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
 Seq. No.
                   223569
                   LIB3165-048-Q1-K1-E9
 Seq. ID
 Method
                   BLASTX
                   q1684716
 NCBI GI
 BLAST score
                   363
 E value
                   1.0e-34
 Match length
                   110
                   60
 % identity
 NCBI Description
                   (Y09424) cytochrome P450 [Nepeta racemosa]
 Seq. No.
                   223570
 Seq. ID
                   LIB3165-048-Q1-K1-F1
 Method
                   BLASTX
 NCBI GI
                   g2497742
 BLAST score
                   178
 E value
                   4.0e-13
 Match length
                   35
 % identity
                   94
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
 NCBI Description
                   >gi 995907 (U15153) nonspecific lipid transfer protein
                   precursor [Gossypium hirsutum]
                   223571
 Seq. No.
```

Seq. ID LIB3165-048-Q1-K1-F12

Method BLASTX NCBI GI g3687243 BLAST score 178 E value 3.0e-14



60 Match length 75 % identity (AC005169) putative ribosomal protein [Arabidopsis NCBI Description thaliana] 223572 Seq. No. LIB3165-048-Q1-K1-F2 Seq. ID BLASTX Method g480450 NCBI GI BLAST score 422 E value 1.0e-41 Match length 109 77 % identity ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis NCBI Description thaliana >gi 402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana] 223573 Seq. No. LIB3165-048-Q1-K1-F3 Seq. ID BLASTX Method q3702327 NCBI GI BLAST score 249 E value 3.0e-21 122 Match length 52 % identity NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] 223574 Seq. No. LIB3165-048-Q1-K1-F4 Seq. ID BLASTX Method q1709651 NCBI GI 148 BLAST score 7.0e-10 E value Match length 54 54 % identity NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir S58209 plastocyanin a precursor - black poplar >qi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus nigra] 223575 Seq. No. LIB3165-048-Q1-K1-G1 Seq. ID Method BLASTX g4510373 NCBI GI 349 BLAST score 5.0e-33 E value 117 Match length 60 % identity (AC007017) putative harpin-induced protein [Arabidopsis NCBI Description thaliana] 223576 Seq. No. LIB3165-048-Q1-K1-G10

Seq. ID

BLASTX Method g3288821 NCBI GI BLAST score 640 4.0e-67 E value



Match length 130 92 % identity (AF063901) alanine:glyoxylate aminotransferase; NCBI Description transaminase [Arabidopsis thaliana] 223577 Seq. No. Seq. ID LIB3165-048-Q1-K1-G11 BLASTX Method NCBI GI q1352821 706 BLAST score E value 7.0e-75 129 Match length 100 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223578 LIB3165-048-Q1-K1-G12 Seq. ID BLASTX Method NCBI GI q1781348 BLAST score 540 2.0e-55 E value 118 Match length 89 % identity (Y10380) homologous to plastidic aldolases [Solanum NCBI Description tuberosum] 223579 Seq. No. LIB3165-048-Q1-K1-G4 Seq. ID Method BLASTX q409756 NCBI GI BLAST score 261 1.0e-22 E value Match length 122 45 % identity NCBI Description (L25643) ATP/GTP nucleotide-binding protein [Leishmania infantum] Seq. No. 223580 LIB3165-048-Q1-K1-G5 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g289920
BLAST score 663
E value 8.0e-70
Match length 124
% identity 99

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 223581

Seq. ID LIB3165-048-Q1-K1-G7

Method BLASTX NCBI GI g68200 BLAST score 417

Seq. ID Method

NCBI GI



```
6.0e-41
 E value
                    107
 Match length
                    80
 % identity
                    fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
 NCBI Description
                    chloroplast - spinach >gi 22633_emb_CAA47293_ (X66814)
                    fructose-bisphosphate aldolase [Spinacia oleracea]
                    223582
 Seq. No.
 Seq. ID
                    LIB3165-048-Q1-K1-G9
                    BLASTX
 Method
                    g2462762
 NCBI GI
                    266
 BLAST score
                    2.0e-23
 E value
                    100
 Match length
                    56
 % identity
                    (AC002292) Highly similar to auxin-induced protein
 NCBI Description
                    (aldo/keto reductase family) [Arabidopsis thaliana]
                    223583
 Seq. No.
                    LIB3165-048-Q1-K1-H1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4056456
                    415
 BLAST score
                    8.0e-41
 E value
                    141
 Match length
 % identity
                    62
                    (AC005990) Strong similarity to gb_U20808 auxin-induced
 NCBI Description
                    protein from Vigna radiata and a member of the zinc-binding
                    dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006
                    and gb AA395179 come from this gene. [Arabidopsis thaliana]
                    223584
 Seq. No.
 Seq. ID
                    LIB3165-048-Q1-K1-H10
                    BLASTX
 Method
 NCBI GI
                    q1006610
                    344
 BLAST score
                    2.0e-32
 E value
                    126
Match length
                    52
 % identity
                    (D64005) hypothetical protein [Synechocystis sp.]
 NCBI Description
                    223585
 Seq. No.
 Seq. ID
                    LIB3165-048-Q1-K1-H12
 Method
                    BLASTX
                    q166835
 NCBI GI
 BLAST score
                    252
 E value
                    3.0e-22
                    65
 Match length
                    74
  % identity
                    (M86720) ribulose bisphosphate carboxylase/oxygenase
 NCBI Description
                    activase [Arabidopsis thaliana] >gi_2642170 (AC003000)
                    Rubisco activase [Arabidopsis thaliana]
  Seq. No.
                    223586
```

LIB3165-048-Q1-K1-H2

BLASTX

q100203



```
BLAST score
                  261
                  9.0e-23
E value
Match length
                  91
% identity
                  60
NCBI Description
                  cysteine proteinase (EC 3.4.22.-) precursor - tomato
                  >qi 19195 emb CAA78403 (Z14028) pre-pro-cysteine
                  proteinase [Lycopersicon esculentum]
                  223587
Seq. No.
                  LIB3165-048-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  q3800853
NCBI GI
BLAST score
                  324
                  3.0e-30
E value
                  102
Match length
% identity
                  68
NCBI Description
                   (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase precursor [Zea mays]
                  223588
Seq. No.
                  LIB3165-048-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  q3928084
NCBI GI
BLAST score
                  338
                  9.0e-32
E value
                  119
Match length
% identity
                  59
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  223589
Seq. ID
                  LIB3165-048-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4406049
BLAST score
                   373
                   5.0e - 36
E value
Match length
                  113
% identity
                   58
NCBI Description
                  (AF067604) linalool synthase-like protein [Oenothera
                  arizonica]
                   223590
Seq. No.
                  LIB3165-049-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170168
BLAST score
                   200
                   1.0e-15
E value
Match length
                  108
                   48
% identity
```

HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) NCBI Description

> >gi 549883 (U09332) homeobox protein [Arabidopsis thaliana] >gi 549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi 2245105 emb CAB10527 (Z97343) unnamed protein product

[Arabidopsis thaliana]

223591 Seq. No.

LIB3165-049-Q1-K1-A11 Seq. ID



```
BLASTX
Method
NCBI GI
                  g4128133
                  253
BLAST score
                  9.0e-22
E value
                  97
Match length
                  49
% identity
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
                  223592
Seq. No.
Seq. ID
                  LIB3165-049-Q1-K1-A12
                  BLASTX
Method
                  g1814405
NCBI GI
                  653
BLAST score
E value
                  1.0e-68
                  137
Match length
                  49
% identity
                  (U84890) putative phosphate permease [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  223593
Seq. ID
                  LIB3165-049-Q1-K1-A3
                  BLASTX
Method
NCBI GI
                  g430947
BLAST score
                  471
E value
                  2.0e-47
                  119
Match length
                  80
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  223594
Seq. No.
                  LIB3165-049-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415908
BLAST score
                  154
E value
                  4.0e-10
Match length
                  74
                  46
% identity
NCBI Description
                  (AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.
                  223595
Seq. ID
                  LIB3165-049-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4097547
BLAST score
                  233
E value
                  2.0e-19
Match length
                  49
% identity
                  46
NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]
                  223596
Seq. No.
                  LIB3165-049-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172664
BLAST score
                  264
                  5.0e-23
E value
```

56

Match length



% identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor -Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia] 223597 Seq. No. LIB3165-049-Q1-K1-B5 Seq. ID Method BLASTX g2739375 NCBI GI BLAST score 195 5.0e-15 E value 102 Match length 47 % identity (AC002505) unknown protein [Arabidopsis thaliana] NCBI Description 223598 Seq. No. Seq. ID LIB3165-049-Q1-K1-B6 Method BLASTX q1352821 NCBI GI 555 BLAST score 4.0e-57 E value 109 Match length 95 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir _RKCNSU ribulose-bisphosphate carboxylase $\overline{(EC 4.1.1.39)}$ small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223599 Seq. No. LIB3165-049-Q1-K1-B7 Seq. ID BLASTX Method g4335763 NCBI GI BLAST score 141 E value 1.0e-08 48 Match length 54 % identity NCBI Description (AC006284) unknown protein [Arabidopsis thaliana] 223600 Seq. No. Seq. ID LIB3165-049-Q1-K1-B8 BLASTX Method NCBI GI q1352821 BLAST score 574 2.0e-59 E value 110 Match length 99 % identity

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

Match length

125



```
223601
Seq. No.
Seq. ID
                  LIB3165-049-Q1-K1-C11
Method
                  BLASTX
                  q2754849
NCBI GI
BLAST score
                  492
                  1.0e-51
E value
                  117
Match length
                  81
% identity
                  (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                  [Fritillaria agrestis]
                  223602
Seq. No.
Seq. ID
                  LIB3165-049-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q131399
                  157
BLAST score
                  5.0e-11
E value
Match length
                  54
                  61
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411
                  photosystem II 10K protein precursor - potato
                  >gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                  tuberosum]
                  223603
Seq. No.
Seq. ID
                  LIB3165-049-Q1-K1-C2
                  BLASTX
Method
NCBI GI
                  q3786016
BLAST score
                  255
E value
                  5.0e-22
                  95
Match length
% identity
                  55
                  (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  223604
                  LIB3165-049-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3249084
BLAST score
                  444
E value
                   4.0e-44
Match length
                  114
                  23
% identity
NCBI Description
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
                   qb X92750 from Mus musculus. ESTs gb AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
                   223605
Seq. No.
                  LIB3165-049-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                  g2499967
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
```

% identity 49 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E



B) >gi_632724_bbs_151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 143 aa] [Nicotiana sylvestris]

Seq. No. 223606 Seq. ID LIB3165-049-Q1-K1-D10

Method BLASTX
NCBI GI g505482

BLAST score 425 E value 6.0e-42 Match length 117 % identity 77

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 223607

Seq. ID LIB3165-049-Q1-K1-D12

Method BLASTX
NCBI GI g1055130
BLAST score 186
E value 7.0e-14
Match length 95
% identity 37

NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for

by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA

yk78c2.3

Seq. No. 223608

Seq. ID LIB3165-049-Q1-K1-D5

Method BLASTX
NCBI GI g2499945
BLAST score 521
E value 4.0e-53
Match length 138
% identity 69

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) /

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)

pyrE-F [Arabidopsis thaliana]

Seq. No. 223609

Seq. ID LIB3165-049-Q1-K1-D7

Method BLASTX
NCBI GI g1076315
BLAST score 370
E value 2.0e-35
Match length 83
% identity 81

NCBI Description cytochrome P450 - Arabidopsis thaliana

>gi_853719_emb_CAA60793_ (X87367) CYP90 protein

[Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)

CYP90 protein [Arabidopsis thaliana]

% identity

NCBI Description

84



```
Seq. No.
                   223610
                   LIB3165-049-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1354515
                   289
BLAST score
                   5.0e-26
E value
                   111
Match length
                   57
% identity
                   (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   223611
Seq. No.
                   LIB3165-049-Q1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160158
                   241
BLAST score
E value
                   2.0e-20
Match length
                   44
% identity
                   95
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   223612
Seq. ID
                   LIB3165-049-Q1-K1-E10
                   BLASTX
Method
NCBI GI
                   g3201969
BLAST score
                   456
E value
                   1.0e-45
                   119
Match length
% identity
                   66
                   (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
Seq. No.
                   223613
                   LIB3165-049-Q1-K1-E12
Seq. ID
Method
                   BLASTX
-NCBI GI
                   g2281633
BLAST score
                   440
E value
                   9.0e-44
Match length
                   119
% identity
                   71
                   (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   223614
                   LIB3165-049-Q1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131385
BLAST score
                   518
                   8.0e-53
E value
                   128
Match length
```

THYLAKOID MEMBRANE PROTEIN)

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD



```
Seq. No.
                  223615
Seq. ID
                  LIB3165-049-Q1-K1-E4
                  BLASTX
Method
NCBI GI
                  q2462781
BLAST score
                  151
                  9.0e-10
E value
                  74
Match length
                  49
% identity
                  (U73175) carbamoyl phosphate synthetase small subunit
NCBI Description
                  [Arabidopsis thaliana]
                  223616
Seq. No.
Seq. ID
                  LIB3165-049-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3288821
                  431
BLAST score
                  1.0e-42
E value
                  109
Match length
% identity
                  76
                  (AF063901) alanine:qlyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  223617
Seq. No.
Seq. ID
                  LIB3165-049-Q1-K1-F10
Method
                  BLASTX
                  g3023752
NCBI GI
BLAST score
                  341
                  4.0e-32
E value
Match length
                  114
% identity
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                  223618
                  LIB3165-049-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  q100616
NCBI GI
                  159
BLAST score
E value
                  8.0e-11
Match length
                  45
                  73
% identity
NCBI Description ribulose-bisphosphate carboxylase activase B precursor -
                  barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                  carboxylase activase [Hordeum vulgare] >gi 167095 (M55449)
                  ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                  vulgare]
                  223619
Seq. No.
                  LIB3165-049-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406530
                  352
BLAST score
                  2.0e-33
E value
                  119
Match length
                  63
% identity
```

NCBI Description (AF126870) rubisco activase [Vigna radiata]



```
223620
Seq. No.
                  LIB3165-049-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g2462929
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
                   44
Match length
% identity
                   64
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                   223621
Seq. No.
                  LIB3165-049-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                   g549063
NCBI GI
                   304
BLAST score
                   8.0e-28
E value
                   81
Match length
                   72
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi 1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   223622
Seq. No.
                   LIB3165-049-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g1928981
NCBI GI
                   572
BLAST score
                   4.0e-59
E value
                   126
Match length
% identity
                   90
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   223623
Seq. No.
Seq. ID
                   LIB3165-049-Q1-K1-G11
                   BLASTX
Method
                   q3800853
NCBI GI
BLAST score
                   357
                   4.0e-34
E value
                   101
Match length
                   73
% identity
                   (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                   activase precursor [Zea mays]
Seq. No.
                   223624
                   LIB3165-049-Q1-K1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1352821
BLAST score
                   590
                   3.0e-61
E value
Match length
                   110
% identity
                   98
```

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
223625
Seq. No.
                  LIB3165-049-Q1-K1-G4
Seq. ID
                  {\tt BLASTX}
Method
                  g2828292
NCBI GI
                  281
BLAST score
                  4.0e-25
E value
                  75
Match length
                  72
% identity
                  (AL021687) neoxanthin cleavage enzyme-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  223626
Seq. No.
                  LIB3165-049-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g2828292
NCBI GI
                  381
BLAST score
                  1.0e-36
E value
                  93
Match length
                  76
% identity
                   (ALO21687) neoxanthin cleavage enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  223627
Seq. No.
                  LIB3165-049-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g117290
NCBI GI
                   251
BLAST score
                   2.0e-21
E value
Match length
                   119
                   47
% identity
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
NCBI Description
                   (P36) (E30) >qi 100071 pir S23774 triose
                   phosphate/3-phosphoglycerate/phosphate translocator
                   precursor - garden pea >gi 20691_emb CAA38451_ (X54639)
                   chloroplast import receptor p36 [Pisum sativum]
                   >gi_20853_emb_CAA48210_ (X68077) phosphate translocator
                   [Pisum sativum] >gi 228551_prf__1805409A phosphate
                   translocator [Pisum sativum]
                   223628
Seq. No.
Seq. ID
                   LIB3165-049-Q1-K1-G9
                   BLASTX
Method
NCBI GI
                   q1352821
BLAST score
                   525
                   1.0e-53
E value
                   111
Match length
                   87
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

Seq. No. 223629

Seq. ID LIB3165-050-Q1-K1-A1

NCBI GI



```
BLASTX
Method
                  g1841870
NCBI GI
BLAST score
                  322
                  8.0e-30
E value
                  81
Match length
                  77
% identity
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
                  223630
Seq. No.
                  LIB3165-050-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
                  359
BLAST score
                  3.0e - 34
E value
                  118
Match length
% identity
                  64
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  223631
Seq. No.
                  LIB3165-050-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
                  619
BLAST score
                  1.0e-64
E value
                  116
Match length
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223632
Seq. No.
Seq. ID
                  LIB3165-050-01-K1-A3
Method
                  BLASTX
                  q1168411
NCBI GI
                  248
BLAST score
                  1.0e-21
E value
                  70
Match length
                  76
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  223633
Seq. No.
                  LIB3165-050-Q1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3023752
BLAST score
                  261
                   9.0e-23
E value
Match length
                   81
                   64
% identity
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
                   ferredoxin-I [Lycopersicon esculentum]
                   223634
Seq. No.
                  LIB3165-050-Q1-K1-B2
Seq. ID
Method
                   BLASTX
```

q1168411



```
BLAST score
                  565
                  3.0e-58
E value
Match length
                  136
% identity
                  84
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  223635
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-B3
Method
                  BLASTX
                  g2493146
NCBI GI
                  535
BLAST score
                  8.0e-55
E value
                  142
Match length
                  58
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 755148
NCBI Description
                  (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                  [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275)
                  vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                  223636
                  LIB3165-050-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  g3860308
NCBI GI
BLAST score
                  172
                  3.0e-12
E value
Match length
                  58
% identity
                  64
                 (AJ012681) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                  223637
Seq. ID
                  LIB3165-050-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  q4204267
                  269
BLAST score
E value
                  1.0e-23
Match length
                  146
                  47
% identity
NCBI Description (AC005223) 55585 [Arabidopsis thaliana]
Seq. No.
                  223638
                  LIB3165-050-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1181599
BLAST score
                  503
                   5.0e-51
E value
Match length
                  129
                  77
% identity
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                  223639
                  LIB3165-050-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g3242704
NCBI GI
                  173
BLAST score
                  2.0e-12
E value
Match length
                  51
```

61

% identity



```
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]
                  223640
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1168411
                  529
BLAST score
                  4.0e-54
E value
                  130
Match length
                  83
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  223641
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1363479
                  271
BLAST score
                  2.0e-24
E value
                  78
Match length
                  69
% identity
NCBI Description
                 photosystem I protein psaL - cucumber
                  >gi 801740 dbj BAA09047 (D50456) PsaL [Cucumis sativus]
                  223642
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-C3
                  BLASTX
Method
                  g1709825
NCBI GI
BLAST score
                  449
                  1.0e-44
E value
                  112
Match length
% identity
                  75
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
                  223643
Seq. No.
                  LIB3165-050-Q1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q231610
                  376
BLAST score
E value
                  4.0e-36
                  124
Match length
% identity
                  65
                 ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >qi 19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
Seq. No.
                  223644
Seq. ID
                  LIB3165-050-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1363479
BLAST score
                  325
                  3.0e - 30
E value
Match length
                  88
% identity
                  72
```

NCBI Description photosystem I protein psaL - cucumber



```
>gi 801740 dbj BAA09047 (D50456) PsaL [Cucumis sativus]
Seq. No.
                   223645
                  LIB3165-050-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1753085
BLAST score
                  157
E value
                   1.0e-10
Match length
                   40
                   78
% identity
NCBI Description
                  (U25283) leucine zipper protein [Oryza sativa]
Seq. No.
                   223646
Seq. ID
                  LIB3165-050-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2501578
BLAST score
                   433
                   5.0e-43
E value
Match length
                   93
                   95
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >qi 2129913 pir S60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                   223647
Seq. No.
                  LIB3165-050-Q1-K1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2262176
BLAST score
                   178
                   5.0e-13
E value
Match length
                   106
% identity
                   37
NCBI Description
                   (AC002329) putative RING zinc-finger protein [Arabidopsis
                   thaliana] >gi 3790573 (AF078824) RING-H2 finger protein
                   RHA3a [Arabidopsis thaliana]
Seq. No.
                   223648
                   LIB3165-050-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1170567
BLAST score
                   329
                   6.0e-31
E value
Match length
                   67
                   88
% identity
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                   >gi 1085960 pir__S52648 INO1 protein - Citrus paradisi
```

Seq. No. 223649

Seq. ID LIB3165-050-Q1-K1-D1

Method BLASTX
NCBI GI g1352821
BLAST score 408
E value 4.0e-40
Match length 81
% identity 95

31729

>gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]



```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223650
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q1351271
BLAST score
                  386
                  2.0e-37
E value
                  131
Match length
                  63
% identity
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi 1084309 pir S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi 806312
                  (L36387) triosephosphate isomerase, chloroplast isozyme
                  [Spinacia oleracea]
                  223651
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-D11
                  BLASTX
Method
NCBI GI
                  g131399
BLAST score
                  506
                  2.0e-51
E value
                  125
Match length
                  77
% identity
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411
                  photosystem II 10K protein precursor - potato
                  >qi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                  tuberosum]
Seq. No.
                  223652
                  LIB3165-050-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706261
BLAST score
                  348
                  1.0e-36
E value
Match length
                  83
% identity
                  84
                  CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129_pir_ S59598
NCBI Description
                  cysteine proteinase 2 precursor - maize
                  >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea
                  mays]
                  223653
Seq. No.
                  LIB3165-050-Q1-K1-D2
Seq. ID
                  BLASTX
```

.z.i..

Method BLASTX
NCBI GI g3914442
BLAST score 412
E value 1.0e-40
Match length 94
% identity 83

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)



>gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

```
223654
Seq. No.
                  LIB3165-050-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3288821
NCBI GI
                  322
BLAST score
                  8.0e-30
E value
Match length
                  112
% identity
                  61
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  223655
Seq. No.
                  LIB3165-050-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
                  638
BLAST score
                  7.0e-67
E value
                  118
Match length
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223656
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-E10
                  BLASTX
Method
NCBI GI
                  g1352821
                  571
BLAST score
                   5.0e-59
E value
                  113
Match length
                   94
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223657
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-E11
Method
                   BLASTX
                   q3914605
NCBI GI
BLAST score
                   592
                   2.0e-61
E value
                   135
Match length
                   83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                   PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir_S39551
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                   apple tree >gi 415852 emb CAA79857 (Z21794)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
```

Seq. No. 223658

[Malus domestica]



Seq. ID LIB3165-050-Q1-K1-E4
Method BLASTX
NCBI GI g1352821
BLAST score 434
E value 6.0e-43
Match length 136
% identity 68

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223659

Seg. ID LIB3165-050-Q1-K1-E5

Method BLASTX
NCBI GI g1352821
BLAST score 606
E value 4.0e-63
Match length 114
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223660

Seq. ID LIB3165-050-Q1-K1-F10

Method BLASTX
NCBI GI g266972
BLAST score 204
E value 4.0e-16
Match length 54
% identity 65

NCBI Description

40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf_2113200H ribosomal protein S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_

ribosomal protein S29

Seq. No. 223661

Seq. ID LIB3165-050-Q1-K1-F7

Method BLASTX
NCBI GI g228403
BLAST score 447
E value 2.0e-44
Match length 93
% identity 92

NCBI Description glycolate oxidase [Lens culinaris]



```
Seq. No.
                  223662
Seq. ID
                  LIB3165-050-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  587
E value
                  6.0e-61
                  135
Match length
                  85
% identity
                  60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  223663
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  q4510372
BLAST score
                  152
                  5.0e-10
E value
Match length
                  57
                  53
% identity
                  (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                  thaliana]
                  223664
Seq. No.
Seq. ID
                  LIB3165-050-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g131276
BLAST score
                  637
                  8.0e-67
E value
Match length
                  125
% identity
                  98
                  PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
NCBI Description
                  PROTEIN) >gi 72704 pir QJNT6A photosystem II chlorophyll
                  a-binding protein psbB - common tobacco chloroplast
                  >gi 11856 emb CAA77373 (Z00044) PSII 47kD protein
                   [Nicotiana tabacum] >qi 225224 prf 1211235BF photosystem
                  II P680 apoprotein [Nicotiana tabacum]
                  223665
Seq. No.
                  LIB3165-050-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1885326
BLAST score
                  341
                  1.0e-32
E value
Match length
                  67
                  91
% identity
NCBI Description (Y11248) phosphoribulokinase [Pisum sativum]
Seq. No.
                  223666
                  LIB3165-050-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
```

BLAST score 618

E value 2.0e-64 Match length 115 % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton $>gi_450505$ emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223667

Seq. ID LIB3165-050-Q1-K1-G5

Method BLASTX
NCBI GI g4193388
BLAST score 540
E value 2.0e-55
Match length 124
% identity 84

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 223668

Seq. ID LIB3165-050-Q1-K1-G9

Method BLASTX
NCBI GI g3242704
BLAST score 352
E value 2.0e-33
Match length 133
% identity 52

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 223669

Seq. ID LIB3165-050-Q1-K1-H10

Method BLASTX
NCBI GI g131276
BLAST score 226
E value 9.0e-43
Match length 120
% identity 83

NCBI Description PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47

PROTEIN) >gi 72704 pir QJNT6A photosystem II chlorophyll

a-binding protein psbB - common tobacco chloroplast >gi_11856 emb_CAA77373 (Z00044) PSII 47kD protein

[Nicotiana tabacum] >gi 225224 prf 1211235BF photosystem

II P680 apoprotein [Nicotiana tabacum]

Seq. No. 223670

Seq. ID LIB3165-050-Q1-K1-H11

Method BLASTX
NCBI GI g2501572
BLAST score 249
E value 3.0e-21
Match length 96
% identity 60

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545

(L47118) EMB8 gene product [Picea glauca]

Seq. No. 223671

Seq. ID LIB3165-050-Q1-K1-H3

Method BLASTX
NCBI GI g1332579
BLAST score 357
E value 4.0e-68



```
Match length
                  140
% identity
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  223672
Seq. ID
                  LIB3165-050-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q131270
BLAST score
                  335
                  2.0e-31
E value
Match length
                  130
% identity
                  72
NCBI Description
                  PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
                  PROTEIN) >gi_100129_pir__S12132 photosystem II chlorophyll
                  a-binding protein psbB - Hooker's evening primrose
                  chloroplast >gi_485417_pir__S12129 photosystem II
                  chlorophyll a-binding protein psbB - Appalachian evening
                  primrose chloroplast >gi 11207 emb CAA39388 (X55899) psbB
                  product, chlorophyll a-binding apoprotein (AA 1-508)
                  [Oenothera argillicola]
Seq. No.
                  223673
Seq. ID
                  LIB3165-050-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2583134
BLAST score
                  177
                  6.0e-13
E value
Match length
                  80
% identity
                  51
NCBI Description
                  (AC002387) putative proline-rich protein [Arabidopsis
                  thaliana]
Seq. No.
                  223674
Seq. ID
                  LIB3165-050-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4321096
BLAST score
                  143
E value
                  7.0e-09
                  92
Match length
                  37
% identity
NCBI Description
                  (M84135) flavonol 3-sulfotransferase [Flaveria
                  chloraefolia]
Seq. No.
                  223675
Seq. ID
                  LIB3165-051-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  213
E value
                  1.0e-23
Match length
                  86
                  67
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
```

Seq. No. 223676

Seq. ID LIB3165-051-Q1-K1-A11

Method BLASTX NCBI GI g3135543

31735



```
BLAST score
                  282
                  2.0e-38
E value
Match length
                  113
                  62
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  223677
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-A3
                  BLASTX
Method
                  q1352821
NCBI GI
                  569
BLAST score
                  8.0e-59
E value
                  107
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223678
Seq. No.
                  LIB3165-051-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  q4455246
NCBI GI
BLAST score
                  148
                  2.0e-09
E value
                   60
Match length
                   44
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   223679
Seq. No.
                  LIB3165-051-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   q4115377
NCBI GI
BLAST score
                   210
                   7.0e-17
E value
                   45
Match length
                   87
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   223680
                   LIB3165-051-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   q1352821
NCBI GI
                   118
BLAST score
                   8.0e-09
E value
                   68
Match length
                   57
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
```

Seq. No. 223681

Seq. ID LIB3165-051-Q1-K1-B1

Method BLASTX



q464621 NCBI GI 230 BLAST score 2.0e-19 E value 69 Match length % identity 61

60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 NCBI Description

ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 223682

LIB3165-051-Q1-K1-B2 Seq. ID

BLASTX Method g4091806 NCBI GI 524 BLAST score 1.0e-53 E value 120 Match length 82 % identity

(AF052585) CONSTANS-like protein 2 [Malus domestica] NCBI Description

Seq. No. 223683

LIB3165-051-Q1-K1-B4 Seq. ID

Method BLASTX q166878 NCBI GI 343 BLAST score 2.0e-32 E value 121 Match length 58 % identity

(M95796) St12p protein [Arabidopsis thaliana] NCBI Description

Seq. No. 223684

LIB3165-051-Q1-K1-B6 Seq. ID

BLASTX Method NCBI GI q1352821 BLAST score 189 1.0e-14 E value 69 Match length 59 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223685 Seq. No.

Seq. ID LIB3165-051-Q1-K1-B8

BLASTX Method g2129511 NCBI GI BLAST score 513 2.0e-52 E value Match length 113 84 % identity

glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, NCBI Description

microbody - cucurbit >gi 1304042 dbj_BAA08410_ (D49432)

hydroxypyruvate reductase [Cucurbita sp.]

223686 Seq. No.



```
LIB3165-051-Q1-K1-B9
Seq. ID
Method
                  BLASTX
                  q4406530
NCBI GI
BLAST score
                  339
E value
                  7.0e-32
                  94
Match length
                  74
% identity
NCBI Description
                  (AF126870) rubisco activase [Vigna radiata]
                  223687
Seq. No.
                  LIB3165-051-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913651
BLAST score
                  512
                  4.0e-52
E value
                  122
Match length
% identity
                  80
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                  223688
                  LIB3165-051-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g400890
BLAST score
                  296
                  8.0e-27
È value
                  124
Match length
% identity
                  45
NCBI Description
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
                  >gi 282837 pir S26953 photosystem II 22K protein precursor
                   - spinach >qi \overline{21307} emb CAA48557 (X68552) 22kD-protein of
                  PSII [Spinacia oleracea] >qi 260917 bbs 119338 (S49864)
                  photosystem II 22 kda polypeptide [spinach, Peptide, 274
                  aa] [Spinacia oleracea]
Seq. No.
                  223689
Seq. ID
                  LIB3165-051-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2708741
BLAST score
                  304
E value
                   6.0e-28
Match length
                   99
% identity
                   60
NCBI Description
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
                  223690
Seq. No.
                  LIB3165-051-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  519
E value
```

5.0e-53 Match length 104 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

NCBI GI

BLAST score

g100200

380



precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
Seq. No.
                  223691
                  LIB3165-051-Q1-K1-C8
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g289920
                  723
BLAST score
                  7.0e-77
E value
                  135
Match length
                  99
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  223692
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1352821
                  586
BLAST score
E value
                  8.0e-61
Match length
                  110
                  97
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223693
Seq. ID
                  LIB3165-051-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g100490
BLAST score
                  608
E value
                  2.0e-63
                  124
Match length
% identity
                  25
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
                  223694
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-D12
Method
                  BLASTX
                  q452357
NCBI GI
BLAST score
                   447
E value
                  2.0e-44
Match length
                  91
% identity
                  (Z29591) guanine nucleotide regulatory protein [Vicia faba]
NCBI Description
                  >gi_1098294_prf__2115367B small GTP-binding protein [Vicia
                   faba]
Seq. No.
                  223695
Seq. ID
                  LIB3165-051-Q1-K1-D3
Method
                  BLASTX
```



```
1.0e-36
E value
                  103
Match length
                  71
% identity
                  chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
                  223696
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-D4
                  BLASTX
Method
                  g119905
NCBI GI
BLAST score
                  316
                  1.0e-29
E value
                  74
Match length
                  81
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978
                   (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to
                  308) [Pisum sativum] >gi_226545_prf__1601517A ferredoxin
                  NADP reductase [Arachis hypogaea]
                  223697
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-D6
                  BLASTX
Method
                  q3335341
NCBI GI
BLAST score
                  158
E value
                  1.0e-10
                  35
Match length
                  89
% identity
                  (AC004512) T8F5.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223698
Seq. ID
                  LIB3165-051-Q1-K1-D7
                  BLASTX
Method
NCBI GI
                  q289920
BLAST score
                  190
E value
                  9.0e-15
Match length
                  84
                  54
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  223699
                  LIB3165-051-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  q3913018
NCBI GI
BLAST score
                  684
                  3.0e-72
E value
Match length
                  139
% identity
                  92
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
```

aldolase [Oryza sativa]

Seq. No.

Seq. ID LIB3165-051-Q1-K1-D9

223700

Method BLASTX NCBI GI g1928981



```
BLAST score
                   141
E value
                   9.0e-16
                   82
Match length
% identity
                   65
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                   223701
                  LIB3165-051-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                   q4539545
NCBI GI
                   226
BLAST score
E value
                   2.0e-28
Match length
                   96
                   61
% identity
NCBI Description (Y16644) PRCI [Nicotiana tabacum]
Seq. No.
                   223702
Seq. ID
                  LIB3165-051-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                   q3914437
BLAST score
                   196
E value
                   3.0e-27
Match length
                   73
% identity
                   69
NCBI Description
                  PROFILIN >gi 3183706 emb CAA75312 (Y15042) profilin [Hevea
                  brasiliensis]
Seq. No.
                   223703
Seq. ID
                  LIB3165-051-Q1-K1-E3
                   BLASTX
Method
NCBI GI
                   q625509
BLAST score
                   626
E value
                   2.0e-65
Match length
                   126
                   25
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.
                   223704
Seq. ID
                   LIB3165-051-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   g20729
BLAST score
                   514
                   2.0e-52
E value
Match length
                   135
% identity
                   78
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                   223705
                  LIB3165-051-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g166834
BLAST score
                   677
                   2.0e-71
E value
Match length
                  140
                   91
% identity
NCBI Description
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
```



activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
Rubisco activase [Arabidopsis thaliana]

```
223706
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3650033
BLAST score
                  150
E value
                  1.0e-09
                  74
Match length
                  45
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                  223707
Seq. No.
                  LIB3165-051-Q1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3832512
BLAST score
                  361
E value
                  2.0e-34
Match length
                  123
                  59
% identity
                  (AF097922) granule-bound glycogen (starch) synthase
NCBI Description
                  [Astragalus membranaceus]
Seq. No.
                  223708
Seq. ID
                  LIB3165-051-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3328122
BLAST score
                  663
E value
                  7.0e-70
                  135
Match length
                  99
% identity
                  (AF073473) phosphoglycerate kinase precursor [Solanum
NCBI Description
                  tuberosum]
                  223709
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g131393
BLAST score
                  340
                  5.0e-32
E value
Match length
                  104
% identity
                  72
                  OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 100360 pir S15005 photosystem II oxygen-evolving
                  complex protein 2 - common tobacco
                  >gi 19911 emb CAA39039.1 (X55354) photosystem II 23kDa
                  polypeptide [Nicotiana tabacum]
Seq. No.
                  223710
Seq. ID
                  LIB3165-051-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g231610
BLAST score
                  347
```

8.0e-33

126

E value Match length

Match length

% identity

116 78



```
% identity
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                  >gi 67880_pir__PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
                  223711
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-F4
                  BLASTX
Method
NCBI GI
                  q3150404
BLAST score
                  418
                  4.0e-41
E value
Match length
                  136
                  62
% identity
                  (AC004165) putative mitochondrial carrier protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  223712
Seq. ID
                  LIB3165-051-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q1168411
BLAST score
                  549
                  2.0e-56
E value
Match length
                  132
                  84
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  223713
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-F6
Method
                  BLASTX
                  q1168411
NCBI GI
                  139
BLAST score
                  8.0e-12
E value
Match length
                  91
                  53
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLGROPLAST PRECURSOR
Seq. No.
                  223714
Seq. ID
                  LIB3165-051-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  252
E value
                  1.0e-21
Match length
                  104
% identity
                  51
                  (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
                  barley [Medicago sativa]
Seq. No.
                  223715
                  LIB3165-051-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490321
BLAST score
                  455
E value
                  2.0e-45
```

BLAST score

E value

180 1.0e-13



```
NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]
                  223716
Seq. No.
                  LIB3165-051-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                  g400890
NCBI GI
BLAST score
                  240
                   3.0e-20
E value
                  110
Match length
                   44
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                  >gi_282837_pir__S26953 photosystem II 22K protein precursor
                   - spinach \overline{>}gi \overline{21}307 emb CAA48557
                                                      (X68552) 22kD-protein of
                   PSII [Spinacia oleracea] >gi 260917 bbs 119338 (S49864)
                  photosystem II 22 kda polypeptide [spinach, Peptide, 274
                   aa] [Spinacia oleracea]
                   223717
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                   q2920666
                   203
BLAST score
                   3.0e - 30
E value
                   86
Match length
                   78
% identity
                   (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                   [Glycine max]
                   223718
Seq. No.
Seq. ID
                   LIB3165-051-Q1-K1-H1
Method
                   BLASTX
                   g20733
NCBI GI
                   408
BLAST score
                   6.0e-40
E value
                   81
Match length
% identity
                   (X15188) precursor C-terminal fragment (AA -80 to 367)
NCBI Description
                   [Pisum sativum]
Seq. No.
                   223719
                   LIB3165-051-Q1-K1-H10
Seq. ID
Method
                   BLASTX
                   q2492515
NCBI GI
BLAST score
                   412
                   2.0e-40
E value
Match length
                   100
% identity
                   84
                   CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                   >qi 2129924 pir S58298 ATPase - pepper (fragment)
                   >gi 929013 emb CAA62084 (X90472) ATPase [Capsicum annuum]
                   223720
Seq. No.
Seq. ID
                   LIB3165-051-Q1-K1-H11
Method
                   BLASTX
                   q1545805
NCBI GI
```



```
Match length
                  45
% identity
                  (D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
NCBI Description
                  223721
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-H2
Method
                  BLASTX
                  g1168411
NCBI GI
                  376
BLAST score
                  3.0e-36
E value
                  102
Match length
                  77
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  223722
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-H4
                  BLASTX
Method
NCBI GI
                  g20733
BLAST score
                  359
E value
                  3.0e - 34
                  124
Match length
% identity
                  62
                  (X15188) precursor C-terminal fragment (AA -80 to 367)
NCBI Description
                  [Pisum sativum]
Seq. No.
                  223723
Seq. ID
                  LIB3165-051-Q1-K1-H6
                  BLASTX
Method
                  g2895188
NCBI GI
BLAST score
                  153
                  5.0e-10
E value
                  69
Match length
% identity
                  27
NCBI Description (AF016011) CONSTANS homolog [Brassica napus]
                  223724
Seq. No.
Seq. ID
                  LIB3165-051-Q1-K1-H8
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                   661
                  1.0e-69
E value
Match length
                  139
                  89
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   223725
                  LIB3165-051-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1730910
BLAST score
                  149
E value
                  2.0e-09
                  137
Match length
```

35

% identity

NCBI GI

E value

BLAST score

q2984709

461 4.0e-46



```
HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION
NCBI Description
                  >gi_1256633 (L77246) putative [Bacillus subtilis]
                  >gi 2634609 emb CAB14107 (Z99115) similar to hypothetical
                  proteins [Bacillus subtilis]
                  223726
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-A1
                  BLASTX
Method
                  g115473
NCBI GI
BLAST score
                  199
                  1.0e-15
E value
                  89
Match length
                  52
% identity
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                  DEHYDRATASE) >gi 170219 (M94135) chloroplast carbonic
                  anhydrase [Nicotiana tabacum] >gi 445610 prf 1909357A
                  carbonic anhydrase [Nicotiana tabacum]
                  223727
Seq. No.
                  LIB3165-052-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334200
                  571
BLAST score
                  5.0e-59
E value
                  131
Match length
                  83
% identity
                  GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE
NCBI Description
                  DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
                  >gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor
                  [Solanum tuberosum]
                  223728
Seq. No.
                  LIB3165-052-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  g282833
NCBI GI
BLAST score ,
                  287
E válue
                  1.0e-25
                  69
Match length
                  86
% identity
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
                  223729
Seq. No.
                  LIB3165-052-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  q4406530
NCBI GI
BLAST score
                  353
                  2.0e-33
E value
                  97
Match length
                  75
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  223730
Seq. ID
                  LIB3165-052-Q1-K1-A5
Method
                  BLASTX
```

E value

Match length

% identity

2.0e-27

137 49



```
Match length
                  95
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  223731
Seq. No.
                  LIB3165-052-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023752
BLAST score
                  360
E value
                  3.0e - 34
Match length
                  121
% identity
                  62
NCBI Description
                  FERREDOXIN I PRECURSOR >qi 1418982 emb CAA99756 (Z75520)
                  ferredoxin-I [Lycopersicon esculentum]
                  223732
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q1350930
BLAST score
                  696
E value
                  1.0e-73
                  146
Match length
% identity
                  93
NCBI Description 40S RIBOSOMAL PROTEIN S13
                  223733
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q4467098
BLAST score
                  326
                  3.0e-30
E value
                  134
Match length
% identity
                  56
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                  223734
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  744
E value
                  3.0e-79
Match length
                  146
                  96
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223735
                  LIB3165-052-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                  302
```



```
(U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  223736
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-B3
                  BLASTX
Method
                  g2191138
NCBI GI
BLAST score
                  334
                  3.0e - 31
E value
                  120
Match length
                  62
% identity
                  (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  223737
Seq. No.
                  LIB3165-052-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173345
                  412
BLAST score
E value
                  2.0e-40
                  133
Match length
                  63
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 1076403 pir S51838 sedoheptulose-1,7-biphosphatase -
                  Arabidopsis thaliana >gi 786466 bbs 159034 (S74719)
                   sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37}
                   [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa]
                   [Arabidopsis thaliana]
                  223738
Seq. No.
                  LIB3165-052-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                   q2677828
NCBI GI
BLAST score
                   395
                   2.0e-38
E value
                   109
Match length
% identity
                   68
NCBI Description
                  (U93166) cysteine protease [Prunus armeniaca]
                   223739
Seq. No.
                   LIB3165-052-Q1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3023752
BLAST score
                   352
                   2.0e-33
E value
Match length
                   128
                   59
% identity
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756_ (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
```

223740 Seq. No.

LIB3165-052-Q1-K1-C11 Seq. ID

BLASTX Method g1352821 NCBI GI 706 BLAST score 8.0e-75 E value



Match length 136 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

223741 Seq. No.

LIB3165-052-Q1-K1-C12 Seq. ID

Method BLASTX NCBI GI g4406530 BLAST score 348 E value 7.0e-33 Match length 98 73 % identity

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223742

Seq. ID LIB3165-052-Q1-K1-C2

Method BLASTX NCBI GI g4262239 BLAST score 245 E value 8.0e-21 Match length 115 45 % identity

(AC006200) putative membrane transporter [Arabidopsis NCBI Description

thaliana]

Seq. No. 223743

Seq. ID LIB3165-052-Q1-K1-C7

Method BLASTX NCBI GI q4210948 BLAST score 497 E value 2.0e-50 Match length 98 % identity 96

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 223744

Seq. ID LIB3165-052-Q1-K1-C8

Method BLASTX NCBI GI q1352821 BLAST score 535 E value 8.0e-55 Match length 101 100 % identity

MCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223745 Seq. No.

LIB3165-052-Q1-K1-C9 Seq. ID

Method BLASTX NCBI GI g100616

```
276
BLAST score
E value
                  2.0e-24
                  77
Match length
                  71
% identity
                  ribulose-bisphosphate carboxylase activase B precursor -
NCBI Description
                  barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                  carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
                  ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                  vulgare]
                  223746
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-D10
                  BLASTX
Method
                  g2088651
NCBI GI
BLAST score
                  368
                  3.0e-35
E value
                  133
Match length
                  56
% identity
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                  [Arabidopsis thaliana]
                  223747
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-D11
                  BLASTX
Method
                  g4406809
NCBI GI
BLAST score
                  180
                  4.0e-13
E value
                  48
Match length
                  69
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                  223748
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2765081
                  525
BLAST score
E value
                  1.0e-53
                  138
Match length
                  75
% identity
NCBI Description (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                  223749
                  LIB3165-052-Q1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1352821
BLAST score
                  574
                  2.0e-59
E value
                  108
Match length
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
```

ribulose-bisphosphate carboxylase $(EC \overline{4.1.1.39})$ small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223750

LIB3165-052-Q1-K1-D7 Seq. ID

BLAST score

E value

619 1.0e-64



```
Method
                  BLASTX
NCBI GI
                  g2982453
BLAST score
                  681
                  6.0e-72
E value
                  143
Match length
                  92
% identity
                  (AL022223) fructose-bisphosphate aldolase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  223751
Seq. No.
                  LIB3165-052-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g1168411
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
                  134
Match length
                  84
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  223752
Seq. ID
                  LIB3165-052-Q1-K1-D9
                  BLASTX
Method
NCBI GI
                  q289920
BLAST score
                  560
E value
                  8.0e-58
                  121
Match length
                  87
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  223753
Seq. No.
                  LIB3165-052-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  a2501572
NCBI GI
BLAST score
                  149
                  1.0e-09
E value
                  74
Match length
                  51
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi 1350545
                  (L47118) EMB8 gene product [Picea glauca]
Seq. No.
                  223754
                  LIB3165-052-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  388
E value
                  1.0e-37
Match length
                  110
% identity
                  74
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  223755
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q231688
```



```
Match length
                  117
                  100
% identity
                  CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC
NCBI Description
                  1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675)
                  subunit 2 of cotton catalase [Gossypium hirsutum]
                  223756
Seq. No.
                  LIB3165-052-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                  q131399
NCBI GI
BLAST score
                  465
                  1.0e-46
E value
                  109
Match length
                  82
% identity
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411
                  photosystem II 10K protein precursor - potato
                  >gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                  tuberosum]
Seq. No.
                  223757
Seq. ID
                  LIB3165-052-Q1-K1-E2
Method
                  BLASTX
                  g2739004
NCBI GI
BLAST score
                  258
                  3.0e-22
E value
Match length
                  81
% identity
                  54
NCBI Description (AF022461) CYP82Clp [Glycine max]
                  223758
Seq. No.
                  LIB3165-052-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  374
BLAST score
                  5.0e-36
E value
                  76
Match length
                  96
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223759
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                  g3885341
BLAST score
                  474
E value
                  1.0e-47
```

Match length 107 % identity 76

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 223760

LIB3165-052-Q1-K1-E8 Seq. ID

Method BLASTX

```
g2791834
NCBI GI
BLAST score
                  623
                  4.0e-65
E value
                  120
Match length
                  99
% identity
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                  223761
Seq. No.
                  LIB3165-052-Q1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3395429
                  177
BLAST score
E value
                  7.0e-13
Match length
                  61
                  52
% identity
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  223762
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-F2
Method
                  BLASTX
                   g2055273
NCBI GI
                   634
BLAST score
E value
                   2.0e-66
                  135
Match length
                   88
% identity
                  (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
NCBI Description
                   223763
Seq. No.
Seq. ID
                  LIB3165-052-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                   q2982463
                   491
BLAST score
                   1.0e-49
E value
                   145
Match length
                   70
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                   223764
Seq. No.
                   LIB3165-052-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   q2632109
NCBI GI
BLAST score
                   238
                   5.0e-20
E value
                   121
Match length
% identity
                   48
                  (AJ000508) phospholipid glutathione peroxidase [Pisum
NCBI Description
                   sativum]
Seq. No.
                   223765
Seq. ID
                   LIB3165-052-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3540196
BLAST score
                   266
E value
                   3.0e-23
Match length
                   118
```

(AC004260) Putative amp-binding protein [Arabidopsis

47

% identity

NCBI Description



thaliana]

223766 Seq. No. Seg. ID LIB3165-052-Q1-K1-G1 Method BLASTX g2765081 NCBI GI BLAST score 506 E value 2.0e-51 139 Match length % identity 72 (Y10557) g5bf [Arabidopsis thaliana] NCBI Description Seq. No. 223767 LIB3165-052-Q1-K1-G2 Seq. ID Method BLASTX NCBI GI g3043428 BLAST score 524 2.0e-53 E value Match length 111 % identity 87 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum] NCBI Description 223768 Seq. No. Seq. ID LIB3165-052-Q1-K1-G3 Method BLASTX NCBI GI g4455208 BLAST score 562 6.0e-58 E value Match length 139 % identity (AL035440) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 223769 Seq. ID LIB3165-052-01-K1-G5 Method BLASTX NCBI GI g1352821 BLAST score 113 E value 2.0e-09 Match length 89 % identity 43 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223770 LIB3165-052-Q1-K1-G7 Seq. ID Method BLASTX NCBI GI g68200 BLAST score 565 E value 2.0e-58

Match length 139 83 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

```
Seq. No.
                   223771
Seq. ID
                  LIB3165-052-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3688123
BLAST score
                   369
                  2.0e-35
E value
Match length
                  128
% identity
                   63
NCBI Description
                  (AJ006293) granule-bound starch synthase [Antirrhinum
                  majus]
Seq. No.
                  223772
                  LIB3165-052-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2582822
BLAST score
                  253
E value
                  1.0e-21
Match length
                  124
% identity
                  51
NCBI Description
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
                  Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                  223773
Seq. ID
                  LIB3165-052-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  374
E value
                  6.0e-36
Match length
                  106
% identity
                  71
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  223774
Seq. ID
                  LIB3165-052-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  518
E value
                  6.0e-53
Match length
                  100
% identity
                  97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223775
Seq. ID
                  LIB3165-052-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1345698
BLAST score
                  672
E value
                  7.0e-71
Match length
                  132
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

95

% identity



(CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

a/b-binding protein - upland cotton

>gi 452314 emb CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 223776

Seq. ID LIB3165-052-Q1-K1-H2

Method BLASTX
NCBI GI g267082
BLAST score 634
E value 2.0e-66
Match length 122
% identity 95

NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8

chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

Seq. No. 223777

Seq. ID LIB3165-052-Q1-K1-H3

Method BLASTX
NCBI GI g2388689
BLAST score 214
E value 3.0e-17
Match length 90
% identity 52

NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 223778

Seq. ID LIB3165-052-Q1-K1-H4

Method BLASTX
NCBI GI g4406530
BLAST score 393
E value 4.0e-38
Match length 109
% identity 75

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223779

Seq. ID LIB3165-052-Q1-K1-H5

Method BLASTX
NCBI GI g3126967
BLAST score 333
E value 2.0e-31
Match length 99
% identity 15

NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No. 223780

Seq. ID LIB3165-052-Q1-K1-H7

Method BLASTX
NCBI GI g1354515
BLAST score 282
E value 4.0e-25
Match length 140
% identity 46

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No.

Seq. ID

223786

LIB3165-053-Q1-K1-A4



```
Seq. No.
                  223781
Seq. ID
                  LIB3165-052-Q1-K1-H8
                  BLASTX
Method
NCBI GI
                  q2088647
BLAST score
                  223
                  3.0e-18
E value
Match length
                  78
                  53
% identity
                  (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                  [Arabidopsis thaliana]
                  223782
Seq. No.
                  LIB3165-053-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1421730
BLAST score
                  494
E value
                  5.0e-50
                  118
Match length
                  77
% identity
                  (U43082) RF2 [Zea mays]
NCBI Description
Seq. No.
                  223783
                  LIB3165-053-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3269292
BLAST score
                  183
E value
                  9.0e-14
Match length
                  62
                  56
% identity
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  223784
                  LIB3165-053-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652892
BLAST score
                  127
E value
                  1.0e-12
Match length
                  113
% identity
                   47
                  (D90909) ABC transporter [Synechocystis sp.]
NCBI Description
Seq. No.
                  223785
Seq. ID
                  LIB3165-053-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2501568
BLAST score
                  173
                  2.0e-12
E value
Match length
                  54
% identity
                  54
NCBI Description
                  HYPOTHETICAL 28.8 KD PROTEIN SLL0506
                  >gi 1001342 dbj BAA10829 (D64006) hypothetical protein
                   [Synechocystis sp.]
```



```
BLASTX
Method
                  g3860264
NCBI GI
                  418
BLAST score
                   4.0e-41
E value
Match length
                  86
% identity
                  88
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  223787
Seq. ID
                  LIB3165-053-Q1-K1-A5
Method
                  BLASTX
                  q1778093
NCBI GI
BLAST score
                   419
                  5.0e-43
E value
Match length
                   139
% identity
                   68
                   (U64902) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
Seq. No.
                   223788
Seq. ID
                  ·LIB3165-053-Q1-K1-A7
Method
                  BLASTX
                   g3559807
NCBI GI
                   292
BLAST score
                   1.0e-26
E value
Match length
                   92
% identity
                   63
                  (Y15628) HCF136 protein [Arabidopsis thaliana]
NCBI Description
                   223789
Seq. No.
Seq. ID
                   LIB3165-053-Q1-K1-B1
                   BLASTX
Method
NCBI GI
                   g3080401
                   385
BLAST score
                   3.0e - 37
E value
Match length
                   100
                   72
% identity
                   (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4455265 emb CAB36801.1 (AL035527) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   223790
Seq. ID
                   LIB3165-053-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1170567
BLAST score
                   675
                   3.0e-71
E value
                   139
Match length
                   91
% identity
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                   >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
```

>g1_1085960_p1r__\$52648 1NO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No. 223791

Seq. ID LIB3165-053-Q1-K1-B2

Method BLASTX

NCBI GI

BLAST score



```
g1363526
NCBI GI
BLAST score
                   681
E value
                  6.0e-72
                  138
Match length
                  92
% identity
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
NCBI Description
                  cytochrome b6 - maize chloroplast >gi_902251_emb_CAA60315_
                   (X86563) cytochrome B6 [Zea mays]
                  223792
Seq. No.
Seq. ID
                  LIB3165-053-Q1-K1-B3
                  BLASTX
Method
NCBI GI
                  g3023281
BLAST score
                  457
E value
                  1.0e-45
                  141
Match length
                  64
% identity
                  HIGH AFFINITY AMMONIUM TRANSPORTER
NCBI Description
                  >gi 2065194 emb CAA64475 (X95098) ammonium transporter
                   [Lycopersicon esculentum]
                  223793
Seq. No.
Seq. ID
                  LIB3165-053-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2739375
BLAST score
                  243
                  1.0e-20
E value
                  107
Match length
                  50
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                  223794
Seq. No.
                  LIB3165-053-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129452
BLAST score
                   481
                   2.0e-48
E value
Match length
                  106
% identity
                  16
NCBI Description polyubiquitin - red alga (Gracilaria verrucosa)
Seq. No.
                  223795
Seq. ID
                  LIB3165-053-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                   206
                   6.0e-29
E value
Match length
                  90
% identity
                   80
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                   223796
                  LIB3165-053-Q1-K1-C10
Seq. ID
Method
                  BLASTX
```

g2494175



```
2.0e-16
E value
                  101
Match length
                  49
% identity
                  GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi 1184960 (U46665)
NCBI Description
                  glutamate decarboxylase 2 [Arabidopsis thaliana]
                  >gi 1236619 (U49937) glutamate decarboxylase [Arabidopsis
                  thaliana]
                  223797
Seq. No.
                  LIB3165-053-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  q131773
NCBI GI
                  200
BLAST score
                  8.0e-16
E value
                  78
Match length
% identity
                   65
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >qi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
                  maize
Seq. No.
                   223798
                  LIB3165-053-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                   q1709825
NCBI GI
                   338
BLAST score
                   7.0e-32
E value
                   124
Match length
                   65
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   223799
Seq. No.
Seq. ID
                   LIB3165-053-Q1-K1-C2
                   BLASTX
Method
                   q2114046
NCBI GI
                   642
BLAST score
                   2.0e-67
E value
                   137
Match length
                   91
% identity
NCBI Description (AB002147) water channel protein [Nicotiana excelsior]
                   223800
Seq. No.
Seq. ID
                   LIB3165-053-Q1-K1-C3
                   BLASTX
Method
                   q3252807
NCBI GI
BLAST score
                   159
                   1.0e-12
E value
                   107
Match length
                   44
 % identity
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   223801
Seq. No.
```

Seq. ID LIB3165-053-Q1-K1-C6

Method BLASTX
NCBI GI g1352821
BLAST score 268
E value 6.0e-25



```
78
Match length
                    79
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                    ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                    precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                    ribulose bisphosphate carboxylase [Gossypium hirsutum]
                    223802
 Seq. No.
                    LIB3165-053-Q1-K1-D11
 Seq. ID
 Method
                    BLASTX
                    g3258571
 NCBI GI
 BLAST score
                    463
                    2.0e-46
 E value
                    117
 Match length
                    80
 % identity
 NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
                    223803
 Seq. No.
                    LIB3165-053-Q1-K1-D3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1168411
                    547
 BLAST score
                    3.0e-56
 E value
                    137
 Match length
                    82
  % identity
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                    223804
 Seq. No.
                    LIB3165-053-Q1-K1-D4
 Seq. ID
                    BLASTX
 Method
                    q3023752
 NCBI GI
                    322
 BLAST score
                    7.0e-30
  E value
                    114
 Match length
                    61
  % identity
                    FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756_ (Z75520)
  NCBI Description
                    ferredoxin-I [Lycopersicon esculentum]
                    223805
  Seq. No.
                    LIB3165-053-Q1-K1-D8
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q1352821
                     386
  BLAST score
                    2.0e-37
  E value
                    73
  Match length
                     95
  % identity
  NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                     (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

223806 Seq. No.

LIB3165-053-Q1-K1-E1 Seq. ID

BLASTX Method q4455208 NCBI GI

```
BLAST score
                       531
                       2.0e-54
    E value
                       141
    Match length
                       73
     % identity
    NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                       223807
     Seq. No.
                       LIB3165-053-Q1-K1-E11
     Seq. ID
     Method
                       BLASTX
     NCBI GI
                       q4006872
     BLAST score
                       280
                       6.0e-25
     E value
                       75
    Match length
                       76
     % identity
    NCBI Description
                       (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
                       thaliana]
                       223808
     Seq. No.
                       LIB3165-053-Q1-K1-E12
     Seq. ID
     Method
                       BLASTX
     NCBI GI
                       q231688
     BLAST score
                       613
                       5.0e-64
     E value
                       123
     Match length
                       94
     % identity
                       CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC
     NCBI Description
                       1.11.1.6) - upland cotton > gi_1 = 18488  emb CAA39998 (X56675)
                       subunit 2 of cotton catalase [Gossypium hirsutum]
                       223809
     Seq. No.
     Seq. ID
                       LIB3165-053-Q1-K1-E2
     Method
                       BLASTX
     NCBI GI
                       q2582822
                       203
     BLAST score
                       7.0e-16
     E value
     Match length
                       115
                       48
     % identity
                       (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
     NCBI Description
                       Protein of 32kDa) [Solanum tuberosum]
                       223810
     Seq. No.
                       LIB3165-053-Q1-K1-E4
     Seq. ID
                       BLASTX
     Method
     NCBI GI
                       q2494076
     BLAST score
                       442
                       3.0e-55
     E value
```

Match length 124 84 % identity

NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE NCBI Description

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >qi 1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase

[Nicotiana plumbaginifolia]

223811 Seq. No.

Seq. ID LIB3165-053-Q1-K1-E5

BLAST score

E value Match length 459 6.0e-46



```
BLASTX
Method
                  q1181599
NCBI GI
BLAST score
                  414
                  1.0e-40
E value
                  111
Match length
% identity
                  74
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
                  223812
Seq. No.
                  LIB3165-053-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172664
                  330
BLAST score
                  8.0e-31
E value
                  70
Match length
                  91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                   >qi 419791 pir S31165 photosystem I chain III precursor -
                   Flaveria trinervia >gi 298482 bbs 127083 photosystem I
                   reaction center subunit III, PSI-RC PsaF [Flaveria
                   trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem
                   I subunit III [Flaveria trinervia]
                   223813
Seq. No.
                   LIB3165-053-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1352821
BLAST score
                   482
                   6.0e-49
E value
                   89
Match length
% identity
                   97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase \overline{\text{(EC 4.1.1.39)}} small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223814
Seq. No.
Seq. ID
                   LIB3165-053-Q1-K1-F10
                   BLASTX
Method
                   g125578
NCBI GI
BLAST score
                   214
                   5.0e-21
E value
                   75
Match length
                   73
% identity
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi 167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                   223815
Seq. No.
Seq. ID
                   LIB3165-053-Q1-K1-F12
                   BLASTX
Method
                   g1346155
NCBI GI
```

```
87
```

% identity SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR NCBI Description (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi 481942 pir S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi 437995 emb CAA81078 (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei] Seq. No. 223816 Seq. ID LIB3165-053-Q1-K1-F2 Method BLASTX q2979550 NCBI GI 203 BLAST score 4.0e-16 E value 95 Match length % identity 48 (AC003680) putative 7-ethoxycoumarin O-deethylase NCBI Description [Arabidopsis thaliana] Seq. No. 223817 Seq. ID LIB3165-053-Q1-K1-F4 Method BLASTX g1352821 NCBI GI 627 BLAST score 1.0e-65 E value Match length 116 98 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 223818 Seq. No. LIB3165-053-Q1-K1-F5 Seq. ID BLASTX Method g1709651 NCBI GI 437 BLAST score 2.0e-43E value 138 Match length 62 % identity NCBI Description PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209 plastocyanin a precursor - black poplar >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus nigra] 223819 Seq. No. Seq. ID LIB3165-053-Q1-K1-F6 BLASTX Method NCBI GI g1352821 BLAST score 557 1.0e-57 E value 105 Match length 95 % identity

31764

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223820 Seq. ID LIB3165-053-Q1-K1-G1 Method BLASTX NCBI GI g232031 BLAST score 236 1.0e-19 E value 73 Match length 58 % identity NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224 translation elongation factor eEF-1 beta chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa] Seq. No. 223821 Seq. ID LIB3165-053-Q1-K1-G2 Method BLASTX NCBI GI q2661021 BLAST score 667 E value 3.0e-70 Match length 126 % identity 98 NCBI Description (AF035255) catalase [Glycine max] Seq. No. 223822 LIB3165-053-Q1-K1-G3 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 261 1.0e-22 E value Match length 52 96 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi_450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223823

Seq. ID LIB3165-053-Q1-K1-G4

Method BLASTX NCBI GI g231503 BLAST score 166 E value 2.0e-21 Match length 80 % identity 67

NCBI Description ACTIN 97 >gi_100417 pir S20098 actin - potato

>gi_21544_emb_CAA39280 (X55751) actin [Solanum tuberosum]

223824 Seq. No.

Seq. ID LIB3165-053-Q1-K1-G8

Method BLASTX NCBI GI q3800853 BLAST score 642 E value 3.0e-71



Match length 140 % identity 96

NCBI Description (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase precursor [Zea mays]

Seq. No. 223825

Seq. ID LIB3165-053-Q1-K1-H12

Method BLASTX
NCBI GI g2191136
BLAST score 323
E value 5.0e-51
Match length 140

% identity 70

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 223826

Seq. ID LIB3165-053-Q1-K1-H2

Method BLASTX
NCBI GI g3075400
BLAST score 289
E value 4.0e-26
Match length 73
% identity 71

NCBI Description (AC004484) putative thromboxane-A synthase [Arabidopsis

thaliana] >gi_3413720 (AC004747) putative thromboxin-A

synthase [Arabidopsis thaliana]

Seq. No. 223827

Seq. ID LIB3165-053-Q1-K1-H4

Method BLASTX
NCBI GI g1352821
BLAST score 412
E value 2.0e-40
Match length 137
% identity 64

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223828

Seq. ID LIB3165-053-Q1-K1-H5

Method BLASTX
NCBI GI g1352821
BLAST score 178
E value 3.0e-15
Match length 56
% identity 80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

Seq. ID

Method

223834

BLASTX

LIB3165-055-P1-K1-A6

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223829
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-A1
                  BLASTX
Method
                  g445116
NCBI GI
BLAST score
                  558
                  1.0e-57
E value
                  116
Match length
                  91
% identity
NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]
                  223830
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  g100203
                  291
BLAST score
                  2.0e-26
E value
                  77
Match length
                  73
% identity
                  cysteine proteinase (EC 3.4.22.-) precursor - tomato
NCBI Description
                  >gi 19195 emb CAA78403 (Z14028) pre-pro-cysteine
                  proteinase [Lycopersicon esculentum]
                  223831
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-A11
Method
                  BLASTX
                   g2673914
NCBI GI
                   538
BLAST score
                   3.0e-55
E value
                   117
Match length
                   80
% identity
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   223832
Seq. No.
Seq. ID
                   LIB3165-055-P1-K1-A12
Method
                   BLASTX
                   g4056507
NCBI GI
                   189
BLAST score
                   2.0e-14
E value
Match length
                   55
                   65
% identity
NCBI Description
                   (AC005896) putative RNA binding protein [Arabidopsis
                   thaliana]
                   223833
Seq. No.
Seq. ID
                   LIB3165-055-P1-K1-A5
Method
                   BLASTX
                   q4406530
NCBI GI
BLAST score
                   312
                   9.0e-29
E value
Match length
                   109
% identity
                   62
NCBI Description
                   (AF126870) rubisco activase [Vigna radiata]
```

NCBI GI

BLAST score

q2499945

430



```
NCBI GI
                  g266893
BLAST score
                  586
                  6.0e-61
E value
                  119
Match length
                  94
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir__S28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906_ (X67674) rubisco activase [Cucumis
                  satīvus]
                  223835
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-B10
                  BLASTX
Method
                  g2864617
NCBI GI
                  239
BLAST score
                  3.0e-20
E value
                  108
Match length
                  50
% identity
NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana]
                  223836
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-B8
                  BLASTX
Method
NCBI GI
                  q3869088
                  511
BLAST score
                  4.0e-52
E value
                  97
Match length
                  100
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  223837
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-B9
                  BLASTX
Method
NCBI GI
                  q70644
BLAST score
                  545
E value
                  4.0e-56
                  114
Match length
                  18
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  223838
Seq. No.
                  LIB3165-055-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4406759
                  204
BLAST score
                  4.0e-16
E value
                  92
Match length
% identity
                  47
NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]
                  223839
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-C11
Method
                  BLASTX
```



```
1.0e-42
E value
                  118
Match length
                  67
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi 1076363 pir S46440 orotate
                  phosphoribosyltransferase (EC 2.4.2.10) /
                  orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                  Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)
                  pyrE-F [Arabidopsis thaliana]
                  223840
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2959643
BLAST score
                  137
                  3.0e-13
E value
Match length
                  102
% identity
                  22
NCBI Description (AF001945) rim ABC transporter [Homo sapiens]
Seq. No.
                  223841
Seq. ID
                  LIB3165-055-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                  203
E value
                  5.0e-16
                  97
Match length
% identity
                  51
NCBI Description
                  (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
Seq. No.
                  223842
Seq. ID
                  LIB3165-055-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q1362086
BLAST score
                  496
                  2.0e-50
E value
Match length
                  103
                  91
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
Seq. No.
                  223843
Seq. ID
                  LIB3165-055-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4433048
BLAST score
                  325
E value
                  3.0e-30
Match length
                  92
% identity
                  75
```

NCBI Description (D26578) DNA-binding protein [Daucus carota]

```
Seq. ID
                  LIB3165-055-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1709825
BLAST score
                  277
                  1.0e-24
E value
Match length
                  112
                  62
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
                  223845
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-C8
Method
                  BLASTX
                  g1439609
NCBI GI
                  566
BLAST score
                  1.0e-58
E value
Match length
                  113
                  54
% identity
NCBI Description
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
                  hirsutum]
Seq. No.
                  223846
Seq. ID
                  LIB3165-055-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  364
                  7.0e-35
E value
Match length
                  71
                  99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  223847
Seq. No.
                  LIB3165-055-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3158474
BLAST score
                  324
E value
                  3.0e - 30
                  85
Match length
% identity
                  76
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  223848
Seq. ID
                  LIB3165-055-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  420
                  2.0e-41
E value
Match length
                  109
% identity
                  75
```

223844

Seq. No.

31770

NCBI Description (L08199) peroxidase [Gossypium hirsutum]



Seq. No. 223849

Seq. ID LIB3165-055-P1-K1-D3

Method BLASTX
NCBI GI g3122232
BLAST score 228
E value 6.0e-19
Match length 95
% identity 55

NCBI Description MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR

>gi 1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana]

>gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis
mitochondrion-localized small heat shock protein

(AtHSP23.6-mito) [Arabidopsis thaliana]

Seq. No. 223850

Seq. ID LIB3165-055-P1-K1-D4

Method BLASTX
NCBI GI g1352821
BLAST score 505
E value 2.0e-51
Match length 104
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505 emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223851

Seq. ID LIB3165-055-P1-K1-D6

Method BLASTX
NCBI GI g118564
BLAST score 562
E value 4.0e-58
Match length 113
% identity 92

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi_65955 pir DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi_18264_emb_CAA41434_ (X58542) NADH-dependent
hydroxypyruvate reductase [Cucumis sativus]
>gi_18275_emb_CAA32764_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 223852

Seq. ID LIB3165-055-P1-K1-D8

Method BLASTX
NCBI GI g4406530
BLAST score 292
E value 2.0e-26
Match length 80
% identity 75

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223853

Seg. ID LIB3165-055-P1-K1-D9

Method BLASTX

Match length



```
g100196
NCBI GI
BLAST score
                   441
                   6.0e-44
E value
                   98
Match length
                   83
% identity
                  chlorophyll a/b-binding protein (cab-11) - tomato
NCBI Description
                   223854
Seq. No.
                   LIB3165-055-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4164408
BLAST score
                   461
                   3.0e-46
E value
                   97
Match length
                   88
% identity
                   (AJ132228) amino acid carrier [Ricinus communis]
NCBI Description
                   223855
Seq. No.
                   LIB3165-055-P1-K1-E8
Seq. ID
                   BLASTX
Method
                   g3510254
NCBI GI
BLAST score
                   362
E value
                   1.0e-34
                   104
Match length
                   72
% identity
                   (AC005310) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   223856
                   LIB3165-055-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g2765817
NCBI GI
BLAST score
                   149
                   1.0e-09
E value
                   57
Match length
                   54
% identity
                   (Z95352) AtMlo-h1 [Arabidopsis thaliana]
NCBI Description
                   >qi 3892049 gb AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
                   223857
Seq. No.
                   LIB3165-055-P1-K1-F10
Seq. ID
                   {\tt BLASTX}
Method
                   g289920
NCBI GI
BLAST score
                   571
                   4.0e-59
E value
                   108
Match length
                    97
 % identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
 Seq. No.
                    223858
                    LIB3165-055-P1-K1-F11
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q4406530
 BLAST score
                    278
                    7.0e-25
 E value
```



```
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  223859
Seq. No.
                  LIB3165-055-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  q477280
NCBI GI
                  427
BLAST score
                  3.0e-42
E value
                  110
Match length
                  73
% identity
NCBI Description mitochondrial processing peptidase (EC
                                                             4.99.41) 55K
                  protein precursor - potato >gi_4106 :
                                                                 7/0 cytochrome
                  c reductase-processing peptidase subunit 1,
                  P55 [potatoes, var. Marfona, tuber, Peptide Mil chondrial,
                  534 aa]
                  223860
Seq. No.
                  LIB3165-055-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1737492
BLAST score
                  142
                  7.0e-09
E value
                  110
Match length
                  33
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
                  223861
Seq. No.
                  LIB3165-055-P1-K1-F3
Seq. ID
                  BLASTX
Method
                   g100602
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
                   97
Match length
                   65
% identity
NCBI Description infection-related protein - barley
                   223862
Seq. No.
                   LIB3165-055-P1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q729252
BLAST score
                   199
                   2.0e-29
E value
                   104
Match length
                   59
% identity
                  CYTOCHROME B5 >qi 167140 (M87514) cytochrome b-5 [Brassica
NCBI Description
                   oleracea] >gi_384338_prf__1905426A cytochrome b5 [Brassica
                   oleracea]
                   223863
Seq. No.
                   LIB3165-055-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   q289920
NCBI GI
BLAST score
                   578
E value
                   6.0e-60
```

110

97

Match length % identity



```
(L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  223864
Seq. No.
                  LIB3165-055-P1-K1-F9
Seq. ID
                  {\tt BLASTX}
Method
                  g2511693
NCBI GI
                  376
BLAST score
                  3.0e-36
E value
                  100
Match length
                  73
% identity
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
                  223865
Seq. No.
                  LIB3165-055-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g3914435
NCBI GI
                   450
BLAST score
                   6.0e-45
E value
                   93
Match length
% identity
                   88
                  PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
NCBI Description
                   [Glycine max]
                   223866
Seq. No.
                   LIB3165-055-P1-K1-G2
Seq. ID
Method
                   BLASTX
                   g1352821
NCBI GI
                   486
BLAST score
                   3.0e-49
E value
                   99
Match length
% identity
                   96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223867
Seq. No.
Seq. ID
                   LIB3165-055-P1-K1-G3
                   BLASTX
Method
                   g2499931
NCBI GI
BLAST score
                   268
                   1.0e-23
E value
                   65
Match length
% identity
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
NCBI Description
                   >gi_2129534_pir__S71272 adenine phosphoribosyltransferase
                   (EC 2.4.2.7) - Arabidopsis thaliana
                   >gi 1321681 emb CAA65609 (X96866) adenine
                   phosphoribosyltransferase [Arabidopsis thaliana]
                   223868
Seq. No.
Seq. ID
                   LIB3165-055-P1-K1-G4
Method
                   BLASTX
```

g3688125

274

NCBI GI BLAST score



2.0e-24 E value 97 Match length 64 % identity (AJ006294) granule-bound starch synthase [Antirrhinum NCBI Description majus] 223869 Seq. No. Seq. ID LIB3165-055-P1-K1-G5 Method BLASTX NCBI GI g1352821 517 BLAST score 8.0e-53 E value 108 Match length 94 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223870 Seq. ID LIB3165-055-P1-K1-G7 BLASTX Method g1703292 NCBI GI 312 BLAST score 8.0e-29 E value 98 Match length 69 % identity HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb CAA53473 NCBI Description (X75879) amt1 [Arabidopsis thaliana] Seq. No. 223871 Seq. ID LIB3165-055-P1-K1-H1 BLASTX Method NCBI GI q68200 BLAST score 285 1.0e-25 E value 78 Match length 77 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea] 223872 Seq. No. LIB3165-055-P1-K1-H10 Seq. ID Method BLASTX q4239845 NCBI GI 190 BLAST score 2.0e-14 E value 118 Match length % identity 40

NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 223873

LIB3165-055-P1-K1-H11 Seq. ID

Method BLASTX NCBI GI g1172664



BLAST score 186 E value 5.0e-14 Match length 39 92 % identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_419791_pir_ S31165 photosystem I chain III precursor -Flaveria trinervia >gi 298482 bbs 127083 photosystem I

reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem

I subunit III [Flaveria trinervia]

223874 Seq. No.

Seq. ID LIB3165-055-P1-K1-H12

Method BLASTX NCBI GI g100616 BLAST score 396 1.0e-38 E value 108 Match length 69 % identity

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

223875 Seq. No.

Seq. ID LIB3165-055-P1-K1-H2

Method BLASTX NCBI GI g1168408 BLAST score 518 E value 6.0e-53 Match length 113 % identity 91

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 223876

LIB3165-055-P1-K1-H3 Seq. ID

Method BLASTX NCBI GI q421826 BLAST score 308 E value 3.0e-28 Match length 98 62 % identity

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb CAA50712 (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 223877

Seq. ID LIB3165-055-P1-K1-H5

Method BLASTX NCBI GI g2492782 BLAST score 284 E value 2.0e-25

```
59
Match length
                  78
% identity
                  ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
NCBI Description
                  (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi 504489 (L27992)
                  alpha-galactosidase [Coffea arabica]
                  223878
Seq. No.
Seq. ID
                  LIB3165-055-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g3292814
                  173
BLAST score
                  2.0e-12
E value
                  100
Match length
                  46
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  223879
Seq. No.
                  LIB3165-055-P1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2435517
BLAST score
                  312
                  8.0e-29
E value
                  107
Match length
                  55
% identity
                   (AF024504) contains similarity to peptidase family A1
NCBI Description
                   [Arabidopsis thaliana]
                  223880
Seq. No.
                  LIB3165-055-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g1684851
NCBI GI
BLAST score
                  262
                  6.0e-23
E value
                  81
Match length
% identity
                   64
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
                  223881
Seq. No.
                  LIB3165-056-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1076748
BLAST score
                   178
                   2.0e-13
E value
                   59
Match length
                   59
% identity
                  major intrinsic protein - rice >qi 440869 dbj BAA04257
NCBI Description
                   (D17443) major intrinsic protein [Oryza sativa]
Seq. No.
                   223882
Seq. ID
                   LIB3165-056-P1-K1-A3
Method
                   BLASTX
                   g1168411
NCBI GI
BLAST score
                   403
                   2.0e-39
E value
                  106
Match length
% identity
                   80
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
```

Seq. No. 223883

Seq. ID LIB3165-056-P1-K1-B1

Method BLASTX
NCBI GI g2554675
BLAST score 202
E value 4.0e-16
Match length 66
% identity 68

NCBI Description Three-Dimensional Structure Of Glycolate Oxidase With Bound

Active-Site Inhibitors >gi 2624594 pdb 1AL7

Three-Dimensional Structures Of Glycolate Oxidase With

Bound Active-Site Inhibitors

Seq. No. 223884

Seq. ID LIB3165-056-P1-K1-B10

Method BLASTX
NCBI GI g3023752
BLAST score 238
E value 4.0e-20
Match length 93
% identity 56

NCBI Description FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No. 223885

Seq. ID LIB3165-056-P1-K1-B12

Method BLASTX
NCBI GI g1352821
BLAST score 457
E value 8.0e-46
Match length 93
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223886

Seq. ID LIB3165-056-P1-K1-B2

Method BLASTX
NCBI GI g131393
BLAST score 144
E value 2.0e-09
Match length 66
% identity 56

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360 pir S15005 photosystem II oxygen-evolving

complex protein 2 - common tobacco

>gi_19911_emb CAA39039.1 (X55354) photosystem II 23kDa

polypeptide [Nicotiana tabacum]

Seq. No. 223887

Seq. ID LIB3165-056-P1-K1-C12

Method BLASTX



```
NCBI GI
                  g2754849
BLAST score
                  312
E value
                  3.0e-29
Match length
                  77
                  86
% identity
NCBI Description
                  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]
Seq. No.
                  223888
Seq. ID
                  LIB3165-056-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q121344
BLAST score
                  165
E value
                  1.0e-11
Match length
                  68
                  53
% identity
                  GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR
NCBI Description
                  (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)
                  >gi 68597 pir AJPMQ2 glutamate--ammonia ligase (EC
                  6.3.1.2) delta precursor, chloroplast - garden pea
                  >gi_169059 (M20664) glutamine synthetase (chloroplast GS2)
                  (EC 6.3.1.2) [Pisum sativum]
                  223889
Seq. No.
Seq. ID
                  LIB3165-056-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  565
E value
                  2.0e-58
Match length
                  114
% identity
                  89
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
                  (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  223890
Seq. No.
Seq. ID
                  LIB3165-056-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1565225
BLAST score
                  151
E value
                  2.0e-13
Match length
                  66
% identity
                  39
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                  223891
                  LIB3165-056-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  g4455235
                  181
                  3.0e-16
```

NCBI GI BLAST score E value Match length 63 % identity 78

(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA NCBI Description

SUBUNIT-like [Arabidopsis thaliana]

Seq. No. 223892

```
Prints and A.
```

```
LIB3165-056-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169528
BLAST score
                  164
E value
                  4.0e-13
                  57
Match length
% identity
                  81
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                  223893
Seq. ID
                  LIB3165-056-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1711355
BLAST score
                  232
                  2.0e-19
E value
                  90
Match length
                  59
% identity
                  SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
NCBI Description
                  >gi_421786_pir__S34678 short-chain alcohol dehydrogenase -
                  Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain
                  alcohol dehydrogenase [Picea abies]
Seq. No.
                  223894
Seq. ID
                  LIB3165-056-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2760537
BLAST score
                  137
                  9.0e-09
E value
Match length
                  34
% identity
                  79
NCBI Description (Y16088) cytosolic form of cyclophilin [Lupinus luteus]
                  223895
Seq. No.
Seq. ID
                  LIB3165-057-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3282092
BLAST score
                  160
                  6.0e-11
E value
Match length
                  106
% identity
                  38
NCBI Description (AJ007446) hypothetical protein [Thermotoga neapolitana]
                  223896
Seq. No.
Seq. ID
                  LIB3165-057-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4220518
BLAST score
                  232
                  2.0e-19
E value
Match length
                  111
                  47
% identity
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
```

Method BLASTX

223897

LIB3165-057-P1-K1-B10

Seq. No.

Seq. ID



```
q1352821
NCBI GI
BLAST score
                   577
                   8.0e-60
E value
Match length
                   118
                   96
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223898
Seq. No.
Seq. ID
                   LIB3165-057-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2829916
BLAST score
                   167
                   1.0e-11
E value
Match length
                   48
                   75
% identity
                   (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   223899
Seq. No.
                   LIB3165-057-P1-K1-B4
Seq. ID
Method
                   BLASTX
                   q1352821
NCBI GI
                   541
BLAST score
                   2.0e-55
E value
Match length
                   115
                   92
 % identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   223900
 Seq. No.
                   LIB3165-057-P1-K1-B6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3660471
 BLAST score
                   379
 E value
                   9.0e-37
                   91
 Match length
                   82
 % identity
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
 NCBI Description
                   subunit [Arabidopsis thaliana]
                   223901
 Seq. No.
                   LIB3165-057-P1-K1-C1
 Seq. ID
 Method
                   BLASTX
                   g430947
 NCBI GI
                   338
 BLAST score
```

1.0e-32 E value 97 Match length 76 % identity

(U01103) PSI type III chlorophyll a/b-binding protein NCBI Description

[Arabidopsis thaliana]

```
223902
Seq. No.
Seq. ID
                  LIB3165-057-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g320622
BLAST score
                  593
E value
                  1.0e-61
Match length
                  123
% identity
NCBI Description probable protein kinase - maize (fragment) >gi_168618
                  (M62985) protein kinase [Zea mays]
Seq. No.
                  223903
                  LIB3165-057-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1931640
BLAST score
                  325
                  3.0e-30
E value
Match length
                  90
% identity
                  64
NCBI Description (U95973) Serine carboxypeptidase isolog [Arabidopsis
                  thaliana]
Seq. No.
                  223904
Seq. ID
                  LIB3165-057-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  301
E value
                  1.0e-27
Match length
                  96
                  72
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  223905
Seq. ID
                  LIB3165-057-P1-K1-E4
Method
                 BLASTX
NCBI GI
                 g134892
BLAST score
                  223
               3.0e-19
E value
                  114
Match length
                  55
% identity
NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
                  (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                  >gi_88607_pir__A29440 signal recognition particle receptor
                  - human >gi_30866_emb_CAA29608_ (X06272) docking protein
                  [Homo sapiens] >gi_4507223_ref NP 003130.1 pSRPR signal
                  recognition particle receptor ('docking protein')
Seq. No.
                  223906
Seq. ID
                 LIB3165-057-P1-K1-G11
Method
                  BLASTX
NCBI GI
                 g1352821
BLAST score
                  432
                  8.0e-43
E value
Match length
                 101
% identity
                  89
```

31782

(RUBISCO SMALL SUBUNIT) >gi_279581 pir RKCNSU

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223907 Seq. TD LIB316

Seq. ID LIB3165-057-P1-K1-H11

Method BLASTX
NCBI GI g4056493
BLAST score 202
E value 7.0e-16
Match length 97
% identity 40

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 223908

Seq. ID LIB3165-058-P1-K1-A8

Method BLASTX
NCBI GI g3914603
BLAST score 188
E value 1.0e-14
Match length 58
% identity 62

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

Seq. No. 223909

Seq. ID LIB3165-058-P1-K1-B1

Method BLASTX
NCBI GI g3747111
BLAST score 267
E value 2.0e-23
Match length 67
% identity 72

NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 223910

Seq. ID LIB3165-058-P1-K1-B11

Method BLASTX
NCBI GI g1488043
BLAST score 171
E value 3.0e-12
Match length 56
% identity 66

NCBI Description (U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No. 223911

Seq. ID LIB3165-058-P1-K1-B2

Method BLASTX
NCBI GI g115765
BLAST score 258
E value 7.0e-37
Match length 107
% identity 73

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi 100201 pir S07408 chlorophyll a/b-binding



protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

223912 Seq. No. Seq. ID LIB3165-058-P1-K1-B3 Method BLASTX NCBI GI g231610 BLAST score 182 1.0e-13 E value 48 Match length 79 % identity

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 223913

Seq. ID LIB3165-058-P1-K1-B8

Method BLASTX
NCBI GI g3953473
BLAST score 300
E value 2.0e-27
Match length 113
% identity 66

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 223914

Seq. ID LIB3165-058-P1-K1-C3

Method BLASTX
NCBI GI g2501578
BLAST score 339
E value 5.0e-32
Match length 73
% identity 90

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047

ethylene-responsive protein 1 - Para rubber tree

>gi_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 223915

Seq. ID LIB3165-058-P1-K1-C8

Method BLASTX
NCBI GI g4510376
BLAST score 186
E value 5.0e-14
Match length 69
% identity 54

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 223916

Seq. ID LIB3165-058-P1-K1-C9

Method BLASTX



57

223921

% identity

Seq. No.

NCBI Description

```
NCBI GI
                  g3914605
BLAST score
                  166
                  6.0e-12
E value
                  77
Match length
                  52
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__$39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857_ (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Malus domestica]
                  223917
Seq. No.
                  LIB3165-058-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2879811
BLAST score
                  149
                  1.0e-21
E value
                  62
Match length
                  74
% identity
                 (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
Seq. No.
                  223918
Seq. ID
                  LIB3165-058-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q2501578
BLAST score
                  575
                  2.0e-59
E value
Match length
                  122
% identity
                  96
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  223919
Seq. No.
Seq. ID
                  LIB3165-058-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g542087
                  196
BLAST score
                  4.0e-32
E value
Match length
                  112
                  67
% identity
                  sucrose transport protein - potato >gi 439294 emb CAA48915
NCBI Description
                  (X69165) sucrose transport protein [Solanum tuberosum]
                  223920
Seq. No.
                  LIB3165-058-P1-K1-G12
Seq. ID
                  BLASTX
Method
                  g1181599
NCBI GI
BLAST score
                  122
E value
                  5.0e-10
                  74
Match length
```

31785

(D83007) subunit of photosystem I [Cucumis sativus]

Match length

% identity

55



```
Seq. ID
                  LIB3165-058-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1352821
                  308
BLAST score
                  9.0e-29
E value
Match length
                  63
% identity
                  94
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223922
                  LIB3165-058-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2655098
BLAST score
                  202
                  6.0e-16
E value
Match length
                  82
                  44
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                  223923
Seq. ID
                  LIB3165-059-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g121080
BLAST score
                  143
                  3.0e-09
E value
Match length
                  64
                  56
% identity
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                  >gi_1070638_pir__GCPMH glycine cleavage system protein H
                  precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H
                  protein [Pisum sativum] >gi_169093 (J05164) H-protein of
                  glycine decarboxylase precursor (EC 2.1.2.10) [Pisum
                  sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum
                  sativum]
Seq. No.
                  223924
Seq. ID
                  LIB3165-059-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4406530
                  250
BLAST score
                  2.0e-21
E value
Match length
                  85
% identity
                  64
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                  223925
Seq. No.
Seq. ID
                  LIB3165-059-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1684851
BLAST score
                  191
                  1.0e-14
E value
```

NCBI Description



(U77935) DnaJ-like protein [Phaseolus vulgaris]

```
223926
Seq. No.
                  LIB3165-059-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  140
                  5.0e-09
E value
                  41
Match length
                  71
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223927
                  LIB3165-059-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g541951
NCBI GI
BLAST score
                  123
                  1.0e-13
E value
                  68
Match length
                  58
% identity
NCBI Description SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
                  [Glycine max]
                  223928
Seq. No.
                  LIB3165-059-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2565305
BLAST score
                  366
                  3.0e-35
E value
Match length
                  99
                  73
% identity
                 (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
NCBI Description
                  Triticum sp.]
                  223929
Seq. No.
                  LIB3165-059-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g2995384
NCBI GI
BLAST score
                  262
E value
                  4.0e-23
Match length
                  86
                  63
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                  223930
Seq. ID
                  LIB3165-059-P1-K1-E5
Method
                  BLASTX
                  q1352821
NCBI GI
                  152
BLAST score
                  2.0e-10
E value
Match length
                  33
                  94
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
```



(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223931

Seq. ID LIB3165-059-P1-K1-F11

Method BLASTX
NCBI GI g1168411
BLAST score 162
E value 4.0e-15
Match length 83
% identity 67

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 223932

Seq. ID LIB3165-059-P1-K1-G11

Method BLASTX
NCBI GI g3702339
BLAST score 154
E value 2.0e-10
Match length 59
% identity 56

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 223933

Seq. ID LIB3165-059-P1-K1-G12

Method BLASTX
NCBI GI g2119719
BLAST score 192
E value 6.0e-15
Match length 80
% identity 56

NCBI Description heat-shock cognate protein 70-3 - tomato >gi_762844

(L41253) Hsc70 [Lycopersicon esculentum]

Seq. No. 223934

Seq. ID LIB3165-059-P1-K1-H10

Method BLASTX
NCBI GI g1431629
BLAST score 165
E value 8.0e-12
Match length 57
% identity 61

NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No. 223935

Seq. ID LIB3165-060-Q1-K1-A1

Method BLASTX
NCBI GI g2507153
BLAST score 189
E value 3.0e-14
Match length 134
% identity 35

NCBI Description VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS16

>gi_2133204_pir_S62031 vacuolar protein sorting-associated

protein VPS16 - yeast (Saccharomyces cerevisiae)

>gi_1171414 (U44030) Vsp16p: Vacuolar sorting protein
[Saccharomyces cerevisiae]

Seq. No. 223936 Seq. ID LIB3165

Seq. ID LIB3165-060-Q1-K1-A3

Method BLASTX
NCBI GI g3914603
BLAST score 517
E value 3.0e-62
Match length 134
% identity 83

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

Seq. No. 223937

Seq. ID LIB3165-060-Q1-K1-A4

Method BLASTX
NCBI GI g2832783
BLAST score 488
E value 2.0e-49
Match length 98
% identity 91

NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]

Seq. No. 223938

Seq. ID LIB3165-060-Q1-K1-A5

Method BLASTX
NCBI GI g232029
BLAST score 377
E value 1.0e-36
Match length 74
% identity 99

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_100154_pir__S21989 translation elongation factor eEF-1

alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)

elongation factor 1A [Daucus carota]

Seq. No. 223939

Seq. ID LIB3165-060-Q1-K1-A6

Method BLASTX
NCBI GI g1928981
BLAST score 510
E value 5.0e-52
Match length 109
% identity 93

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 223940

Seq. ID LIB3165-060-Q1-K1-A8

Method BLASTX
NCBI GI g3121825
BLAST score 322
E value 7.0e-30
Match length 123

Seq. ID

Method

NCBI GI

```
% identity
NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
                    ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                    bas1 protein [Spinacia oleracea]
Seq. No.
                     223941
                    LIB3165-060-Q1-K1-B1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1351408
BLAST score
                    437
E value
                    2.0e-43
Match length
                    104
% identity
                    78
NCBI Description
                    VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
                    >gi_1076563_pir__S51117 cystein proteinase - sweet orange
>gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by
                    similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                    vascular processing protease [Citrus sinensis]
Seq. No.
                    223942
Seq. ID
                    LIB3165-060-Q1-K1-B11
Method
                    BLASTX
NCBI GI
                    g2501353
BLAST score
                    438
E value
                    1.0e-43
Match length
                    89
% identity
                    93
                    TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
NCBI Description
                    (fragment) > gi\_664901\_emb\_CAA86607\_ (Z46646) transketolase
                    [Craterostigma plantagineum]
Seq. No.
                    223943
Seq. ID
                    LIB3165-060-Q1-K1-B12
Method
                    BLASTX
NCBI GI
                    g3421102
BLAST score
                    332
E value
                    3.0e-31
Match length
                    77
% identity
NCBI Description
                   (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
                    thaliana]
Seq. No.
                    223944
                    LIB3165-060-Q1-K1-B2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2832643
BLAST score
                    281
E value
                    3.0e-25
Match length
                    70
% identity
NCBI Description
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    223945
```

31790

LIB3165-060-Q1-K1-B3

BLASTX

g4325041

Seq. No.

Seq. ID

Method

223950

BLASTX

LIB3165-060-Q1-K1-C11

```
BLAST score
                   478
E value
                   2.0e-48
Match length
                   102
% identity
                   94
NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana
Seq. No.
                   223946
Seq. ID
                   LIB3165-060-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   q1684851
BLAST score
                   318
E value
                   2.0e-29
Match length
                   114
% identity
                   60
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
Seq. No.
                   223947
Seq. ID
                   LIB3165-060-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   g20729
BLAST score
                   392
E value
                   4.0e-38
Match length
                   108
% identity
                   74
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                   223948
Seq. ID
                   LIB3165-060-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   431
E value
                   9.0e-43
Match length
                   83
% identity
                   98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   223949
Seq. ID
                   LIB3165-060-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g267120
BLAST score
                   198
E value
                   2.0e-15
Match length
                   83
% identity
                   55
NCBI Description THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi 100070 pir S20929
                   thioredoxin f precursor - garden pea
                   >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum
                   sativum] \overline{>}gi_{\overline{1}388086} (\overline{U}35830) thioredoxin f [Pisum sativum]
```



```
NCBI GI
                   g1351271
BLAST score
                   181
E value
                   9.0e-17
                   97 .
Match length
                   60
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                  >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi 806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                  223951
Seq. ID
                  LIB3165-060-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1130682
BLAST score
                  642
E value
                  2.0e-67
Match length
                  127
% identity
                  100
NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
Seq. No.
                  223952
Seq. ID
                  LIB3165-060-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4206194
BLAST score
                  462
E value
                  3.0e-46
Match length
                  131
% identity
                  66
NCBI Description
                  (AF071527) GH3-like protein [Arabidopsis thaliana]
                  >gi_4262168_gb_AAD14468 (AC005275) putative GH3-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  223953
Seq. ID
                  LIB3165-060-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2943789
BLAST score
                  269
E value
                  1.0e-23
Match length
                  90
% identity
NCBI Description (AB000875) RD22BP1 [Arabidopsis thaliana]
Seq. No.
                  223954
Seq. ID
                  LIB3165-060-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q68200
BLAST score
                  438
E value
                  1.0e-43
```

Match length 113 % identity 80

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 223955

Seq. ID LIB3165-060-Q1-K1-D3



```
Method
                   BLASTX
NCBI GI
                   q1532135
BLAST score
                   495
E value
                   3.0e-50
Match length
                  106
% identity
                  86
NCBI Description
                  (U49442) chloroplast mRNA-binding protein CSP41 precursor
                   [Spinacia oleracea]
Seq. No.
                  223956
Seq. ID
                  LIB3165-060-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4091806
BLAST score
                  377
E value
                  2.0e-36
Match length
                  96
                  72
% identity
NCBI Description
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
                  223957
Seq. No.
Seq. ID
                  LIB3165-060-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  169
E value
                  4.0e-12
Match length
                  56
% identity
                  66
NCBI Description
                  (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  223958
Seq. ID
                  LIB3165-060-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q1946368
BLAST score
                  452
E value
                  3.0e-45
Match length
                  104
% identity
                  85
NCBI Description
                  (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  223959
Seq. ID
                  LIB3165-060-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3024126
BLAST score
                  444
E value
                  3.0e-44
Match length
                  87
                  97
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                  synthetase 1 [Catharanthus roseus]
```

223960 Seq. No.

Seq. ID LIB3165-060-Q1-K1-E11

Method BLASTX NCBI GI g3822036 BLAST score 221

BLAST score

Match length

% identity

E value

482

96

95

1.0e-48



```
E value
                  4.0e-18
Match length
                  115
% identity
                  45
NCBI Description
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                  223961
Seq. No.
Seq. ID
                  LIB3165-060-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q4204849
BLAST score
                  515
E value
                  1.0e-52
Match length
                  120
% identity
                  81
NCBI Description (U55875) protein kinase [Arabidopsis thaliana]
                  223962
Seq. No.
Seq. ID
                  LIB3165-060-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q3127838
BLAST score
                  220
E value
                  3.0e-18
Match length
                  88
% identity
                  49
NCBI Description (AL023496) hypothetical protein [Streptomyces coelicolor]
Seq. No.
                  223963
Seq. ID
                  LIB3165-060-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3023752
BLAST score
                  160
E value
                  3.0e-11
Match length
                  54
% identity
                  65
NCBI Description FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
                  ferredoxin-I [Lycopersicon esculentum]
                  223964
Seq. No.
                  LIB3165-060-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170897
BLAST score
                  288
E value
                  4.0e-26
Match length
                  67
                  87
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi 1076276 pir S52039 NAD-malate dehydrogenąse - cucumber
                  >gi 695311 (L31900) glyoxysomal malate dehydrogenase
                  [Cucumis sativus]
                  223965
Seq. No.
Seq. ID
                  LIB3165-060-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1352821
```